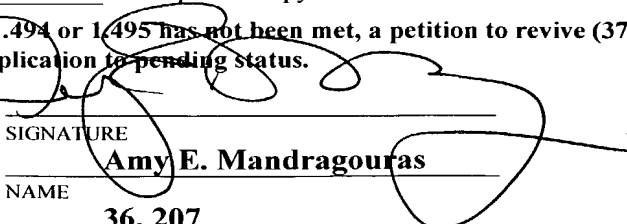


FORM PTO-1390 (REV 10-2000)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY'S DOCKET NUMBER GIN-6727CPUS
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C.371			U.S. APPLIC./ 09/856231
INTERNATIONAL APPLICATION PCT/JP99/06412	INTERNATIONAL FILING DATE 17 November 1999 (17.11.99)	PRIORITY DATE CLAIMED 17 November 1998 (17.11.98)	
TITLE OF INVENTION HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS			
APPLICANT(S) FOR DO/EO/US SAGAMI CHEMICAL RESEARCH, et al.			
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:			
<ol style="list-style-type: none"> 1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C.371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input type="checkbox"/> This is an express request to promptly begin national examination procedures (35 U.S.C. 371(f)). 4. <input type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (PCT Article 31). 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)) <ol style="list-style-type: none"> a. <input type="checkbox"/> is attached hereto (required only if not communicated by the International Bureau). b. <input checked="" type="checkbox"/> has been communicated by the International Bureau. c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C 371(c)(2)) 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)) <ol style="list-style-type: none"> a. <input type="checkbox"/> are attached hereto (required only if not communicated by the International Bureau). b. <input type="checkbox"/> have been communicated by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input checked="" type="checkbox"/> have not been made and will not be made. 8. <input type="checkbox"/> An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 9. <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). (unexecuted) (4 Sheets); 10. <input type="checkbox"/> An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). 			
Items 11. to 16. below concern document(s) or information included:			
<ol style="list-style-type: none"> 11. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1. 12. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included 13. <input type="checkbox"/> A FIRST preliminary amendment <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. 14. <input type="checkbox"/> A substitute specification. 15. <input type="checkbox"/> A change of power of attorney and/or address letter. 16. <input checked="" type="checkbox"/> Other items or information: Transmittal Letter (2 sheets in duplicate); Check (\$1260) based on large entity; Certificate of First Class Mailing (1 sheet); and Return Postcard. 			

U.S. APPLICATION NO. 09/856231		INTERNATIONAL APPLICATION NO. PCT/JP99/06412		ATTORNEY'S DOCKET NO. GIN-6727CPUS																																																																													
17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) .(a/o November 1, 2000): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO..... \$1000 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$860 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.455(a)(2)) paid to USPTO \$710 International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4)..... \$690 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4)..... \$100 ENTER APPROPRIATE BASIC FEE AMOUNT = Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input checked="" type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)). <table border="1" style="width:100%; border-collapse: collapse;"><thead><tr><th style="width:20%;">CLAIMS</th><th style="width:20%;">NUMBER FILED</th><th style="width:20%;">NUMBER EXTRA</th><th style="width:20%;">RATE</th><th style="width:20%;"></th><th style="width:20%;"></th></tr></thead><tbody><tr><td>Total claims</td><td>10 -20 =</td><td></td><td>X \$18.00</td><td>\$</td><td></td></tr><tr><td>Independent claims</td><td>2-3 =</td><td></td><td>X \$80.00</td><td>\$</td><td></td></tr><tr><td colspan="3">MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td><td>+ 270.00</td><td>\$270.00</td><td></td></tr><tr><td colspan="4">TOTAL OF ABOVE CALCULATIONS =</td><td>\$1260.00</td><td></td></tr><tr><td colspan="4"><input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.</td><td>\$</td><td></td></tr><tr><td colspan="4">SUBTOTAL =</td><td>\$1260.00</td><td></td></tr><tr><td colspan="4">Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).</td><td>\$</td><td></td></tr><tr><td colspan="4">TOTAL NATIONAL FEE =</td><td>\$990.00</td><td></td></tr><tr><td colspan="4">Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property</td><td>\$</td><td></td></tr><tr><td colspan="4">TOTAL FEES ENCLOSED =</td><td>\$1260.00</td><td></td></tr><tr><td colspan="4"></td><td>Amount to be: refunded</td><td>\$</td></tr><tr><td colspan="4"></td><td>charged</td><td>\$</td></tr></tbody></table>				CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE			Total claims	10 -20 =		X \$18.00	\$		Independent claims	2-3 =		X \$80.00	\$		MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ 270.00	\$270.00		TOTAL OF ABOVE CALCULATIONS =				\$1260.00		<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				\$		SUBTOTAL =				\$1260.00		Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$		TOTAL NATIONAL FEE =				\$990.00		Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property				\$		TOTAL FEES ENCLOSED =				\$1260.00						Amount to be: refunded	\$					charged	\$
				CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE																																																																										
Total claims	10 -20 =		X \$18.00	\$																																																																													
Independent claims	2-3 =		X \$80.00	\$																																																																													
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ 270.00	\$270.00																																																																													
TOTAL OF ABOVE CALCULATIONS =				\$1260.00																																																																													
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				\$																																																																													
SUBTOTAL =				\$1260.00																																																																													
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$																																																																													
TOTAL NATIONAL FEE =				\$990.00																																																																													
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property				\$																																																																													
TOTAL FEES ENCLOSED =				\$1260.00																																																																													
				Amount to be: refunded	\$																																																																												
				charged	\$																																																																												
a. <input checked="" type="checkbox"/> A check in the amount of \$ <u>1260.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. _____ in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>12-0080</u>. A duplicate copy of this sheet is enclosed. NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status. SEND ALL CORRESPONDENCE TO: Amy E. Mandragouras, Esq. LAHIVE & COCKFIELD, LLP 28 State Street Boston, Massachusetts 02109 United States of America (617)227-7400 Date: 17 May 2001 <div style="text-align: right;">SIGNATURE  NAME Amy E. Mandragouras REGISTRATION NUMBER 36, 207</div>																																																																																	

098562309/856231
JC18 Rec'd PCT/PTO 17 MAY 2001

(Atty. Docket No.: GIN-6727CPUS)

IN THE UNITED STATES PATENT DESIGNATED OFFICE (DO/US)

In re the
application of: **SAGAMI CHEMICAL RESEARCH *et al.***

International Application No.: **PCT/JP99/06412**

International Filing Date: **17 November 1999**

U.S. Serial No.: **Not Yet Assigned**

Filed: **Herewith**

For: **HUMAN PROTEINS HAVING
HYDROPHOBIC DOMAINS AND DNAs
ENCODING THESE PROTEINS**

Attorney Docket No.: **GIN-6727CPUS**

BOX PCT

Commissioner for Patents
Washington, D.C. 20231


Certification Under 37 CFR 1.10

I hereby certify that the attached:

Transmittal Letter (2 sheets in duplicate); Unexecuted Declaration, Petition and Power of Attorney (4 sheets); check (\$1260) based on large entity; Certificate of Express Mailing (1 sheet); and Return Postcard are being deposited by me with the United States Postal Service "Express Mail Post Office to Addressee" service, Mailing Label No. **EL 848 027 401US**, under 37 CFR 1.10 on the date indicated below and is addressed to the Box PCT, Commissioner for Patents, Washington, D.C. 20231.

Date: 17 May 2001

Name: Ilidio P. Cardoso

Signature: 

DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

5

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for genetic diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantity can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like.

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden

potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like have been currently employed as pharmaceuticals. In addition, 5 secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is 10 expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal 15 transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned. 20 It has been clarified that abnormalities of these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the 25 membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which 30 a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of

Fig. 4 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP02956.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02962.

Fig. 6 illustrates the hydrophobicity/hydrophilicity
5 profile of the protein encoded by clone HP03014.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10608.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10609.

10 Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10611.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10617.

Fig. 11 illustrates the hydrophobicity/hydrophilicity
15 profile of the protein encoded by clone HP02837.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02991.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03063.

20 Fig. 14 illustrates the hydrophobicity/hydrophilicity
profile of the protein encoded by clone HP03091.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03092.

Fig. 16 illustrates the hydrophobicity/hydrophilicity
25 profile of the protein encoded by clone HP03116.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10618.

Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10619.

30 Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10622.

Fig. 20 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP10625.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02883.

Fig. 22 illustrates the hydrophobicity/hydrophilicity
5 profile of the protein encoded by clone HP03140.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10628.

Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10629.

10 Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10635.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10636.

15 Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10640.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10644.

Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10656.

20 Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10672.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03194.

25 Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03219.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03236.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03237.

30 Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03267.

Fig. 36 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP03270.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03298.

Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10631.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10658.

Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10663.

Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03165.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03266.

Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03287.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10665.

Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10669.

Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10670.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10671.

Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10673.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10675.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10683.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides a DNA encoding the above-mentioned protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150 as well as an expression vector that is capable of expressing such DNA by in vitro translation or in eukaryotic cells and a transformed eukaryotic cell that is capable of expressing such DNA and of producing the above-mentioned protein.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequence of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the

15 In the case where the protein of the present invention
is produced by expressing the DNA in eukaryotic cells, the
protein of the present invention can be produced as a
secretory protein, or as a membrane protein on the cell-
membrane surface, by introducing the translated region of
20 the cDNA into an expression vector for eukaryotic cells that
has a promoter, a splicing region, a poly(A) addition site
and the like, and then introducing the vector into the
eukaryotic cells. The expression vectors are exemplified by
pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV,
25 EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic
cells to be used in general include mammalian cultured cells
such as monkey kidney COS7 cells, Chinese hamster ovary CHO
cells and the like, budding yeasts, fission yeasts, silkworm
cells, Xenopus oocytes and the like. Any eukaryotic cells
30 may be used as long as they are capable of expressing the
proteins of the present invention. The expression vector can
be introduced into the eukaryotic cells by using a method

known in the art such as the electroporation method, the calcium phosphate method, the liposome method, the DEAE-dextran method and the like.

5 After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated from the culture and purified by a combination of separation procedures known in the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication,
10 enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography and the like.

15 The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments
20 can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the
25 protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be
30 converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where

sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall also come within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)⁺ RNAs extracted from human cells as templates. The human cells may be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for colony or plaque hybridization according to a method known in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-

PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest are synthesized, which are then used as the primers.

5 The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1 summarizes the clone number (HP number), the cells
10 from which the cDNA clone was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

WO 00/29448

PCT/JP99/06412

Table 1

SEQ ID NO	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP02539	Saos-2	4485	647
2, 12, 22	HP02770	HT-1080	1509	350
3, 13, 23	HP02869	KB	3059	206
4, 14, 24	HP02956	KB	2367	213
5, 15, 25	HP02962	KB	2355	595
6, 16, 26	HP03014	Liver	1024	264
7, 17, 27	HP10608	Saos-2	1237	343
8, 18, 28	HP10609	KB	1332	244
9, 19, 29	HP10611	KB	1932	303
10, 20, 30	HP10617	HT-1080	1124	160
31, 41, 51	HP02837	HT-1080	4473	1445
32, 42, 52	HP02991	KB	2630	582
33, 43, 53	HP03063	HT-1080	1472	410
34, 44, 54	HP03091	Liver	1652	483
35, 45, 55	HP03092	Liver	2112	607
36, 46, 56	HP03116	KB	1087	314
37, 47, 57	HP10618	HT-1080	1694	94
38, 48, 58	HP10619	HT-1080	1522	218
39, 49, 59	HP10622	Liver	1591	460
40, 50, 60	HP10625	Liver	1249	216
61, 71, 81	HP02883	KB	4027	392
62, 72, 82	HP03140	HT-1080	2495	497
63, 73, 83	HP10628	HT-1080	1617	417
64, 74, 84	HP10629	WERI-RB	3269	649
65, 75, 85	HP10635	WERI-RB	458	93
66, 76, 86	HP10636	HT-1080	1712	425
67, 77, 87	HP10640	WERI-RB	1055	149
68, 78, 88	HP10644	WERI-RB	1616	396
69, 79, 89	HP10656	PMA-U937	1860	350
70, 80, 90	HP10672	Thymus	783	153
91, 101, 111	HP03194	KB	3438	303

92, 102, 112	HP03219	PMA-U937	1144	283
93, 103, 113	HP03236	HT-1080	2339	488
94, 104, 114	HP03237	HT-1080	1765	182
95, 105, 115	HP03267	Liver	1418	184
96, 106, 116	HP03270	PMA-U937	1211	140
97, 107, 117	HP03298	PMA-U937	1099	153
98, 108, 118	HP10631	WERI-RB	3489	173
99, 109, 119	HP10658	HT-1080	931	75
100, 110, 120	HP10663	PMA-U937	1123	159
121, 131, 141	HP03165	KB	3234	636
122, 132, 142	HP03266	HT-1080	2490	318
123, 133, 143	HP03287	Thymus	1465	82
124, 134, 144	HP10665	HT-1080	917	247
125, 135, 145	HP10669	WERI-RB	1306	206
126, 136, 146	HP10670	WERI-RB	2022	432
127, 137, 147	HP10671	Thymus	1227	306
128, 138, 148	HP10673	Thymus	2210	555
129, 139, 149	HP10675	Thymus	1493	250
130, 140, 150	HP10683	PMA-U937	1264	174

5 The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

10 In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150 shall come within the scope of the present

invention.

Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come
5 within the scope of the present invention, as long as the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

The cDNAs of the present invention also include cDNA
10 fragments (of 10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA
15 fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention
20 may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of
25 polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention
30 can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use;

as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern
5 gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source
10 of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of
15 expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example,
20 in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors
25 of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit
30 another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological

fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to
5 isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction.
10 Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for
15 commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory
20 Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

25 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases
30 the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the

form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

5 Cytokine and Cell Proliferation/Differentiation
Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or
10 may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of
15 cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165,
20 HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in
25 Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol.
30 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol.

149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a

subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can
10 be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the
15 expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell.
20 Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary
25 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected
30 with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class

II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses
 5 and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In
 10 vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly
 15 Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse
 20 Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify,
 25 among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
 30 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994;

Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

5 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 10 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 15 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et 20 al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the 25 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells 30 alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) 5 useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as 10 thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic 15 utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or 20 ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among 25 other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence 30 embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as
 5 open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

10 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming
 15 cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by
 20 inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or
 25 other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing
 30 protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including
15 vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

25 A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

The activity of a protein of the invention may, among

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

5 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

10 A protein of the invention may also exhibit one or more
of the following additional activities or effects:
inhibiting the growth, infection or function of, or killing,
infectious agents, including, without limitation, bacteria,
viruses, fungi and other parasites; effecting (suppressing
15 or enhancing) bodily characteristics, including, without
limitation, height, weight, hair color, eye color, skin, fat
to lean ratio or other tissue pigmentation, or organ or body
part size or shape (such as, for example, breast
augmentation or diminution, change in bone form or shape);
20 effecting biorhythms or circadian cycles or rhythms;
effecting the fertility of male or female subjects;
effecting the metabolism, catabolism, anabolism, processing,
utilization, storage or elimination of dietary fat, lipid,
protein, carbohydrate, vitamins, minerals, cofactors or
25 other nutritional factors or component(s); effecting
behavioral characteristics, including, without limitation,
appetite, libido, stress, cognition (including cognitive
disorders), depression (including depressive disorders) and
violent behaviors; providing analgesic effects or other pain
30 reducing effects; promoting differentiation and growth of
embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

10

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

25

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO 98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO 97/33993), the cDNA library of epidermoid carcinoma cell line KB (WO 98/11217) and the cDNA library of liver tissue delivered by the operation (WO 98/21328) were used as the

30

cDNA libraries. Additionally, the cDNA libraries constructed from phorbol ester-stimulated histiocytic lymphoma cell line U937 (ATCC CRL 1593) mRNA, human retinoblastoma cell line WERI-RB (ATCC HTB 169) mRNA and human thymus mRNA (Clontech) were also used. Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. A clone that has a hydrophobic region being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 μl containing 12.5 μl μ of T_NT rabbit reticulocyte lysate, 0.5 μl of a buffer solution (attached to the kit), 2 μl of an amino acid mixture (without methionine), 2 μl of [³⁵S]methionine (Amersham) (0.37 MBq/μl), 0.5 μl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO₂. After the medium was exchanged for a medium containing
5 [35S]cystine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

10 <HP02539> (SEQ ID NOS: 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP02539 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 188-bp 5'-untranslated region, a 1944-bp ORF,
15 and a 2353-bp 3'-untranslated region. The ORF encodes a protein consisting of 647 amino acid residues and there existed a putative secretory signal at the N-terminus and six putative transmembrane domains at the C-terminus. Figure 1 depicts the hydrophobicity/hydrophilicity profile,
20 obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse frizzled-1 (GenBank
25 Accession No. AF054623). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse frizzled-1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the
30 present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 90.4% in the entire

WO 00/29448

PCT/JP99/06412

44

region.

```

HP MAEEEEAPKKSRAAGGGASWELCAGALSARLTEEGSGDAGRRRPPVDPRRLARQLLLLLLW
    ****.*.*.*.**** * * ****.*.*.*.* * * *.*...****.*.*****
5 MM MAEEAAPSESRAA--GRLSLELCAEALPGRREEVGHEDTASHRRPRADPRRWASGLLLLLLW
HP LLEAPILLGVRAQAAGQGPGQGPGGPGQPPPPQQQQSGQQYNGERGISVPDHGYCQPIS
    ***** ** .*****.*****.*****.*****.*****
MM LLEAPILLGVRAQAA----QOVSGPGQQAPPPQPQQSGQQYNGERGISIPDHGYCQPIS
HP IPLCTDIAYNQTIMPNNLLGHTNQEDAGLEVHQFYPLVKVQCSAELKFFLCSMYAPVCTVL
10 *****.*****.*****.*****.*****.*****.*****.*****
MM IPLCTDMAYNQTIMPNNLLGHTNQEDAGLEVHQFYPLVKVQCSAELKFFLCSMYAPVCTVL
HP EQALPPCRSLCERARQGCEALMNKFGFQWPDTLKCEKFPVHGAGELCVGQNTSDKGTPTP
    *****
MM EQALPPCRSLCERARQGCEALMNKFGFQWPDTLKCEKFPVHGAGELCVGQNTSDKGTPTP
15 HP SLLPEFWTSNPQHGGGGHRRGGFPGGAGASERGFSCPRALKVPSYLYNYHFLGEKDCGAPC
    *****.*****.*.*.*****.*****.*****.*****.*****
MM SLLPEFWTSNGQHGGGGYRGYPGGAGTVERGKFSCPRALRVPSYLYNYHFLGEKDCGAPC
HP EPTKVYGLMYFGPEELRFSRTWIGIWSVLCCASTLFTVLTYLVDMMRRFSYPERPIIFLSG
    *****.***** **
20 MM EPTKVYGLMYFGPEELRFSRTWIGIWSVLCCASTLFTVLTYLVDMPRFSYPERPIISLSG
HP CYTAVAVAYIAGFLLDRVVCNDKFAEDGARTVAQGTKEGCTILFMMLYFFSMASIIWW
    *****.*****.*****.*****.*****.*****.*****
MM CYTAVAVAYIAGFLLDRVVCNDKFAEDGARTVAQGTNKEGCTILFMMLYFFSMASIIWW
HP VILSLTWFLAAGMKWGHEAIEANSQYFHLAAWAVPAIKTITILALGQVDGDVLSGVCFLG
25 *****.*
MM VILSLTWFLAAGMKWGHEAIEANSQYFHLAAWAVPAIKTITILALGQVDGDVLSGVCFLG
HP LNNVDALRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGKTEKLEKLMVRIGVF
    *****
MM LNNVDALRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGKTEKLEKLMVRIGVF
30 HP SVLYTVPATIVIACYFYEQAFRDQWERSWVAQSCSKSYAIPCPHLQAGGGAPPHPPMSPDF
    *****.*.*.*****
MM SVLYTVPATIVIACYFYEQAFRDQWERSWVAQSCSKSYAIPCPHLQGGGGVPPHPPMSPDF
HP TVFMIKYLMTLIVGITSGFVIWSGKTLNSWRKFYTRLTNSKOGETTV
    *****
35 MM TVFMIKYLM-----TLNSWRKFYTRLTNSKOGETTV

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA010020) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10

<HP02770> (SEQ ID NOS: 2, 12, and 22)

Determination of the whole base sequence of the cDNA insert of clone HP02770 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 252-bp 5'-untranslated region, a 1053-bp ORF, and a 204-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed two putative transmembrane domains. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was somewhat larger than the molecular weight of 38,274 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human RING zinc finger protein (GenBank Accession No. AF037204). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human RING zinc finger protein (ZN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

30

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA434312) among ESTs. However, since they are partial sequences, it can not be judged whether or

not they encode the same protein as the protein of the present invention.

<HP02869> (SEQ ID NOS: 3, 13, and 23)

5 Determination of the whole base sequence of the cDNA
insert of clone HP02869 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 229-bp 5'-untranslated region, a 621-bp ORF,
and a 2209-bp 3'-untranslated region. The ORF encodes a
10 protein consisting of 206 amino acid residues and there
existed two putative transmembrane domains. Figure 3 depicts
the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
15 of 22 kDa that was almost identical with the molecular
weight of 22,367 predicted from the ORF.

Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA278247) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
present invention.

25 <HP02956> (SEQ ID NOS: 4, 14, and 24)

Determination of the whole base sequence of the cDNA
insert of clone HP02956 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 68-bp 5'-untranslated region, a 642-bp ORF,
30 and a 1657-bp 3'-untranslated region. The ORF encodes a
protein consisting of 213 amino acid residues and there
existed three putative transmembrane domains. Figure 4

Table 4

	HP	MHY
5	TS MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGGFD HP YRYSNAKVSCWYKYLIFSINIIFWLAGVVFLGVGLWAWSEKGVLSDLTKVTRMHGIDPVV	
	TS PVWLFLVVGVMFILGFAGCIGALRENTFLKFFSVFLGIIFLELTAGVLAFVFKDWIK HP LVLVGVVMTLGFAGCVGALRENICLLNFNQCCGAYGPEDWDLNVYFNCSGASYSREKC	
10	TS DQLYFFINNNIRAYRDDIDLQNLIDFTQEYWQCCGAFGADDWNLNIYFNCTDSNASRERC HP GVPFSCCVPDPAQKVNTQCGYDVRIQLKSKWDESIKTKGCIQALESWLPRNIYIVAGVF *****. *****.*****.* . . . *.*****.*****. *. *****. TS GVPFSCCTKDPADVINTQCGYDARQKPEVDQQIVYTKGCVQFEKWLQDNLITIVAGIF HP IAISLLQIFGIFLARTLISDIEAVKAGHHF *.*.*****. *****.*****.*. TS IGIALLOIFGICLAQNLVSDIEAVRASW	

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. T05279) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

<HP02962> (SEQ ID NOS: 5, 15, and 25)

30 Determination of the whole base sequence of the cDNA
insert of clone HP02962 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 19-bp 5'-untranslated region, a 1788-bp ORF,
and a 548-bp 3'-untranslated region. The ORF encodes a

protein consisting of 595 amino acid residues and there
 existed a putative secretory signal at the N-terminus.
 Figure 5 depicts the hydrophobicity/hydrophilicity profile,
 obtained by the Kyte-Doolittle method, of the present
 5 protein. In vitro translation resulted in formation of a
 translation product of 70 kDa that was somewhat larger than
 the molecular weight of 67,549 predicted from the ORF. In
 this case, the addition of a microsome led to the formation
 of a product of 85 kDa to which sugar chains are presumably
 10 attached. Application of the (-3,-1) rule, a method for
 predicting the cleavage site of the secretory signal
 sequence, allows to expect that the mature protein starts
 from alanine at position 23. In addition, there exist in the
 amino acid sequence of this protein four sites at which N-
 15 glycosylation may occur (Asn-Thr-Thr at position 75, Asn-
 Gln-Thr at position 153, Asn-Tyr-Thr at position 237 and
 Asn-Ser-Ser at position 360).

The search of the protein data base using the amino
 acid sequence of the present protein revealed that the
 20 protein was similar to the human hypothetical protein
 KIAA0584 (GenBank Accession No. AB011156). Table 5 shows the
 comparison between amino acid sequences of the human protein
 of the present invention (HP) and the human hypothetical
 protein KIAA0584 (KI). Therein, the marks of -, *, and .
 25 represent a gap, an amino acid residue identical with that
 of the protein of the present invention, and an amino acid
 residue similar to that of the protein of the present
 invention, respectively. The both proteins shared a homology
 of 52.9% in the entire region.

[illegible]

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse WW domain-binding protein 1 (GenBank Accession No. U40825). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse WW domain-binding protein 1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W24575) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10608> (SEQ ID NOS: 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10608 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure
 5 consisting of a 23-bp 5'-untranslated region, a 1032-bp ORF, and a 182-bp 3'-untranslated region. The ORF encodes a protein consisting of 343 amino acid residues and there existed five putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained
 10 by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 37 kDa that was somewhat smaller than the molecular weight of 40,584 predicted from the ORF. When expressed in COS7 cells, an expression product of about 36
 15 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35406) among ESTs. However, since
 20 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10609> (SEQ ID NOS: 8, 18, and 28)

25 Determination of the whole base sequence of the cDNA insert of clone HP10609 obtained from cDNA library of the human epidermoid carcinoma cell line KB revealed the structure consisting of a 38-bp 5'-untranslated region, a 735-bp ORF, and a 559-bp 3'-untranslated region. The ORF
 30 encodes a protein consisting of 244 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 8 depicts the hydrophobicity/hydrophilicity

profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,756 predicted from the ORF. When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Mycobacterium tuberculosis hypothetical protein Rv1147 (GenBank Accession No. Z95584). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Mycobacterium tuberculosis hypothetical protein Rv1147 (MT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 31.7% in the entire region.

Table 7

	HP MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF
5	MT MTSGAAASASRVDHPLFARIWPVVAHEAEAIRAL
	HP QIKGLTGASGKVALLELGCCTGANFQFYPPGC-RVTCLDPNPHFEKFLTKSMAENRHLQY
	*. * *. * *. * *. * *. * *. * . *. * *. * . . * . . .
	MT RRENLAGLSGRV--LEVGAGVGTNFAYYPVAVEQVIAMEPEPRLAA-KARIAAADAPVPI
	HP ERFVVAPGEDMRQLADGSMDDVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEP
10	. . * . * * . * . * . * . * . * . * . . . * . * . * . * .
	MT -VVTDKTVEEFRD--TETFDVVCVSLVLCVSDPGAVLAHLRSLLRGGELRYLEHVASA
	HP YGSWAFMWQQVFETWVKHIGDGCCLTRETWKLLENQFSEIQMERQPPPLKW--LPVGP
	* * . . * * * . * . * . * * .
	MT -GARGRVQRFVDATFWPRLAGNCHTHRHTERAILDAGFVVDSSRREWAFPAWVPLPVSEL
15	HP IMGKAVK
	* . * .
	MT ALGRAHRT

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. T60981) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

<HP10611> (SEQ ID NOS: 9, 19, and 29)

30 Determination of the whole base sequence of the cDNA
insert of clone HP10611 obtained from cDNA library of the
human epidermoid carcinoma cell line KB revealed the
structure consisting of a 37-bp 5'-untranslated region, a
912-bp ORF, and a 983-bp 3'-untranslated region. The ORF

encodes a protein consisting of 303 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was somewhat smaller than the molecular weight of 33,856 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 36 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 34. When expressed in COS7 cells, an expression product of about 35 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the 218 amino acid residues at the C-terminus of the protein matched with the amino acid sequence of human glucosidase II (SWISS-PROT Accession No. Q06003). However, no similarity was observed at the N-terminal portion.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H14054) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10617> (SEQ ID NOS: 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10617 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure

consisting of a 72-bp 5'-untranslated region, a 483-bp ORF, and a 569-bp 3'-untranslated region. The ORF encodes a protein consisting of 160 amino acid residues and there existed four putative transmembrane domains. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 17 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H67672) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP02837> (SEQ ID NOS: 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP02837 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 44-bp 5'-untranslated region, a 4338-bp ORF, and a 91-bp 3'-untranslated region. The ORF encodes a protein consisting of 1445 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 150 kDa that was almost identical with the molecular weight of 161,657 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 22. In addition, there exist in the amino acid sequence of this protein 18 sites at which N-glycosylation
5 may occur.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α -2 macroglobulin (SWISS-PROT Accession No. P01023). Table 8 shows the comparison
10 between amino acid sequences of the human protein of the present invention (HP) and the human α -2 macroglobulin (MG). Therein, the marks of - and * represent a gap and an amino acid residue identical with that of the protein of the present invention, respectively. The both proteins shared a
15 homology of 29.5% in the entire region.

WO 00/29448

PCT/JP99/06412

61

Table 8

	HP	MOGPPLL--TAAHLLCVCTAALA-VAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVT
		* * * * * * * * * *
5	MG	MGKNKLLHPSLVLLLLLVLLPTDASVSGKPQYMLVP-SLLHTETTEKGCVLLSYLNETVT
	HP	VKAELLKTASN-LTVSVLEAE-GVFEGKSFKTLTLPSLPLNSADEIYELRVTGRTQDEIL
		* * * * * * * * * *
	MG	VSASLESVRGNRSLFTDLEAENDVLHCVAF---AVPKSSSNEEVMFLTQVKGPTQ---E
	HP	FSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSNLIL--IKDPKS
10		* * * * * * * * * *
	MG	FKKRRTVMVKNEDSLVVFQTDKSIYKPGQTVKFRVSMDEFHP-LNELIPLVYIQDPKG
	HP	NLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQ-VNDQTYQSFQVSEYVLPKFVQ
		* * * * * * * * * *
	MG	NRIAQWQSFQLEGGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFVQ
15	HP	LQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVT----LTFLPLSFWGKKKNITKTFKING
		* * * * * * * * * *
	MG	VTVPKIITILEEEMNVSVCGLYTYGKVPVGHVTVSICRKYSDASDCHGEDSQAFCEKFSG
	HP	SANFSFNDEEMKNVMDSSNGLSEY-LDLSFPGPVEILTTVTESVTG----ISRNVTNVF
		* * * * * * * * * *
20	MG	QLNSHGCFYQQVKTQVFKLKRKEYEMKLHTEAQIQEETVVELTGRQSSEITRTITKLSF
	HP	FK--QHDYIIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTEERRNNVVITVTQRNYTEY
		* * * * * * * * * *
	MG	VKVDSHFRQGIPIFFGQVRLVDGKGVPPIPNKVIFIRGN-----EANYYSNATTDHGLV
	HP	WSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSSELQKAYFLGSKSSMAVHSLFK
25		* * * * * * * * * *
	MG	QFSINTTN-VMGTSLTVRVNYKDRSPCYQVWSEEHEEAHTAYLVFSPSKSFVHLEPM
	HP	S--PSKTYIQLKTRDENIKVGSPFELVVSNGKRLKELSYMVVSRLQVAVGKQ--NSTMF
		* * * * * * * * * *
	MG	SHELPCGHTQTVQAHYILNGGTLGLKLSFYLLIMAKGGIVRTGTHGLLVKQEDMKGHF
30	HP	S-LTPENS-WTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVS
		* * * * * * * * * *
	MG	SISIPVKSIDIAPVARLLIYAVLPTGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAH
	HP	LRISVT-QPDSIVGIVAVDKSVNLMNASNDITMENVVHEL-ELYNTG-----
		* * * * * * * * * *
35	MG	LR--VTAAPQSVCALRAVDQSVLLMKPDAELSASSVYNLLPEKDLTGFPGLNDQDDEDC


```

MG RLLLQQVSL-PELPGEYSMKVTGEGCVYLQTSCLKYN----ILPEKEEFPFALGVQTLPT
HP VKENK-DDLNHVLDLNVCTSFSGPGRSGMALMEVNLLSGFMVPSEAISETVKKVEYDHG
      * *           * *      *   * * *      *   * * *      * *   * * *
MG CDEPKAHTSFQISLSVSYTGS-RSASNMAIVDVKMVSGF-----IPLKPTVKMLE----
5  HP KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYIEPRRQAVRSYNSEVKLSSCD
      *   *   *           * * * *           *   *   * *           *
MG ----RSNHVSRTEVSSNHVLIYLDKVSNTLSLFFTVLQDVP----VR-----D
HP LCSDVQGCRCPCEDGASGSHHSSVIFIFCFKLLYFMELWL
      *           *           * * *
10 MG L---KPAIVKVYDYYETDEFAIAEYNAPCSKDL----GNA

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W33075) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20 <HP02991> (SEQ ID NOS: 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02991 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 81-bp 5'-untranslated region, a 1749-bp ORF, and a 800-bp 3'-untranslated region. The ORF encodes a protein consisting of 582 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 66 kDa that was somewhat larger than the molecular weight of 64,244 predicted from the ORF. In

Table 9

	HP	MFPAGPPSHSLRLPLLQLLLLLVQAVGRGLGRASPAGGPLEDVVIERYHIPRACPREVQ
		** .*.***. *...*.***** .*.***.*****.*****.*****
5	MM	MFLVGSSSHTLHRVRILPLLLL-LQTLERGLGRASPAGAPLEDVVIERYHIPRACPREVQ
	HP	MGDFVRYHYNGTFEDGKKFDSSYDRNTLVAIVVGVRGLITGMDRGLMGMCVNERRRLIVP
		*****.*****.*****.*****.*****.*****.*****.*****
	MM	MGDFVRYHYNGTFEDGKKFDSSYDRSTLVAIVVGVRGLITGMDRGLMGMCVNERRRLIVP
	HP	PHLGYGSIGLAGLIPPDATLYFDVLLDVWNKEDTVQVSTLLRPPHCPRMVQDGDVRYH
10		*****.*****.*****.*****.*****.*****.*****.*****
	MM	PHLGYGSIGVAGLIPPDATLYFDVLLDVWNKADTVQSTILLRPPYCPRMVQNSDFVRYH
	HP	YNGTLLDGTSDTSYSKGGTYDTYVGSWLIKMDQGLLMCPGERRKIIIPPFLAYGEK
		*****.***.***.*****.*****.*****.*****.*****
	MM	YNGTLLDGTGFDNSYSRGGTYDTYIGSWGLIKMDQGLLMCPGERRKIIIPPFLAYGEK
15	HP	GYGTVIPPQASLVFHVLLIDVHNPKDAVQLETLELPPGCVRRAGAGDFMRYHYNGSLMDG
		*****.***.*****.*****.*****.*****.*****.*****
	MM	GYGTVIPPQASLVFYVLLDVHNPKDVTQLETLELPQGCVRRVAVAGDFMRYHYNGSLMDG
	HP	TLFDSSYSRNHTYNTYIGQYIIPGMDQGLQGACMGERRRITIPPHLAYGENGTGDKIPG
		*****.*****.*****.*****.*****.*****.*****.*****
20	MM	TLFDSSYSRNHTYNTYVGQYIIPGMDQGLQGACIGERRRITVPPHLAYGENGTGDKIPG
	HP	SAVLIFNVHVIDFHNPAADVVEIRTLSPSETCNETTKLGDFVRYHYNCSSLDDGTQLFTSH
		*****.*****.* ***.*****.*****.***.*****.*****.***.***
	MM	SAVLIFDVHVIDFHNPSDPVEIKTLSPENCNETSKIGDFIRYHYNCSSLDDGTRLFSSH
	HP	DYGAPQEATLGANKVIEGLDTGLQGMCVGERRQLIVPPHLAHGESGARGVPGSAVLLFEV
25		** .*****.*****.*****.*****.*****.*****.*****
	MM	DYEAPQEITLGANKVIEGLDRGLQGMCVGERRQLIVPPHLAHGENGARGVPGSAVLLFEV
	HP	ELVSREDGLPTGYLFVWHKDPPANLFEDMDLNKDGEVPPEEFSTFIKAQVSEGKGRMLPG
		*****.***.***.*****.*****.*****.*****.*****
	MM	ELVSREDGLPTGYLFVWYQDPSTSLFEDMDLNKDGEVPPEEFSSFIKAQVNEGKGRMLPG
30	HP	QDPEKTIGDMFQNQDRNQDGKITVDELKLKSDDEDEERVHEEL
		..*****.*****.*****.*****.*****.*****
	MM	QDPDKTISDMFQNQDRNQDGKITAEELKLKSDDEDQERVHEEL

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse AUP1 (GenBank Accession No. U41736). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse AUP1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 90.2% in the entire region.

Table 10

	HP	MELPSGPGPERLFD	SHRLPGDCFL	LLVLLLYAPV	GFCLLVLR	LFLGLIHV	FLVSCALP	DSV
		**	*	.	*****	.	*	****
5	MM	MEPPPAPGPERLFD	SHRLPSDGF	LLLALLLYAPV	GLCLLVLR	LFLGLHV	FLVSCALP	DSV
	HP	LRRFVVRTMCAVL	GLVARQEDS	GLRDHSVR	VLISNHV	TPFDHN	IVNLLT	CSTPLLNSPP
		*****	.	*****	.	*****	.	*****
	MM	LRRFVVRTMCAVL	GLVARQEDS	GLRDHRVR	VLISNHV	TPFDHN	IVNLLT	CSTPLLNSPP
	HP	SFVCWSRGMEMN	RGELVESL	KRFCASTR	LPPTPL	LLFP	EEEEATN	GREGLLRFSSWPFS
10		*****	.	*	*****	.	*****	.
	MM	SFVCWSRGMEMD	RRVELVES	LKKFCASTR	LPPTPL	LLFP	EEEEATN	GREGLLRFSSWPFS
	HP	IQDVVQPLTLQV	QRPLVSV	TVSDASW	SELLWS	LFVP	FTVYQVR	WLRPVHRQLGEANE
		*****	.	*****	.	*****	.	*****
	MM	IQDVVQPLTLQV	QRPLVSV	TVSDASW	SELLWS	LFVP	FTVYQVR	WLRHPIRRQLGEESE
15	HP	ALRVQQLVAKEL	GQTGTRL	TPADKAEH	MKRQRH	PRLRPQ	SAQSSFP	SPSPDPVQLATL
		*****	.	*****	.	*****	.	*****
	MM	ALRVQQLVAKEL	GQIGTRL	TPADKAEH	MKRQRH	PRLRPQ	SVQSSFP	SPSPSSDVQLTTL
	HP	AQRVKEVLPHV	PLGVIQ	RDLAGT	GCVDLT	ITNL	LEGAVAF	MPEDITKGTQSLPTAS
		*	*****	.	*****	.	*****	.
20	MM	AHRVKEVLPHV	PLNVIQ	RDLAGT	GCVDLT	ITNL	LEGAVAF	MPEDVTEGSQSP
	HP	PSSGPVTPQPT	ALTFAK	SSWARQES	LQERKQ	ALY	YARRR	FTERRAQEAD
		****	.	*****	.	*****	.	*****
	MM	PSSGLATPQPT	ALTFAK	SSWARQES	LQERKQ	ALY	YARRR	FRERQAQAE

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA131932) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

30

<HP03091> (SEQ ID NOS: 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03091 obtained from cDNA library of human liver revealed the structure consisting of a 16-bp 5'-untranslated region, a 1452-bp ORF, and a 184-bp 3'-untranslated region. The ORF encodes a protein consisting of 483 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 34.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human OS-9 protein (SWISS-PROT Accession No. Q13438). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human OS-9 protein (OS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 27.8% in the N-terminal region of 281 amino acid residues. The positions of eight cysteines were conserved between the two proteins.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI016020) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03116> (SEQ ID NOS: 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP03116 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 32-bp 5'-untranslated region, a 945-bp ORF, and a 110-bp 3'-untranslated region. The ORF encodes a protein consisting of 314 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 20. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 167, Asn-Asn-Ser at position 200 and Asn-Ile-Ser at position 273).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human Prostasin (SWISS-PROT Accession No. Q16651). Table 13 shows the comparison between amino acid sequences of the human protein of the present

invention (HP) and the human Prostasin (PR). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.8% in the entire region.

Table 13

10	HP	MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPW
		..*.* . . * ** *. ***** . ****.*.*.* *.*.*
	PR	MAQKGVLGPGQLGAVAILLYLGLLRSGTG-AEGAEAPCG-VAPQARITGSSAVAGQWPW
	HP	QGSLRLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAY
		* *. . ***** **.*.*.*.*.*.*.*.*. *.*.*. . *. .
15	PR	QVSITYEGVHVCGGSLVSEQWVLSAAHCF---PSEHHKEAYEVKLGA-HQLDSY---SED
	HP	YTRYFVSNIIYLSPRYLGNSPY-DIALVKLSAPVITYTKHIQPICLQASTFEFENRTDCWVT
	* *** .. *****.*
	PR	AKVSTLKDIIHPHPSYLQEGSQGDIALQLSRPITFSRYIRPICLPAANASFPNGLHCTVT
	HP	GWGYIKEDEALPSPHTLQEVQVAIINNSMCNHLF-LKYSFRKDIF--GDMVCAGNAQGGK
20		****.. . . * ..*
	PR	GWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGK
	HP	DACFGDSGGPLACNKNGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMS
		*** *****.* ..***** .*.***** .** ..***** * . *****.
	PR	DACQGDSSGGLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVTELQPR
25	HP	QPDPSWPLLFFPLLWALPLLGPV
	PR	VVPQTQESQPDNLCGSHLAFSSAPAQGLLRPILFLPLGLALGLLSPWLSEH

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA159101) among ESTs. However, since they are partial sequences, it can not be judged whether or

Determination of the whole base sequence of the cDNA insert of clone HP10619 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 11-bp 5'-untranslated region, a 657-bp ORF, and a 854-bp 3'-untranslated region. The ORF encodes a protein consisting of 218 amino acid residues and there existed a putative transmembrane domain at the N-terminus.

Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z43089) among ESTs. However, since they are partial sequences, it can not be judged whether or
10 not they encode the same protein as the protein of the present invention.

<HP10622> (SEQ ID NOS: 39, 49, and 59)

Determination of the whole base sequence of the cDNA
15 insert of clone HP10622 obtained from cDNA library of the human liver revealed the structure consisting of a 43-bp 5'-untranslated region, a 1383-bp ORF, and a 165-bp 3'-untranslated region. The ORF encodes a protein consisting of 460 amino acid residues and there existed a putative
20 secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the
25 mature protein starts from serine at position 17. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Ser-Ser at position 23, Asn-Met-Ser at position 115, Asn-Glu-Thr at position 296 and Asn-Tyr-Thr at position 357).

30 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human angiopoietin-1 (GenBank

Accession No. U83508). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human angiopoietin-1 (AN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 28.2% in the entire region and a homology of 39.1% in the C-terminal region of 215 amino acid residues.

example, Accession No. R86161) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5

<HP10625> (SEQ ID NOS: 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10625 obtained from cDNA library of the human liver revealed the structure consisting of a 133-bp 5'-untranslated region, a 651-bp ORF, and a 465-bp 3'-untranslated region. The ORF encodes a protein consisting of 216 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

15

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R59052) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20

<HP02883> (SEQ ID NOS: 61, 71, and 81)

Determination of the whole base sequence of the cDNA insert of clone HP02883 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 191-bp 5'-untranslated region, a 1179-bp ORF, and a 2657-bp 3'-untranslated region. The ORF encodes a protein consisting of 392 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained

25

30

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F11409) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP03140> (SEQ ID NOS: 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP03140 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 29-bp 5'-untranslated region, a 1494-bp ORF, and a 972-bp 3'-untranslated region. The ORF encodes a protein consisting of 497 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 51 kDa that was almost identical with the molecular weight of 54,245 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELC50D2 (GenBank Accession No. AF040642). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CELC50D2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the N-terminal region of 393 amino acid residues.

5

Table 16

	HP	MALWRGSAYAGFLALAVGCVFLLEPELPGSALRSIWSSSLCLGPAPAPPGPVSPEGR	LAAA
			* * . . .
	CE	MFSETFVPSIFS	YKHRLHLSV
	HP	WDALIVRPVRRWRRVAVGVNACVDVVL	SGVKLLQALGLSPGNGKDHSILHSRNDLEEAFI
10		*. **.* *	* **.* *
	CE	WERAIVKPGAMFKKAVIGFNCNVDLIVSGVRVVDALNTTCSE	GKDQETLET
	HP	HFMWKGAAAERFFSDKET	FDIAQVASEFPGAQHYVGGNAALIGQKFAAN-SDLKVLLCG
		** *	* *
15	CE	HFFQRGAAAERYMSS	EDQFNLLVAESEASTRSHHHIGGNAALMADRIAANFPSTEVYLVG
	HP	PVGPRLHELLDDNVFVPPESLQ	EVDEFHLILEYQAGEEWGQLKAPHANRFIFSHDLSNGA
		* *	* *
	CE	PIGPRSQALLHPSVKRTNSTRILKDELHVILEYKQGEILGDWVAPSSSR	FITSHDFSGS
	HP	MNMLEFVVSLEEFQPD	LVVLSGLHMMEGQSKELQRKRLLLEVVT
20		* *	* *
	CE	MVVMEMFFKAIAQFRPDLV	VITGVHLLFQSKEMRQEKMR
	HP	SMTNRELMSSIVHQVFP	AVTSLGLNEQELLFLTQSASGPH-SSLSSWNGVPDVG
		* *	* *
	CE	SLAD-EIFSTDVINKILPYVDSL	GINEQELTFLSHIANGPHMEEYPVQAGTVHVHKVEM
25	HP	LFWILKEHGR-----	SKSRASDLTRIHFHTLVYHILATVDGHWANQLAAVAAGARVAGT
		* * *	* *
	CE	LHWLLKTYGRDPTGQIASKTGYRLSRIHFHCLTYHIMVSSGTDWSNLAAGLAAGARIAGR	
	HP	QAC--ATETIDTSRVSLRAPQEFMTSHSEAGSRIVLNP	KNPKPVVEWHREGISFHFTPVLVC
		* *	
30	CE	LSCNIGANTMDSELLEIRTPANFVLDKKIEKNYQFEAHKYMLTPFNIARCSTR	LIRRKPP
	HP	KDPIRTVGLGDAISAEG	LFYSEVHPHY
	CE	GGGILDEGVTFS	DVHNVLNPTTRLPYPEEQ

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356000) among ESTs. However, since
5 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10628> (SEQ ID NOS: 63, 73, and 83)

10 Determination of the whole base sequence of the cDNA insert of clone HP10628 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 66-bp 5'-untranslated region, a 1254-bp ORF, and a 297-bp 3'-untranslated region. The ORF encodes a
15 protein consisting of 417 amino acid residues and there existed four putative transmembrane domains. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
20 product of 46 kDa that was almost identical with the molecular weight of 45,461 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Schistosoma mansoni ATP-cassette
25 family protein (GenBank Accession No. L26286). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Schistosoma mansoni ATP-cassette family protein (SM). Therein, the marks of -, *, and . represent a gap, an amino
30 acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. U66688) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10629> (SEQ ID NOS: 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10629 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 259-bp 5'-untranslated region, a 1950-bp ORF, and a 1060-bp 3'-untranslated region. The ORF encodes a protein consisting of 649 amino acid residues and there existed at least eight putative transmembrane domains. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELF38B6 (GenBank Accession No. U40060). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CELF38B6 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.1% in the C-terminal region of 445 amino acid residues.

Table 18

	HP MIPNQHNAGAGSHQPAVFRMAVLDTDLDHILPSSVLPPFWAKLVVGSVAIVCFARSYDGD
	CE MKYAEINVNSGKHFRNLNYKLHETS
5	HP FVFDDSEAIVNKNVAGVVGRADLLCALFFLLSFLGYCKAFRESNKEGAHSSTFWLLSIF
	CE TLGYHVNIICHTVATLVFYKLGKQLEHIFDFFNIAFSASILFAVHPVHTEAVANITGRA
	HP LGAVAMLCKEQGITVLGLNAVFDILVIGKFNVLIVQKVLHKDKSLENLGMRLNGGLLFR
	CE ELLMTIFSLAALILHVKNREINCKFVLLVILSTLSKEQGLMTIPIAICIDFLAHRSCRSN
	HP MTLTSGGAGMLYVRWRIMGTGPPAFTEVDNPASFADSMVLRAVNYNYYYSLNAWLLLC
10	..* .. * ... **.....* ... ** ..*...*
	CE FVRMICLLVAIGFLRMVNGFEAAKFTKLDNPTAFLNSKFYRMINYTYIWLYHAYLLVIP
	HP WWLCFDWSMGCIPLIKSIDWRVIALAALWFCLIGLICQALCEDGHKRRILTLGLGLV
	****.....** ..*... ..* ..* ..*... ..*
	CE VNLCFDYSMGCISSITM--WDLRALSPVLIFTIVIIGVKF----QNECRAFTLSSIMGI
15	HP IPFLPASNLFFRVGFVVAERVLVLPISIGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFI
	*.....** *** ..*.....* ..* ..* ..* ..* ..* ..* ..*
	CE ISFLPASNIFFTVGFSIAERVLVLPISAGFCILCAIIFKKLSVHFKNADVLSITLILLIS
	HP NTLRCVLRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAIRYYREAVRLN
	..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
20	CE KTYR--RSGEWKTELSLYSSGLSVCPTNAKIHYNLGKVLGDNGLTKDAEKYWNNAIKLD
	HP PKYVHAMNNLGNILKERNELQEAELLSLAVQIQPDFAAAWMNLGIVQNSLKRFEAAEQS
	* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
	CE PSYEQALNNLGNLLEKSGDSKTAESLLARAVTLRPSFAVAMNLGISQMNLLKYYEAEKS
	HP YRTAIKHRRKYPDCYYNLGRLYADLNRHVDALNAWRNATVLKPEHSLAWNMIILLDNTG
25* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
	CE LKNLLIRPNSAHCLFNLGVLYQRTNRDEMAMSAWKNATRIDPSHSQSWTNLFVVDHLS
	HP NLAQAEAVGREALELIPNDHSLMFLANVLGKSQKYKESEALFLKAIKANPNAASYHGNI
	..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
	CE QCSQVIDLSYQALSSVPNESRVHMQIGSCHAKHSNFTAENHIKSAIDLNPSTSVLFHANL
30	HP AVLYHRWGHLDLAKKHYEISLQLDPTASGTKENYGLLRKLELMQKKAV
	***..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
	CE GILYQRMSRHKESQYRIVLALDSKNIVAKQNLQKLEEHNCYNSTLP

35 Furthermore, the search of the GenBank using the base

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA450191) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10635> (SEQ ID NOS: 65, 75, and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10635 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 65-bp 5'-untranslated region, a 282-bp ORF, and a 111-bp 3'-untranslated region. The ORF encodes a protein consisting of 93 amino acid residues and there existed two putative transmembrane domains. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 9,489 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA516481) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10636> (SEQ ID NOS: 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10636 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure

consisting of a 179-bp 5'-untranslated region, a 1278-bp ORF, and a 255-bp 3'-untranslated region. The ORF encodes a protein consisting of 425 amino acid residues and there existed ten putative transmembrane domains. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z43270) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10640> (SEQ ID NOS: 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10640 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 52-bp 5'-untranslated region, a 450-bp ORF, and a 553-bp 3'-untranslated region. The ORF encodes a protein consisting of 149 amino acid residues and there existed at least two putative transmembrane domains. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was almost identical with the molecular weight of 16,829 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical

protein F27F23.14 (GenBank Accession No. AC003058). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Arabidopsis thaliana hypothetical protein F27F23.14 (AT).
 5 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire
 10 region other than the N-terminal region.

Table 19

	HP	METLYRVPFLVLECPNLKCLKPPWLHMPSAMTVYA
15		*** * *.*** * . .***.*****
	AT	MAPRSDSQTGSSVSDGSDQSSMDPIFHLIRIVPFSFLRPPRLRLKIPS-FTLPSPMTVYA
	HP	LVVVSFYFLITGGIIYDVIVEPPSVGSMTD-EHGHQRPVAFLAYRVNGQYIMEGLASSFLF
		*....***.....*****..** * . * ***.*.. *****.***.*.*
	AT	LILLTYFLVSGFVYDVIVEPPGIGSTQDPTTGTIRPVVFMSSGRVNGQYIIEGLSSGFMF
20	HP	TMGGLGFIILDRSNAPNIPKLNRFLLLFIGFVCVLLSFFMARVFMRMKLPGYLMG
		..***.*....** . . * . * . * *.....*.....*
	AT	VLGGIGIVMLDLALDKNKAKSVKASYAVAGVSSIVIAVMSMLFIRIKIPGYLY

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N34717) among ESTs. However, since they are partial sequences, it can not be judged whether or
 30 not they encode the same protein as the protein of the present invention.

<HP10644> (SEQ ID NOS: 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10644 obtained from cDNA library of the human retinoblastoma cell line WERI-RB revealed the structure consisting of a 221-bp 5'-untranslated region, a
 5 1191-bp ORF, and a 204-bp 3'-untranslated region. The ORF encodes a protein consisting of 396 amino acid residues and there existed two putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

10 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein B0511.8 (GenBank Accession No. AF067608). Table 20 shows the comparison between amino acid
 15 sequences of the human protein of the present invention (HS) and the *Caenorhabditis elegans* hypothetical protein B0511.8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that
 20 of the protein of the present invention, respectively. The both proteins shared a homology of 31.3% in the region of 361 amino acid residues other than the N-terminal region and the C-terminal region.

Table 20

	HS	MAMIELGFGRQNFHPLKRKSSLLLKL
	CE	CDKNGQYLSVQEEIDAENKVQRKIAPGLNEKVLERVQTQMLMKQEKSTETETMIWLKNLRVP
5	HS	IAVVFAVLLFCEFLIYYLAIFQCNWPEVKTTASDGEQTTREPVLKAMFLADTHLLGEFLG
		* * * * * * *
	CE	ILLAILLVYNEYFIFFIASFSSCQWP-----CKYGRCS-ESSVKAFMISDTHLLGKING
	HS	HWLDKLRREWQMERAFQTALWLLQPEVVFILGDIFDEGKWSTPEAWADDVERFQKMFRRHP
		***** * * * * *
10	CE	HWLDKLRREWQMYQSFWISTWIHSPDVTFFLGDLMDEGKWAGRPVFEAYAERFKKLF--G
	HS	SHVQLKVAGNHDIGFHYEMNTYKVERFEKVFSSERLFSWKGINFVMVNSVALNGDGCGI
	 ***** * * * *
	CE	DNEKVITLAGNHDLGFHYAL----VQTFATHLTPT--VELKNYLLIMPETLEMFKKEFRR
	HS	CSETEAELIEVSHRLNCSREARG-SSR-CGPGPL-----LPTSAPVLLQHYPLYRRS
15		. * * * * * * *
	CE	GLIDEMKIKKHRFVLINSMAMHGDGCRLCHEAELILEKIKSRNPKNRPIVLQHFPLYRKS
	HS	DANCSGEDAAPAEERDIPFKENYDVLREASQKLLWWLQPRVLVSGHHSAC-----EVH
		** . * * * * *
	CE	DAECDQVDEQHEIDLKEMYREQWDTLSKESLQIIDSLNPKAVFGGHTHKMCKKKWNKTG
20	HS	HGGRVPELSVPSFSWRNRNPNPSFIMGSIPTDYTLSCYLPREDVVLIIYC-GVVGFLVV
	 * . * * * * *
	CE	NSEYFYEYTVNSFSWRNGDVPAMLLVVIDGDNVLVSSCRLPSEILQIMVYIFGGIGILAK
	HS	LTLTHFGLLASPFLSGLNLLGKRKTR
25	CE	MYNDLITPAPLEWNVNNIAVCTAILVMIINVALIFTIFWCLRSKDEGGEIDSNGVVIN

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R88381) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10656> (SEQ ID NOS: 69, 79, and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10656 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure consisting of a 68-bp 5'-untranslated region, a 1053-bp ORF, and a 739-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed two putative transmembrane domains. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 41 kDa that was almost identical with the molecular weight of 40,043 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa to which sugar chains are presumably attached. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Cys-Thr at position 148, Asn-Tyr-Thr at position 155, Asn-Gln-Thr at position 162 and Asn-Lys-Ser at position 190).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA917816) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10672> (SEQ ID NOS: 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10672 obtained from cDNA library of the

human thymus revealed the structure consisting of a 244-bp 5'-untranslated region, a 462-bp ORF, and a 77-bp 3'-untranslated region. The ORF encodes a protein consisting of 153 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. When expressed in COS cells, a product of 17 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N48700) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03194> (SEQ ID NOS: 91, 101, and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03194 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 120-bp 5'-untranslated region, a 912-bp ORF, and a 2406-bp 3'-untranslated region. The ORF encodes a protein consisting of 303 amino acid residues and there existed four putative transmembrane domains. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the mouse hyperpolarization-activated cation channel HAC3 (GenBank Accession No. AJ225124). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the mouse hyperpolarization-activated cation channel HAC3 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 92.5% in the N-terminal region of 293 amino acid residues.

Table 21

15	HS	MEAEQRPAAGASEGATPGLEAVPPVAPPPATAASGPIPKSGPEPKRRHLGTLLQPTVNKF
		.***.****. *. **.*..* **** .*.*****.*****
	MM	MEEEARPAAGAGEAATPARET-PPAAPAQARAASGGVPESAPEPKRRQLGTLLQPTVNKF
	HS	SLRVFGSHKAVEIEQERVKSAGAWIIHPYSDFRFYWDLIMLLLMVGNLIVLPVGITFFKE

20	MM	SLRVFGSHKAVEIEQERVKSAGAWIIHPYSDFRFYWDLIMLLLMVGNLIVLPVGITFFKE
	HS	ENSPPWIVFNVLSDTFFLLDLVLNFRGTGIVVEEGAEILLAPRAIRTRYLRTWFLVDLISS

	MM	ENSPPWIVFNVLSDTFFLLDLVLNFRGTGIVVEEGAEILLAPRAIRTRYLRTWFLVDLISS
	HS	IPVDYIFLVVELEPRLDAEVYKTARALRIVRFTKILSLRLRLRLSLIRYIHQWEEIFHM
25		*****
	MM	IPVDYIFLVVELEPRLDAEVYKTARALRIVRFTKILSLRLRLRLSLIRYIHQWEEIFHM
	HS	TYDLASAVVRIFNLIGMMLLLCHWDGCLQFLVPMLQDFPPDCWVSINHMVVRSPHSSAFP
		*****.*****.***.*
	MM	TYDLASAVVRIFNLIGMMLLLCHWDGCLQFLVPMLQDFPSDCWVSMNRMVNHWSGRQYSH
30	HS	GPS
	MM	ALFKAMSHMLCIGYGQAPVGMPDVWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRQY

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI571225) among ESTs. However, since
5 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03219> (SEQ ID NOS: 92, 102, and 112)

10 Determination of the whole base sequence of the cDNA insert of clone HP03219 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 55-bp 5'-untranslated region, a 852-bp ORF, and a 237-bp 3'-untranslated region. The ORF encodes a protein consisting
15 of 283 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
20 of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human putative membrane protein 54Tm (GenBank Accession No. AF004876). Table 22 shows the
25 comparison between amino acid sequences of the human protein of the present invention (HS) and the human putative membrane protein 54Tm (TM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino
30 acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 56.5% in the entire region.

Determination of the whole base sequence of the cDNA insert of clone HP03236 obtained from cDNA library of human

10 The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the *Caenorhabditis elegans*
hypothetical protein ZC513.5 (GenBank Accession No. U53155).
Table 23 shows the comparison between amino acid sequences
15 of the human protein of the present invention (HS) and the
Caenorhabditis elegans hypothetical protein ZC513.5 (CE).
Therein, the marks of -, *, and . represent a gap, an amino
acid residue identical with that of the protein of the
present invention, and an amino acid residue similar to that
20 of the protein of the present invention, respectively. The
both proteins shared a homology of 39.5% in the intermediate
region of 365 amino acid residues.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human intestinal membrane A4 protein (SWISS-PROT Accession No. Q04941). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the human intestinal membrane A4 protein (IM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the intermediate region of 111 amino acid residues.

Determination of the whole base sequence of the cDNA insert of clone HP03267 obtained from cDNA library of human liver revealed the structure consisting of a 148-bp 5'-untranslated region, a 555-bp ORF, and a 715-bp 3'-untranslated region. The ORF encodes a protein consisting of 184 amino acid residues and there existed two putative transmembrane domains. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 21 kDa that was almost identical with the molecular

weight of 20,733 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human polyposis locus protein 1 (SWISS-PROT Accession No. Q00765). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the human polyposis locus protein 1 (PL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 59.1% in the entire region.

15

Table 25

HS	MDGLRQ RVEHFLEQRNLVTEVLGALEAKTGVEKRYLAAGAVTLLSLYLLFGYGASLLCNL
	.*. * * * * * *
PL	MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVEFGYGASLLCNL
20	HS IGFVYPAYASIKAIESP SKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYVVGKCAFL
	*** ** * * * * * *
PL	IGFGYPAYISIKAIESP NKEDDTQWLTYWVVYGVFSIAEFFSDIFLSWFPFYMLKCGFL
HS	LFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSGRALDAAAGITRNVKPSQTPQ
	* * * . . . * * * * *
25	PL LWCMA PPSNGAELLYKRIIRPF FLKHESQMDSVVKDLKDKSKETADAITKEAKKATVNL
HS	PKDK
PL	LGEEKKST

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. R09702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5

<HP03270> (SEQ ID NOS: 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP03270 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 132-bp 5'-untranslated region, a 423-bp ORF, and a 656-bp 3'-untranslated region. The ORF encodes a protein consisting of 140 amino acid residues and there existed four putative transmembrane domains. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was somewhat larger than the molecular weight of 15,864 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schizosaccharomyces pombe* hypothetical protein (EMBL Accession No. AL031854). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the *Schizosaccharomyces pombe* hypothetical protein (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.4% in the entire region.

Determination of the whole base sequence of the cDNA insert of clone HP03298 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 182-bp 5'-untranslated region, a 462-bp ORF, and a 455-bp 3'-untranslated region. The ORF encodes a protein consisting of 153 amino acid residues and there existed at least one putative transmembrane domain. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17.5 kDa that was almost identical with the molecular

weight of 17,360 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Schizosaccharomyces pombe hypothetical protein SPBC119.09c (EMBL Accession No. AL022117). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the Schizosaccharomyces pombe hypothetical protein SPBC119.09c (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.9% in the entire region other than the N-terminal region.

Table 27

20	HS	MNVGVAHSEVNPNTNTRVMNSRGMWLTALGVGLLHIVLL
		. * . * * *
	SP	MGSSSSRRRSSSLVTKVPKPTIDDRLDQGSATNYSNWNVNYKGAWVIHIVLIAALRLIFH
	HS	SIPFFSVPAWTLTNIIHNLGMYVFLHAVKGTPTFETPDQKARLLTHWEQLDYGVOFTSS
		. ** * * * *
	SP	AIPSVSRELAWTLTNLTYMAGSFIMFHWVTGTPFEFNGGAYDR-LTMWEQLDEGNQYTPA
25	HS	RKFFTISPIILYFLASFYTKYDPTHFILNTASLLSVLIPKMPQLHGVRIFGINKY
		** * * *
	SP	RKYLLVLPILFLMSTHYTHYNGWMFLVNIWALFMVLIPKLPVHRKRIFGIQKLSLRDD

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA043039) among ESTs. However, since

they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP10631> (SEQ ID NOS: 98, 108, and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10631 obtained from cDNA library of the human retinoblastoma cell line WERI-RB revealed the structure consisting of a 226-bp 5'-untranslated region, a
10 522-bp ORF, and a 2741-bp 3'-untranslated region. The ORF encodes a protein consisting of 173 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

15 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W26443) among ESTs. However, since they are partial sequences, it can not be judged whether or
20 not they encode the same protein as the protein of the present invention.

<HP10658> (SEQ ID NOS: 99, 109, and 119)

Determination of the whole base sequence of the cDNA
25 insert of clone HP10658 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 24-bp 5'-untranslated region, a 228-bp ORF, and a 679-bp 3'-untranslated region. The ORF encodes a protein consisting of 75 amino acid residues and there
30 existed two putative transmembrane domains. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 14 kDa or less that was almost identical with the molecular weight of 8,625 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T85006) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10663> (SEQ ID NOS: 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10663 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure consisting of a 67-bp 5'-untranslated region, a 480-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 159 amino acid residues and there existed two putative transmembrane domains. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA336522) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03165> (SEQ ID NOS: 121, 131, and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03165 obtained from cDNA library of human

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human β -galactosidase (GenBank Protein ID No. AAA51822). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human β -galactosidase (GL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.8% in the entire region.

HP RNQYIK

GL FVDRPVIGSSVTYDHPSKPVEKRLMPPPPQKNKDSWLDHV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA054017) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03266> (SEQ ID NOS: 122, 132, and 142)

15

Determination of the whole base sequence of the cDNA insert of clone HP03266 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 69-bp 5'-untranslated region, a 957-bp ORF, and a 1464-bp 3'-untranslated region. The ORF encodes a protein consisting of 318 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was almost identical with the molecular weight of 35,363 predicted from the ORF.

25

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana putative ribitol dehydrogenase (GenBank Protein ID No. AAC23625). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the

30

Arabidopsis thaliana putative ribitol dehydrogenase (AT).
 Therein, the marks of -, *, and . represent a gap, an amino
 acid residue identical with that of the protein of the
 present invention, and an amino acid residue similar to that
 5 of the protein of the present invention, respectively. The
 both proteins shared a homology of 39.0% in the region of
 483 residues other than the N-terminal region.

Table 29

10

HP MVELMFPLLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE
 * * *

15

AT MGIYGVMTGKKGKSGFGSASTAEDVTQAIDASHLTAITGGTSGIGLEAARV
 HP LAQRGARVYLACRDVEKGELVAKEIQTTTGNQQVLVRKLDLSDTKSIRAFAGKFLAEKHX
 ** ***. * . * * . . . * * *** . .
 AT LAMRGAHVIAARNPKAANESKEMILQMNPNARVDYLQIDVSSIKSVRSFVDQFLALNVP
 HP LHVLIINAGVMMCPYSKTADGFEMHIGVNHGFLHLLTHLLEKLK-----ESAPSRIVNV
 * * * * * * *

20

AT LNILINAGVMFCPFKLTEDGIESQFATNHIGHFLLTNLLLDKMKSTARESGVQGRIVNL
 HP SSLAH---HLGRIHFHNLQGEKFYNAGLAYCHSKLANILFTQELARRLKSGS--VTTYSV
 ** . . . * * * * * *
 AT SSIAHTYTYSEGIKFQGINDPAGYSERRAYGQSKLSNLLHSNALSRRRLQEEGVNITINSV
 HP HPGTVQSELVRHSSFMRWMLFSF-FIKTPQQAQTSILHCALTEGLEILSGNHFSDCNV
 *** * . . * * * * * *

25

AT HPGLVTTNLFYSGFSMKVFRAMTFLFWKNIPQGAATTCYVALHPDLEGVTGKYFGDCNI
 HP AWVSAQARNETIARRLWDVSCDLLGLPID
 . * * * . . . * . . . * . . .
 AT VAPSKFATNNSLADKLWDFSVFLIDSISK

30

Furthermore, the search of the GenBank using the base
 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. D17020) among ESTs. However, since

they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP03287> (SEQ ID NOS: 123, 133, and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03287 obtained from cDNA library of human thymus revealed the structure consisting of a 83-bp 5'-untranslated region, a 249-bp ORF, and a 1133-bp 3'-untranslated region. The ORF encodes a protein consisting of 82 amino acid residues and there existed one putative transmembrane domain at the N-terminus and one at the C-terminus, respectively. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
10 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
20 protein was similar to the Schizosaccharomyces pombe hypothetical protein 9.0kDa (SWISS-PROT Accession No. 013825). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Schizosaccharomyces pombe hypothetical protein
25 9.0kDa (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 45.7%
30 in the entire region.

Table 30

HP MAFTLYSLQAALLCVNAIAVLHEERFLKNIGWGTDQGIGGFGE-EPGIKSQLMNLIRSV
** .**.*.* **.*** .***. ***. . .***.....***..
 5 SP MFGFGNILYVTLLLLNAVAILSEDRFLGRIGWSQSAAL-GFGDRQDTIKSRILHLIRAI
 HP RTVMRVPLIIVNSIAIVLLLLFG
 ***** *** .**.*** *..*
 SP RTVMTFPLIAINTIVIVYNLVLG

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA853098) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15

<HP10665> (SEQ ID NOS: 124, 134, and 144)

20

Determination of the whole base sequence of the cDNA insert of clone HP10665 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 744-bp ORF, and a 142-bp 3'-untranslated region. The ORF encodes a protein consisting of 247 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,320 predicted from the ORF. In this case, the addition of a microsome led to the formation

25

30

of a product of 27 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from aspartic acid at position 26.

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA055367) among ESTs. However, since they are partial sequences, it can not be judged whether or
10 not they encode the same protein as the protein of the present invention.

<HP10669> (SEQ ID NOS: 125, 135, and 145)

Determination of the whole base sequence of the cDNA
15 insert of clone HP10669 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 73-bp 5'-untranslated region, a 621-bp ORF, and a 612-bp 3'-untranslated region. The ORF encodes a protein consisting of 206 amino acid residues and there
20 existed one putative transmembrane domain. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration
25 of sequences that shared a homology of 90% or more (for example, Accession No. AF086533) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

30

<HP10670> (SEQ ID NOS: 126, 136, and 146)

Determination of the whole base sequence of the cDNA

insert of clone HP10670 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 117-bp 5'-untranslated region, a 1299-bp ORF, and a 606-bp 3'-untranslated region. The ORF encodes a
 5 protein consisting of 432 amino acid residues and there existed seven putative transmembrane domains. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino
 10 acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELM03F8.2 (GenBank Protein ID No. AAB65910). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP)
 15 and the *Caenorhabditis elegans* hypothetical protein CELM03F8.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention,
 20 respectively. The both proteins shared a homology of 39.6% in the N-terminal region of 376 residues.

Table 31

	HP	MDARWWAVVLAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGYLLVQYF
	 ** . . * ** *
5	CE	MDRSIMPIDSPARDKPPD--ELVWPLRLFLILLGYSTVATPAAILIYYV
	HP	RRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLA---PRTEAAETTPMW-----QALKL
		** * * * * *
	CE	RRNRHAFETPYLSIRLLIRS-FAVGNPEYQLIPTGEKQARKENDSIPQTRAQCINVIILL
	HP	LFCATGLQVSYLTWGV LQERVMTSY-GATATSPGERFTDSQFLVLMNRVLALIVA--GL
10		** * * * * *
	CE	LFFFSGIQVTLVAMGVLQERIITRGYRRSDQLEVEDKFGETQFLIFCNRIVALVLSIMIL
	HP	SCVLCKQPRHGAPMYRYSFASLSNVLSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKL
	 * * * * * *
	CE	AKDWTQPPHVPPLYVHSYTSFSNTISSWCQYEALKYVSFPTQTICKASKVVVTMLMGRL
15	HP	VSRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPAT--TLSGLLLAGYIAFDSFTSN
		* * * * * *
	CE	VRGQRYSWFEYGCCTIAFGASLFLSSSSSKGAGSTITYTSFSGMILMAGYLLFDAFTLN
	HP	WQDALFAYK--MSSVQMMFGVNF SCLFTVGSILLEQGALLEGTRFMGRHSEFAAHALLS
		** * * * * *
20	CE	WQKALFDTKPKVSKYQMMFGVNF SAILCAVSLIEQGTWSSIKFGAEHVDFSRDVFLLS
	HP	ICSACGQLFIFYTIGQFGAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAAL
	 * * * * *
	CE	LSGAIGQIFIYSTIERFGPIVFVAVIMTIRQIFIRNTLIRAEDHRGVEMAPPPPPPEPFRLK
	HP	LLRVYARGRLKQRGKKAVPVESPVQKV
25		
	CE	FLSMIIAVIHI

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. 246196) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the

present invention.

<HP10671> (SEQ ID NOS: 127, 137, and 147)

Determination of the whole base sequence of the cDNA
 5 insert of clone HP10671 obtained from cDNA library of human
 thymus revealed the structure consisting of a 74-bp 5'-
 untranslated region, a 921-bp ORF, and a 232-bp 3'-
 untranslated region. The ORF encodes a protein consisting of
 306 amino acid residues and there existed a putative
 10 secretory signal at the N-terminus and one putative
 transmembrane domain at the intermediate region. Figure 47
 depicts the hydrophobicity/hydrophilicity profile, obtained
 by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base
 15 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. AA357141) among ESTs. However, since
 they are partial sequences, it can not be judged whether or
 not they encode the same protein as the protein of the
 20 present invention.

<HP10673> (SEQ ID NOS: 128, 138, and 148)

Determination of the whole base sequence of the cDNA
 insert of clone HP10673 obtained from cDNA library of the
 25 human thymus revealed the structure consisting of a 203-bp
 5'-untranslated region, a 1668-bp ORF, and a 339-bp 3'-
 untranslated region. The ORF encodes a protein consisting of
 555 amino acid residues and there existed one putative
 transmembrane domain. Figure 48 depicts the
 30 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
 Doolittle method, of the present protein. In vitro
 translation resulted in formation of a translation product

of 65 kDa that was somewhat larger than the molecular weight of 61,781 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R96413) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10675> (SEQ ID NOS: 129, 139, and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10675 obtained from cDNA library of the human thymus revealed the structure consisting of a 92-bp 5'-untranslated region, a 753-bp ORF, and a 648-bp 3'-untranslated region. The ORF encodes a protein consisting of 250 amino acid residues and there existed at least one putative transmembrane domain. Figure 49 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356139) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10683> (SEQ ID NOS: 130, 140, and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10683 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure

consisting of a 25-bp 5'-untranslated region, a 525-bp ORF, and a 714-bp 3'-untranslated region. The ORF encodes a protein consisting of 174 amino acid residues and there existed one putative transmembrane domain. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 22 kDa that was somewhat larger than the molecular weight of 19,572 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 24 kDa to which sugar chains are presumably attached. In addition, there exist in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 27).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA482321) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents

30 Organisms that have enhanced, reduced, or modified
expression of the gene(s) corresponding to the
polynucleotide sequences disclosed herein are provided. The

desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; 5 Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed 10 herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or 15 that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been 20 partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, 25 of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, 30 preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153;

5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75%

Table 32

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [†]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC,50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC,50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC,50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC,50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC,50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC,50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC,50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC,50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC,50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺]) + 0.41 (%G+C) · (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing

polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid
sequence selected from the group consisting of SEQ ID NOS: 1
5 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

2. An isolated DNA encoding the protein according to
Claim 1.

3. An isolated cDNA comprising any one of a base
sequence selected from the group consisting of SEQ ID NOS:
10 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.

4. The cDNA according to Claim 3 consisting of any
one of a base sequence selected from the group consisting of
SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and
141 to 150.

15 5. An expression vector that is capable of expressing
the DNA according to any one of Claim 2 to Claim 4 by in
vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of
expressing the DNA according to any one of Claim 2 to Claim
20 4 and of producing the protein according to Claim 1.

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07R 14/705, C12N 15/12		A2	(11) International Publication Number: WO 00/29448
			(43) International Publication Date: 25 May 2000 (25.05.00)
(21) International Application Number: PCT/JP99/06412 (22) International Filing Date: 17 November 1999 (17.11.99) (30) Priority Data: 10/326255 ✓ 17 November 1998 (17.11.98) JP 10/364315 ✓ 22 December 1998 (22.12.98) JP 11/69811 16 March 1999 (16.03.99) JP 11/119299 ✓ 27 April 1999 (27.04.99) JP 11/138169 19 May 1999 (19.05.99) JP (71) Applicants (for all designated States except US): SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 (JP). (72) Inventors; and (75) Inventors/Applicants (for US only): KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 (JP). KIMURA, Tomoko [JP/JP]; 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 (JP).		(74) Agents: AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi, Osaka 540-0001 (JP). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published Without international search report and to be republished upon receipt of that report.	
(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING THESE PROTEINS			
(57) Abstract			
The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs.			

Fig.1

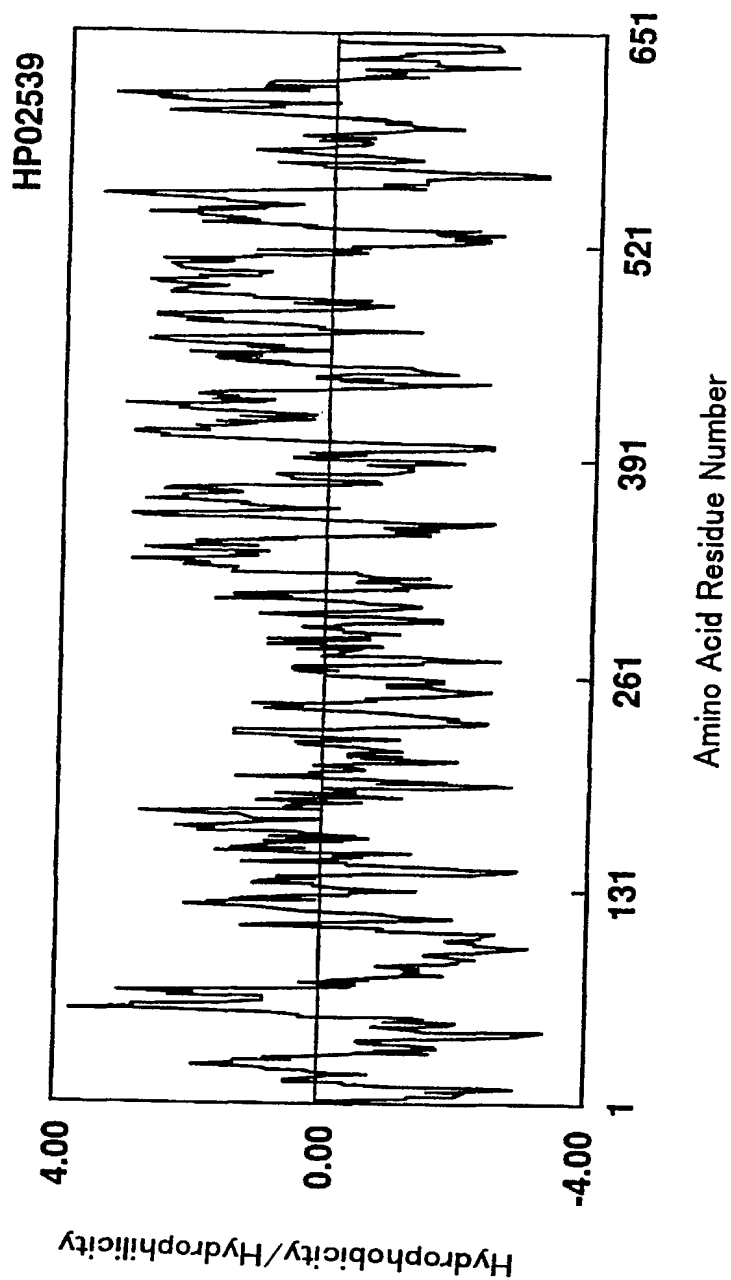


Fig.2

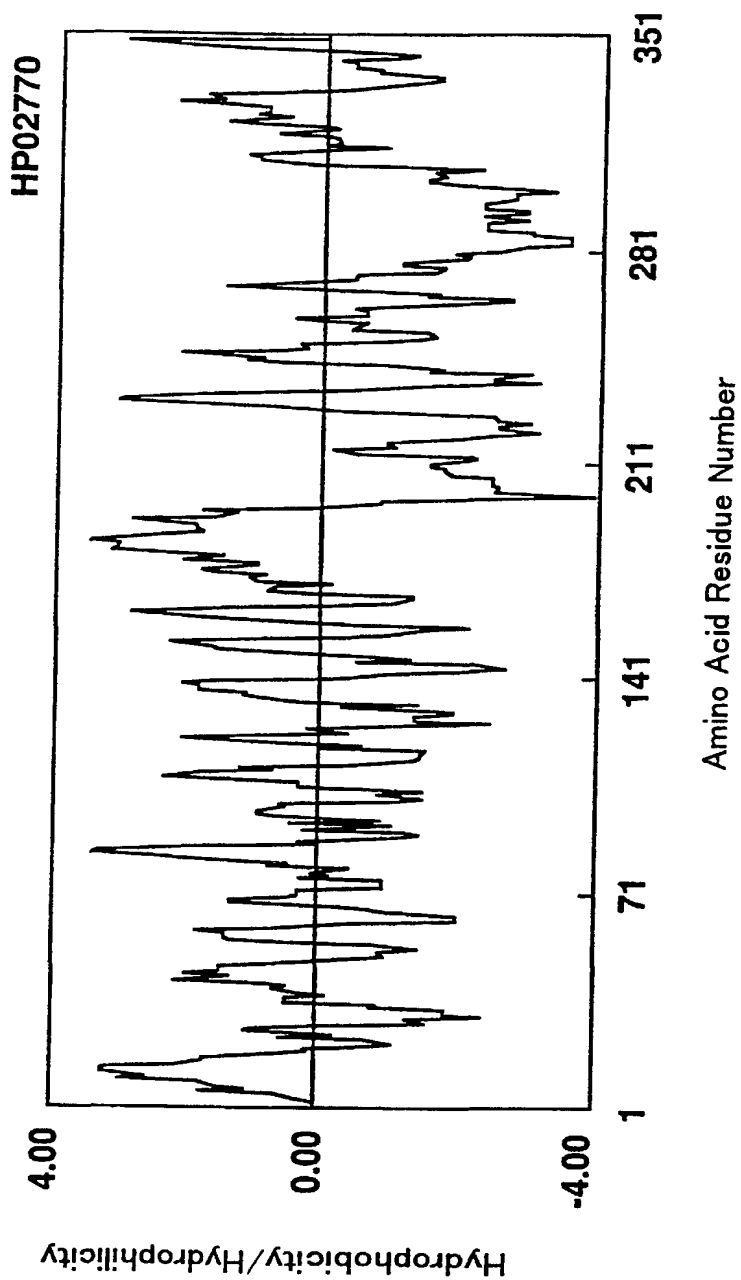


Fig.3

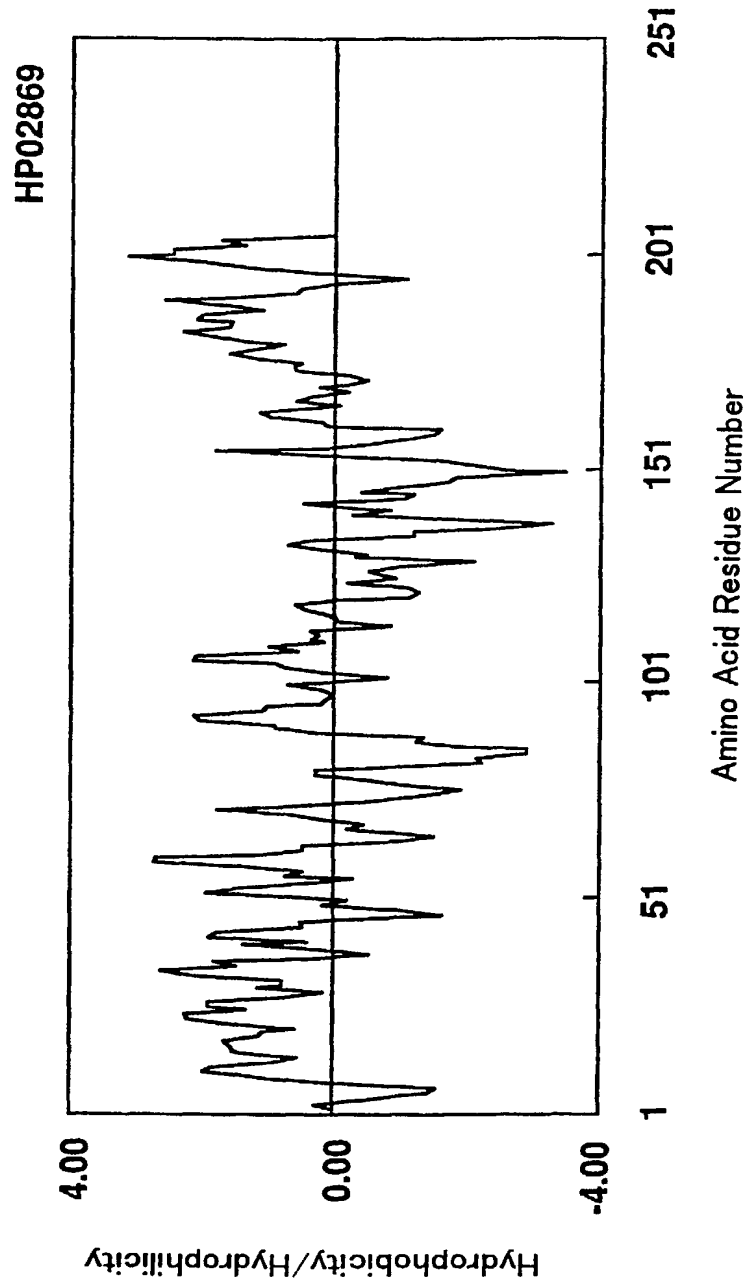


Fig.4

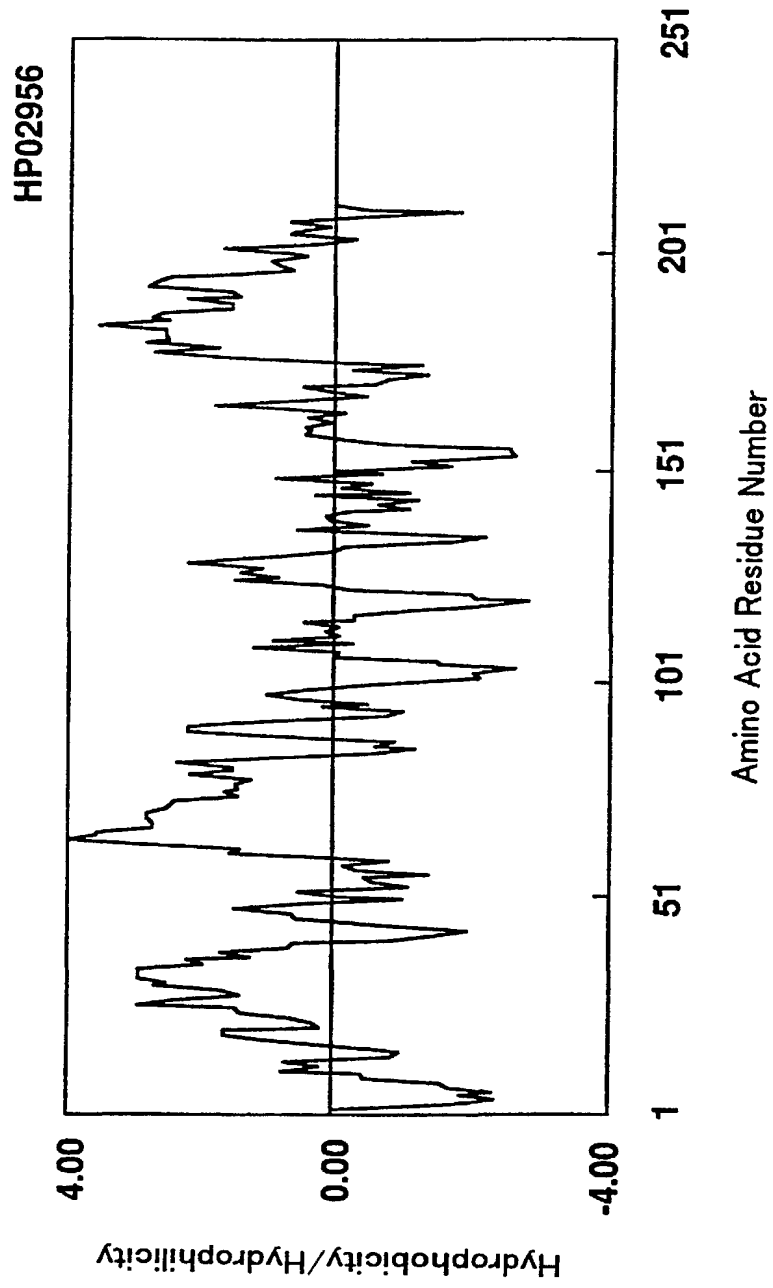
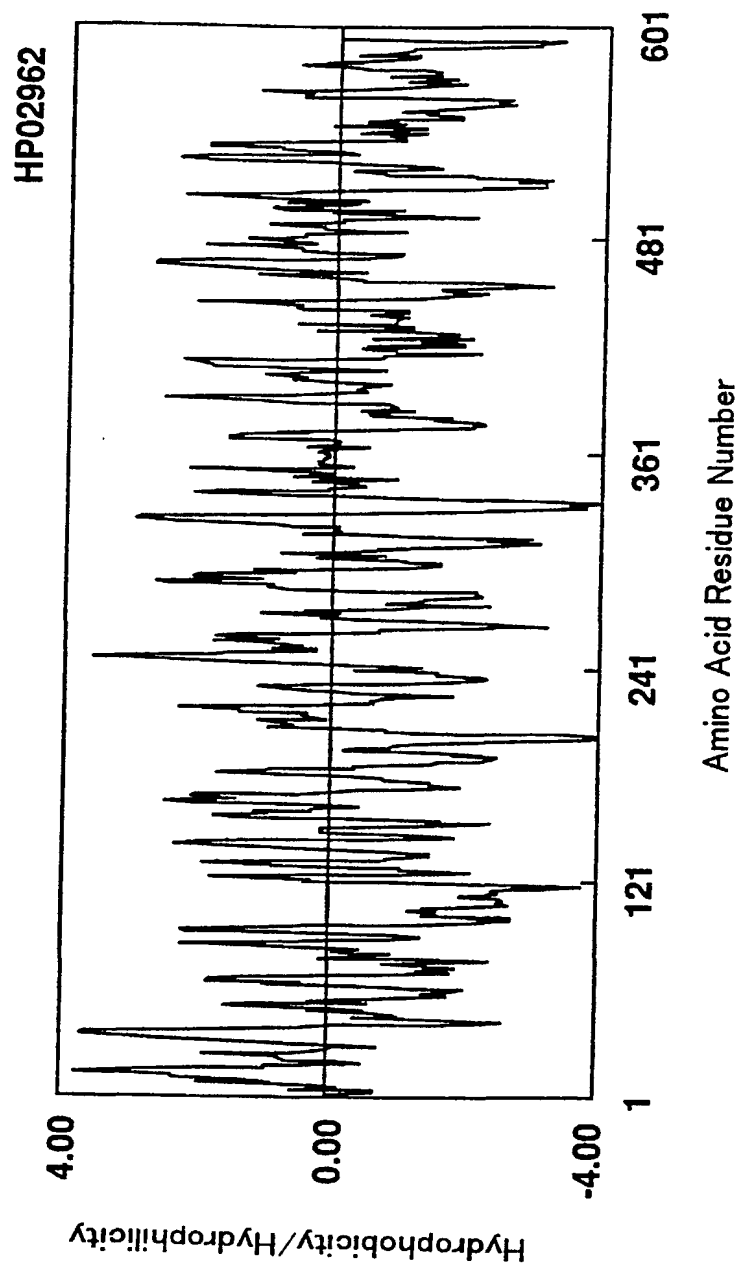


Fig.5



6/50

Fig.6

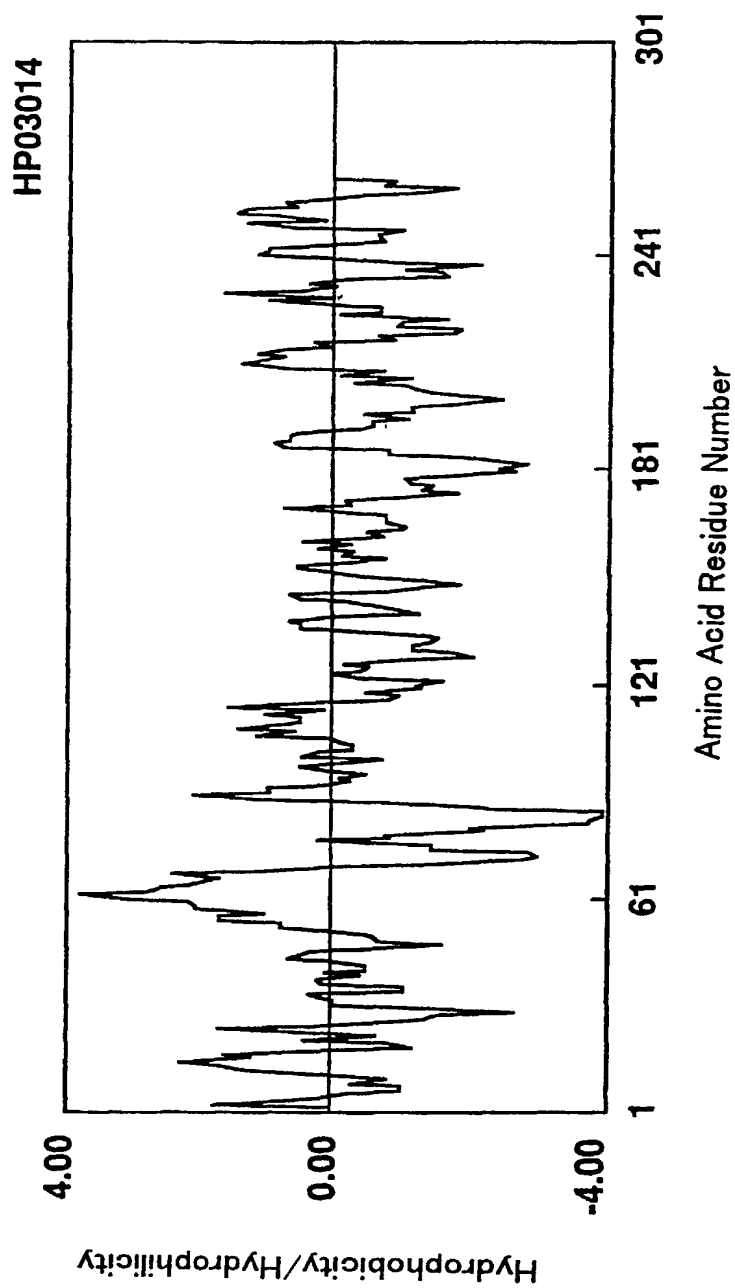


Fig.7

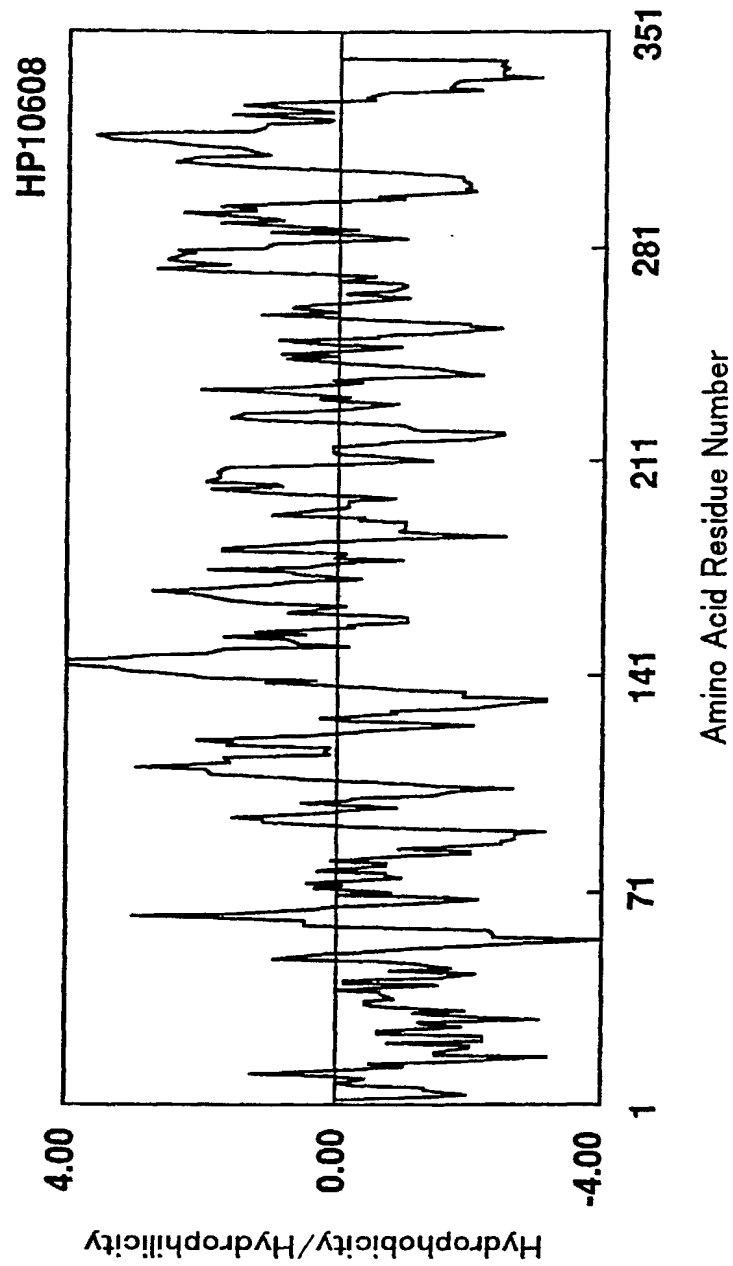
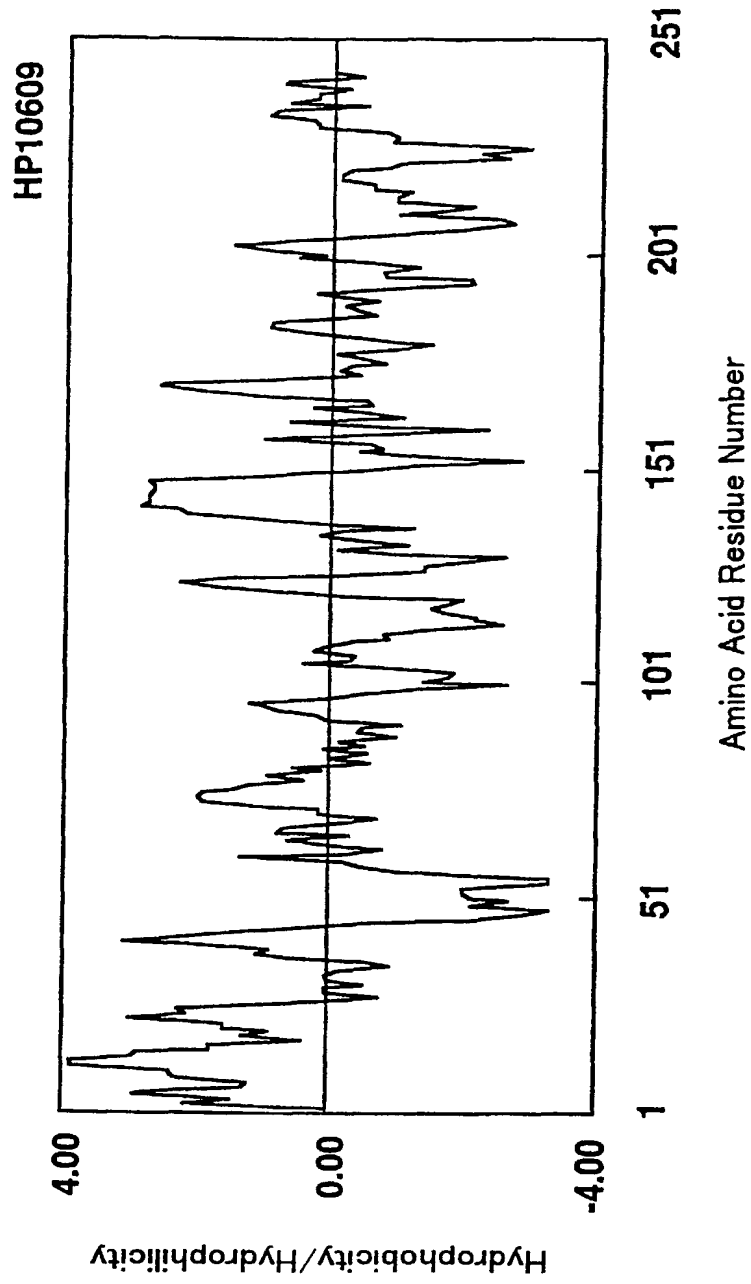


Fig.8



9/50

Fig.9

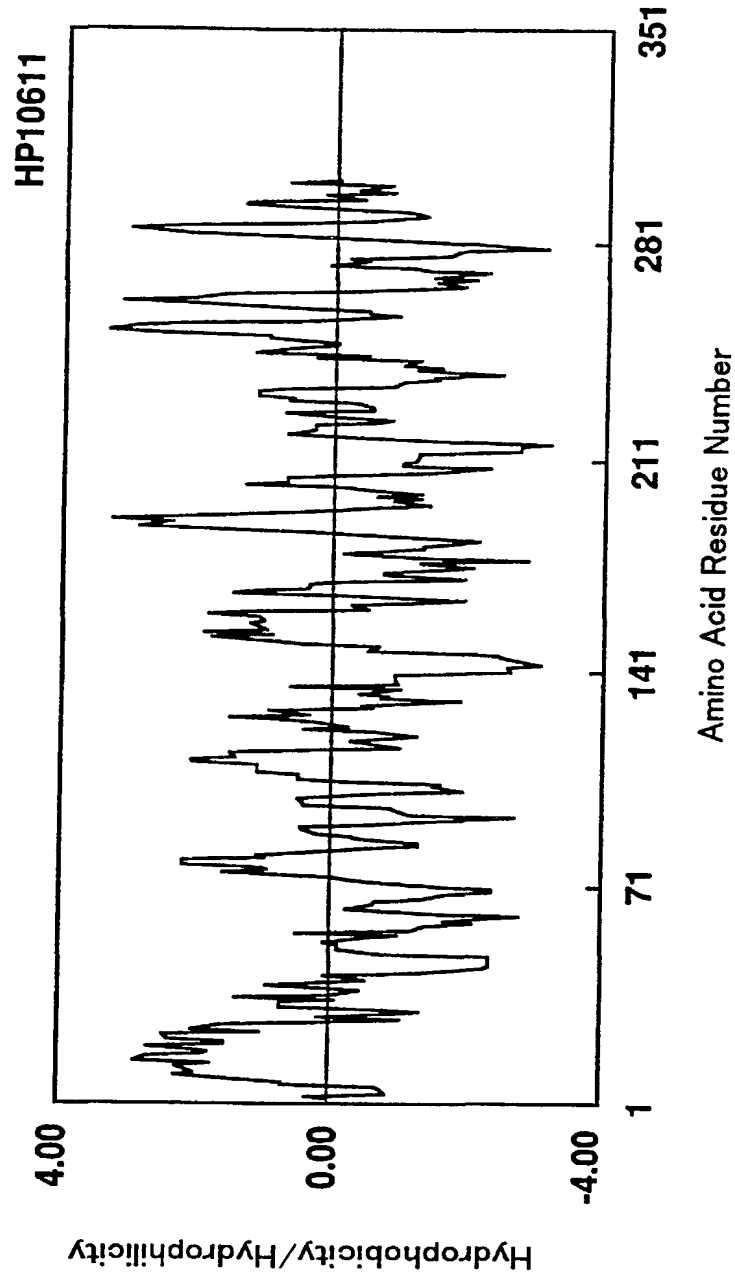
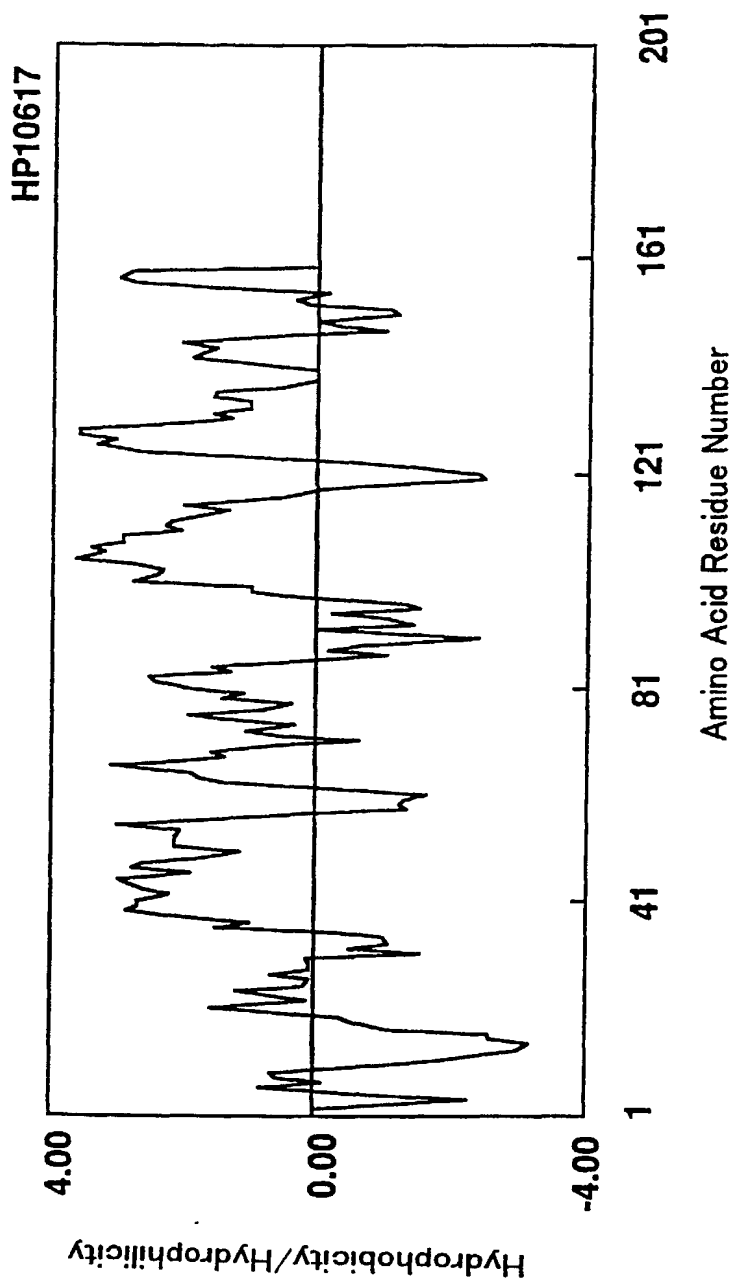


Fig.10



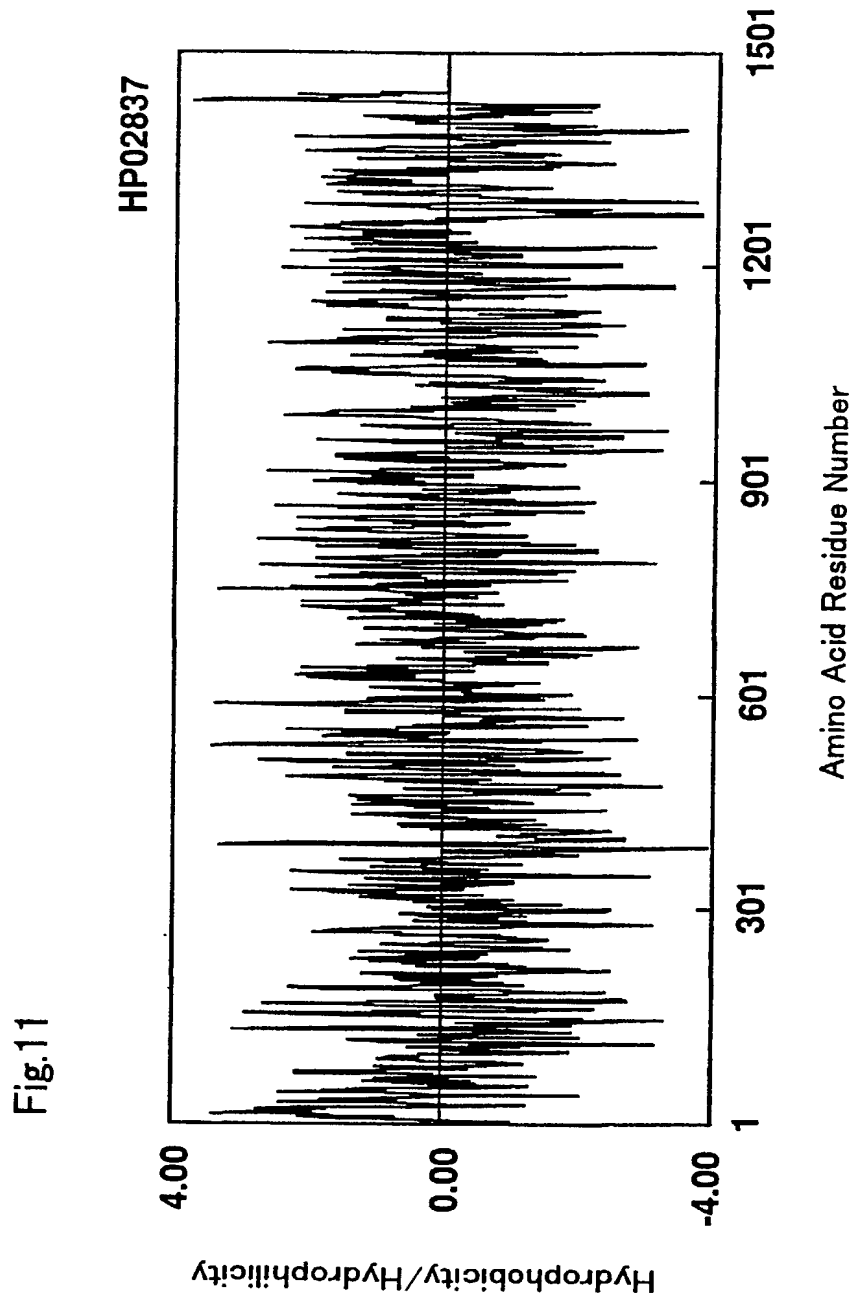
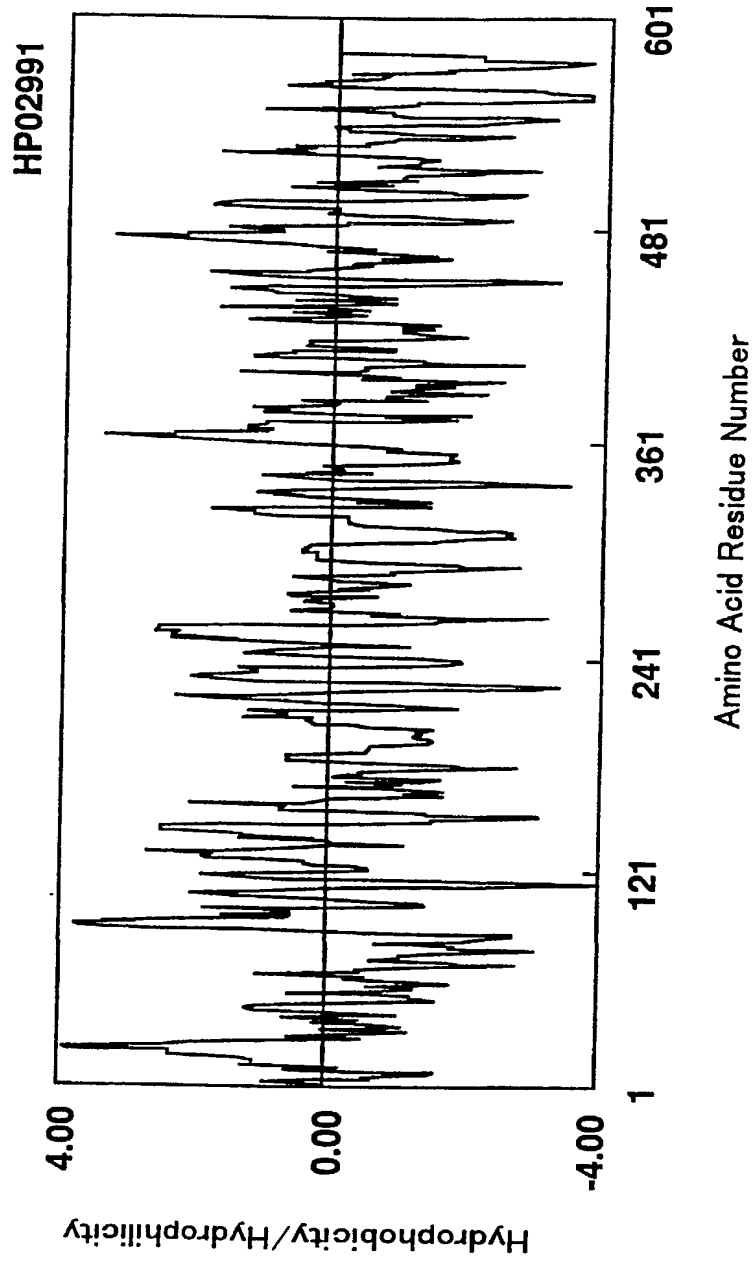


Fig.12



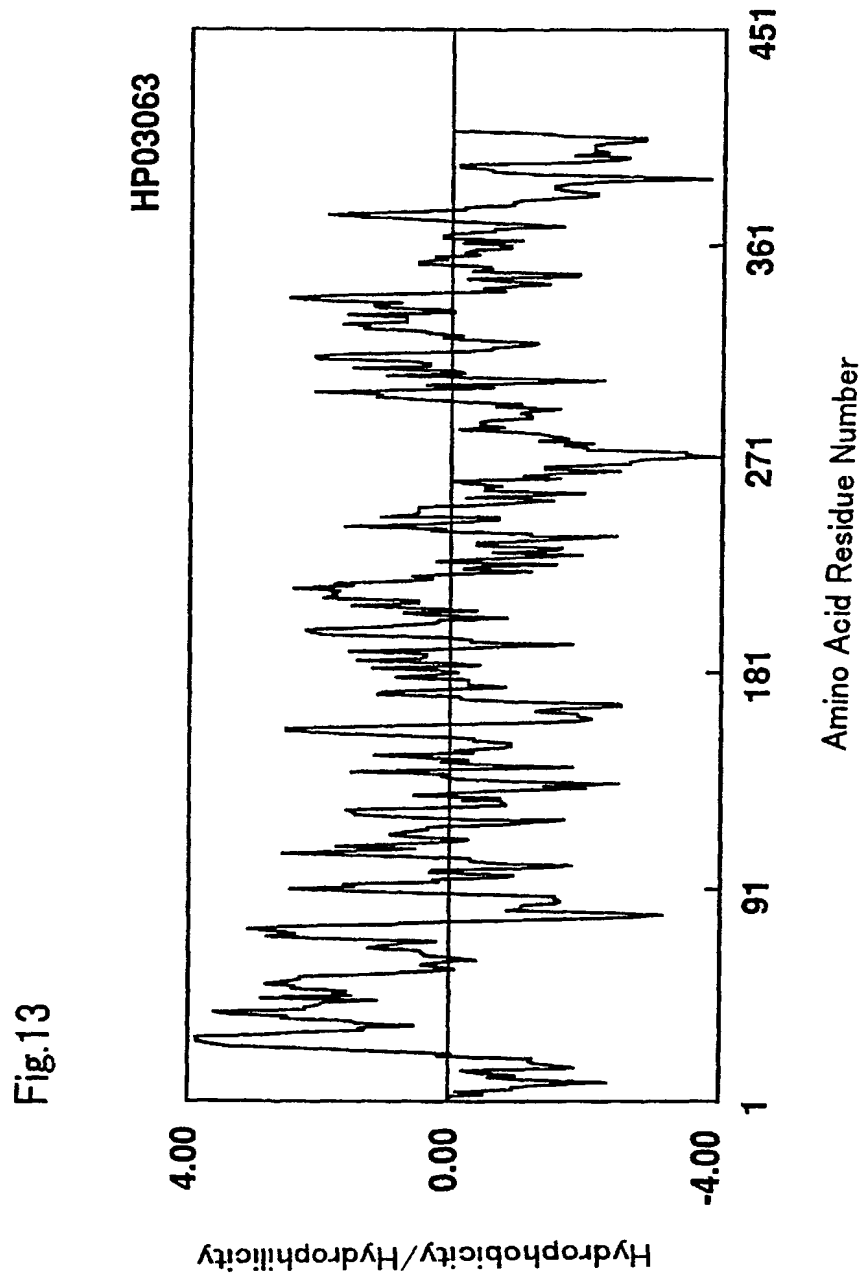


Fig.14

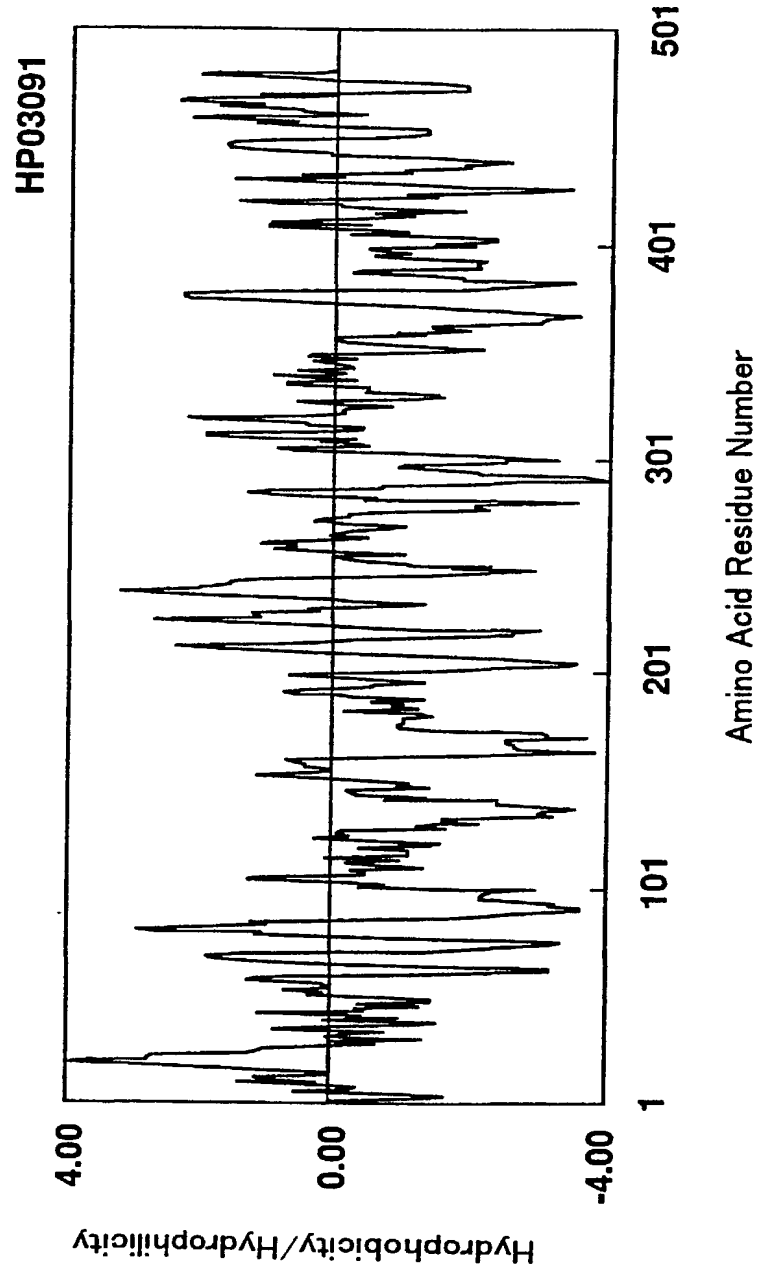


Fig.15

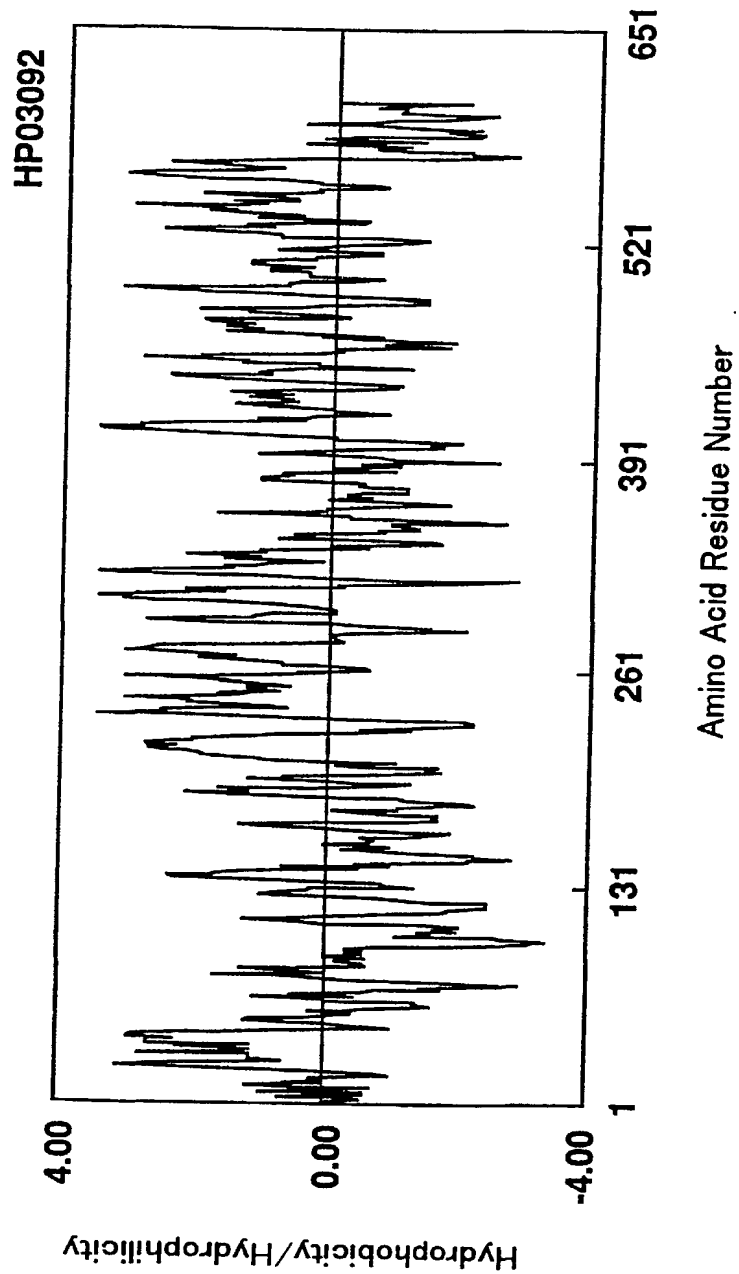


Fig.16

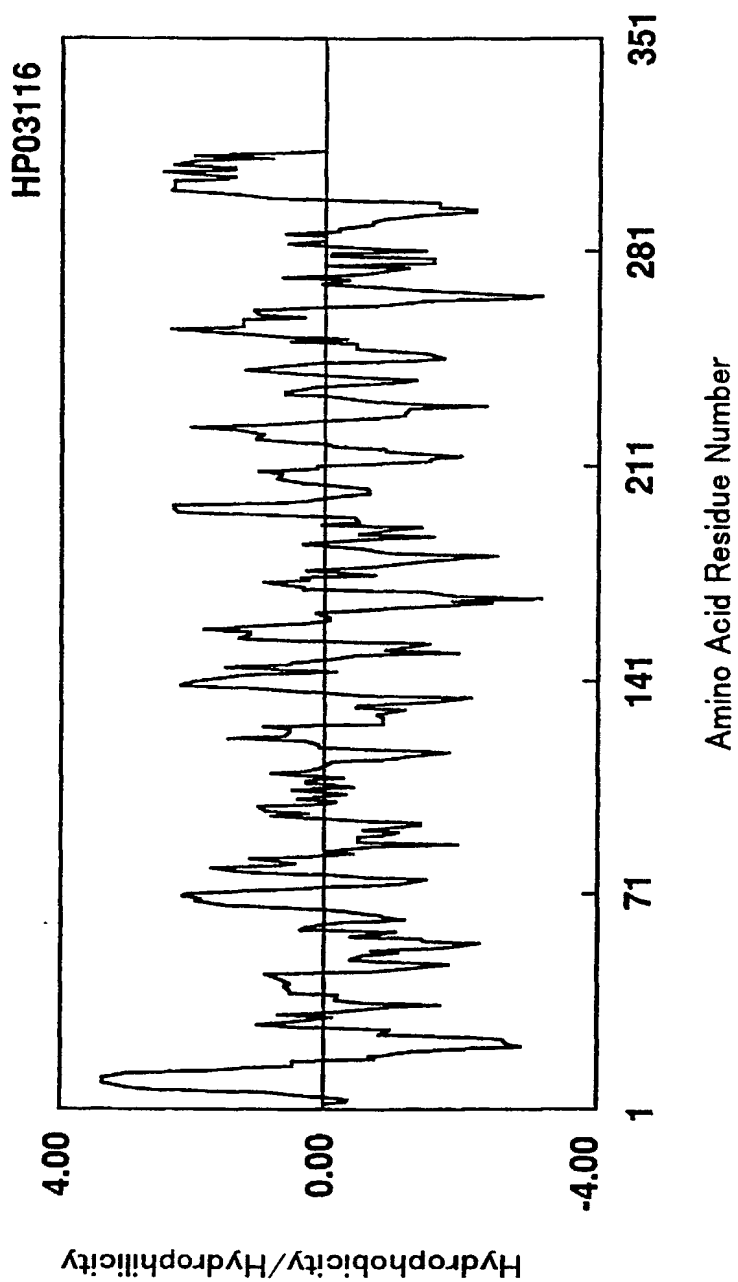
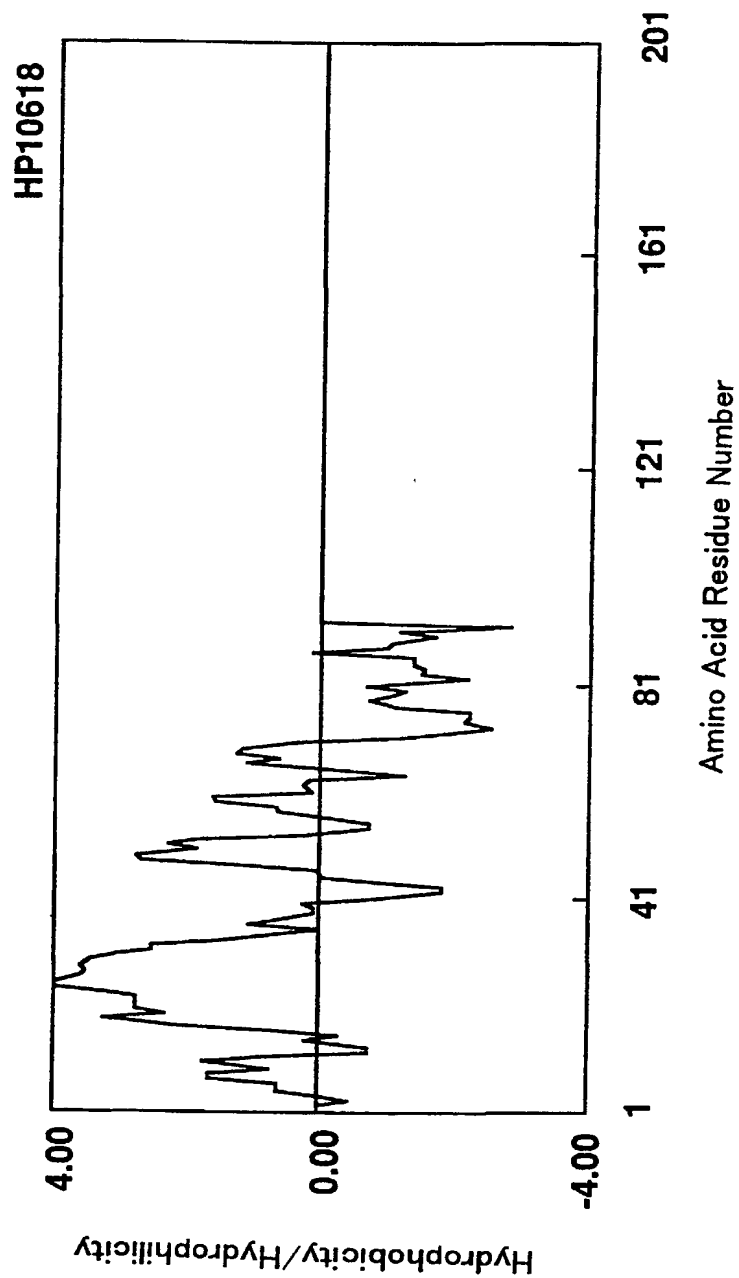


Fig.17



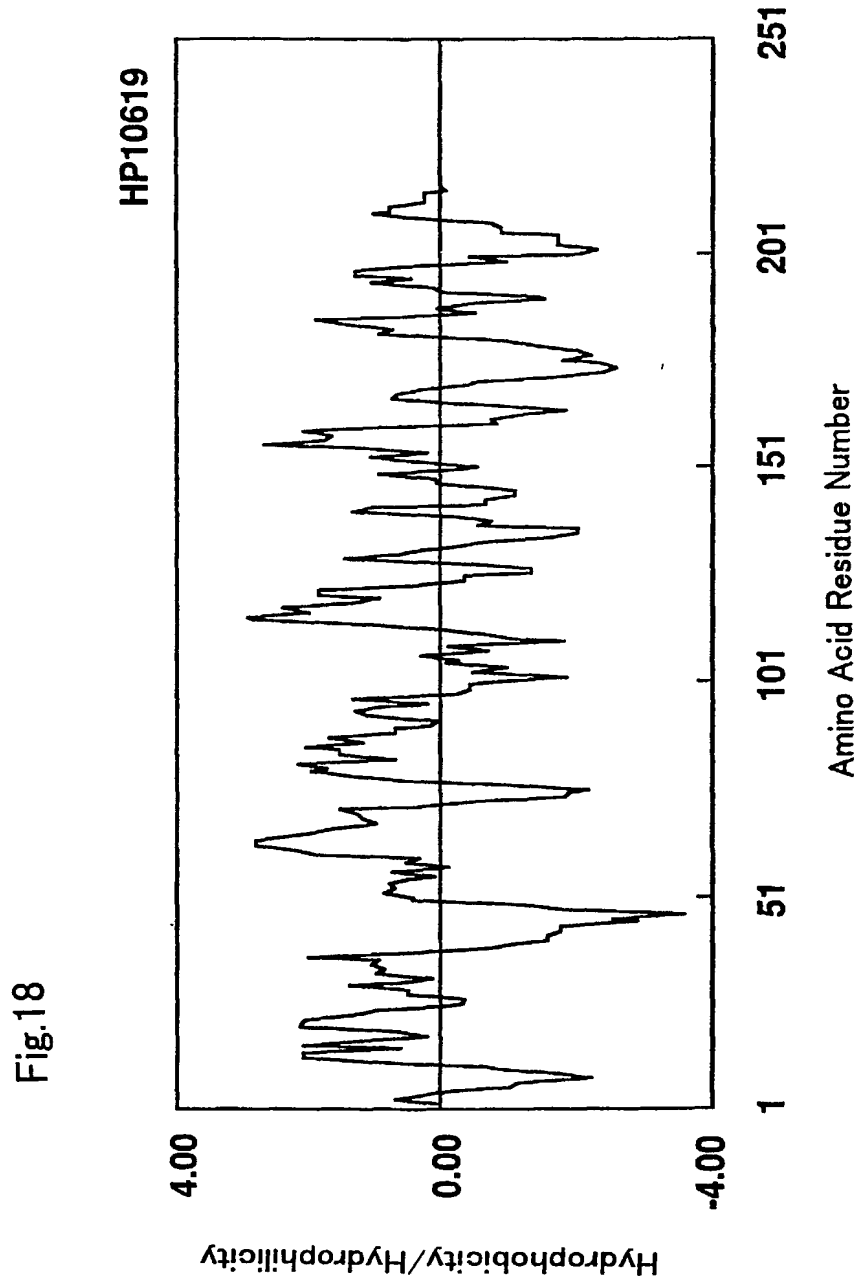
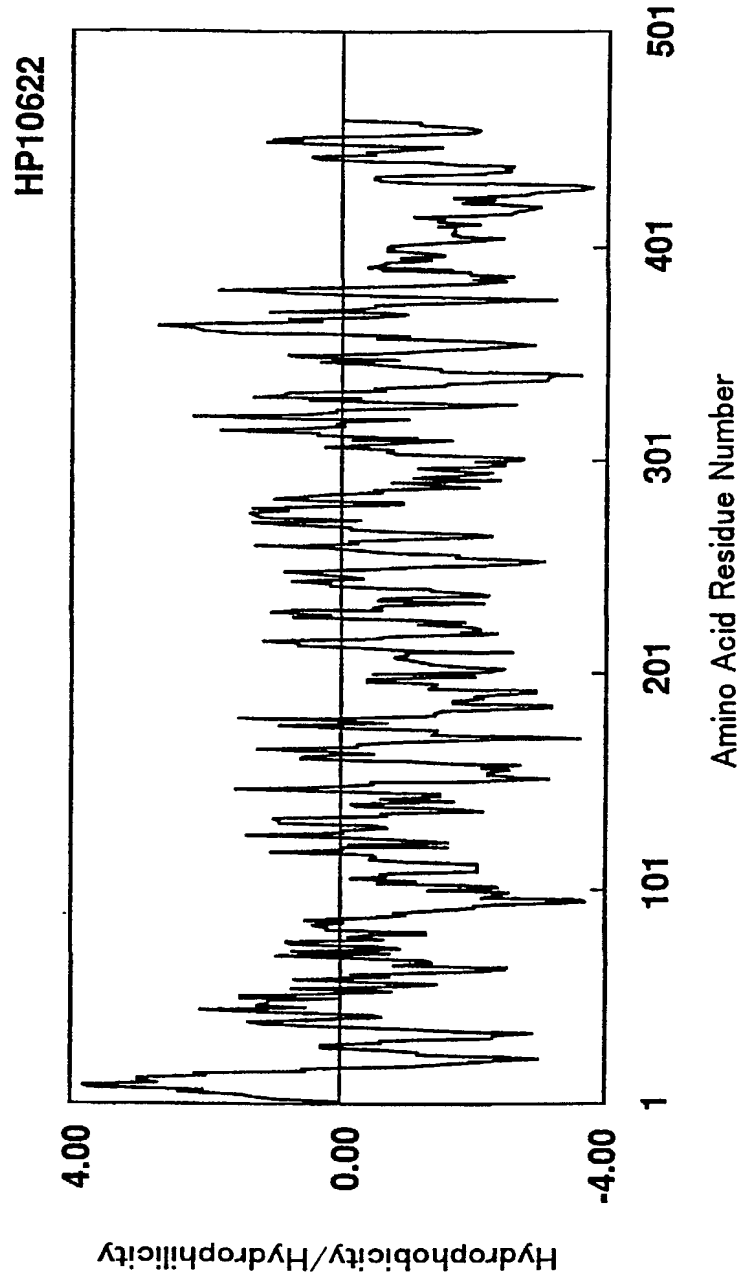


Fig.19



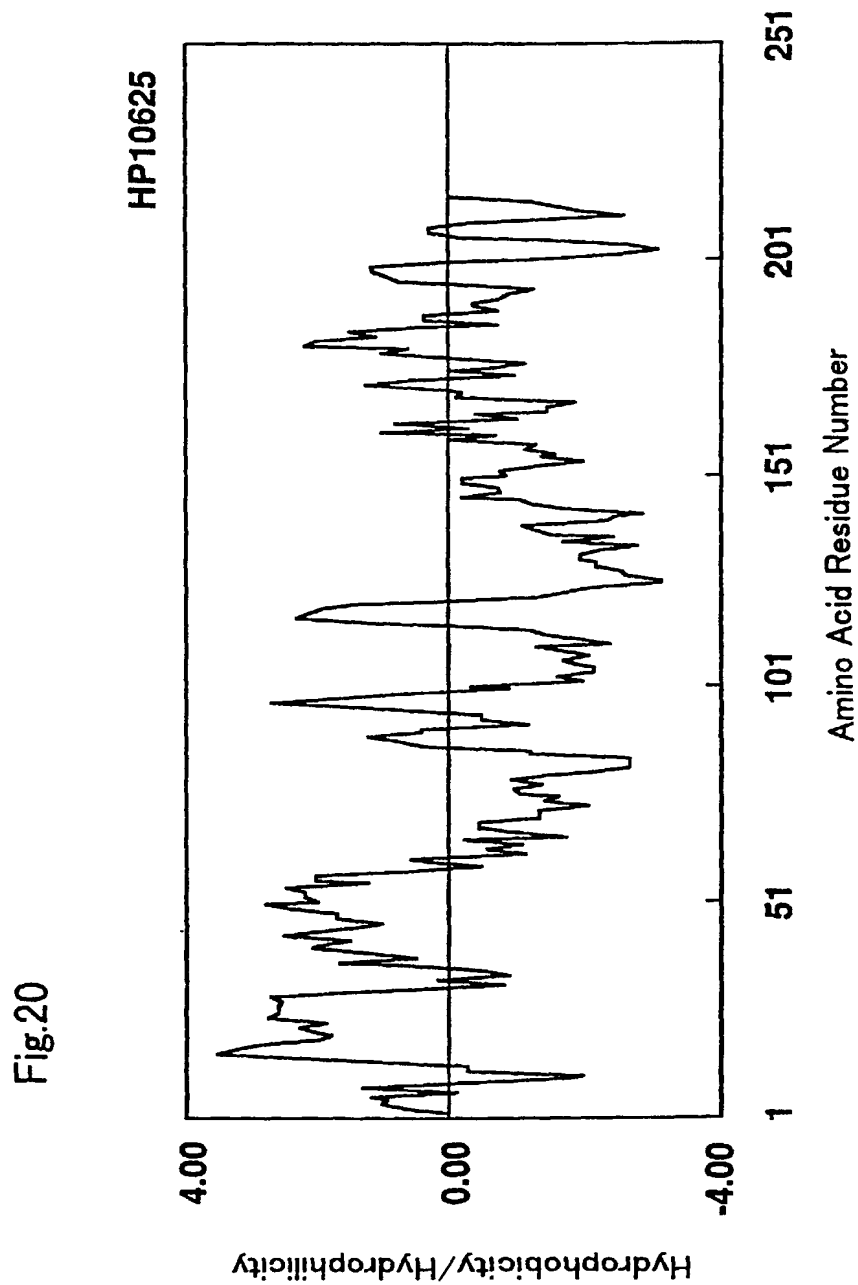


Fig.21

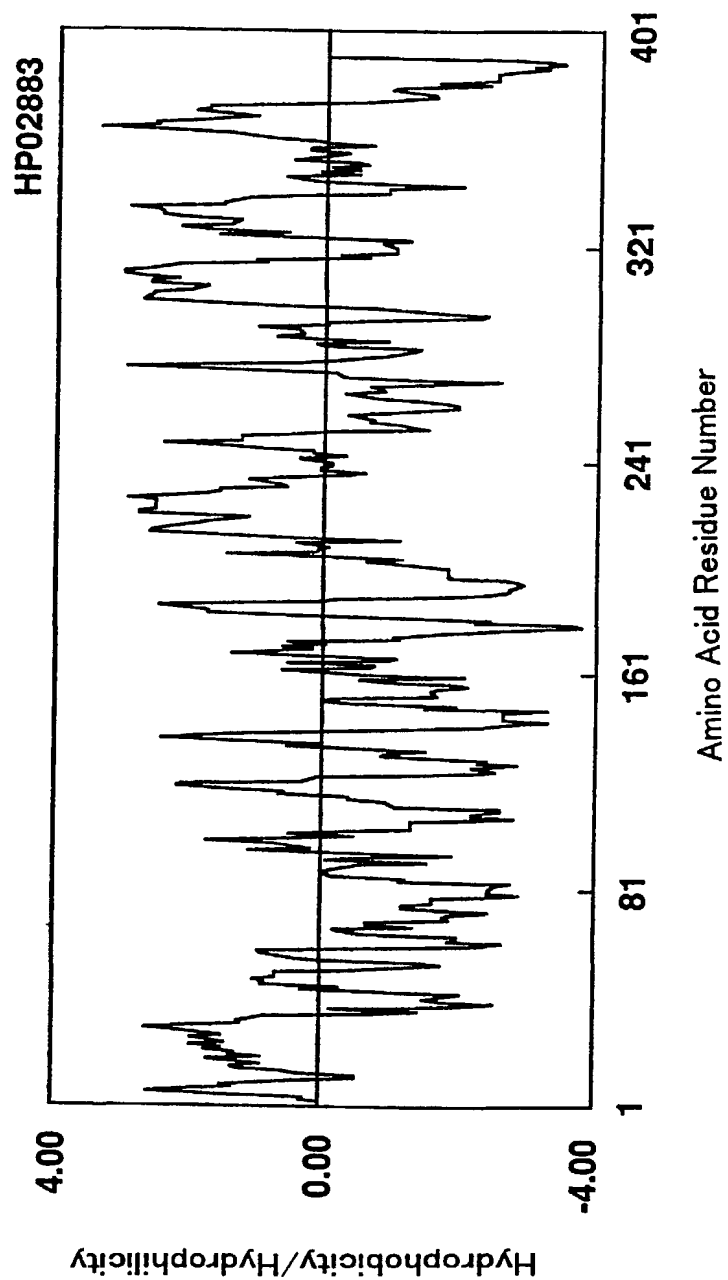


Fig.22

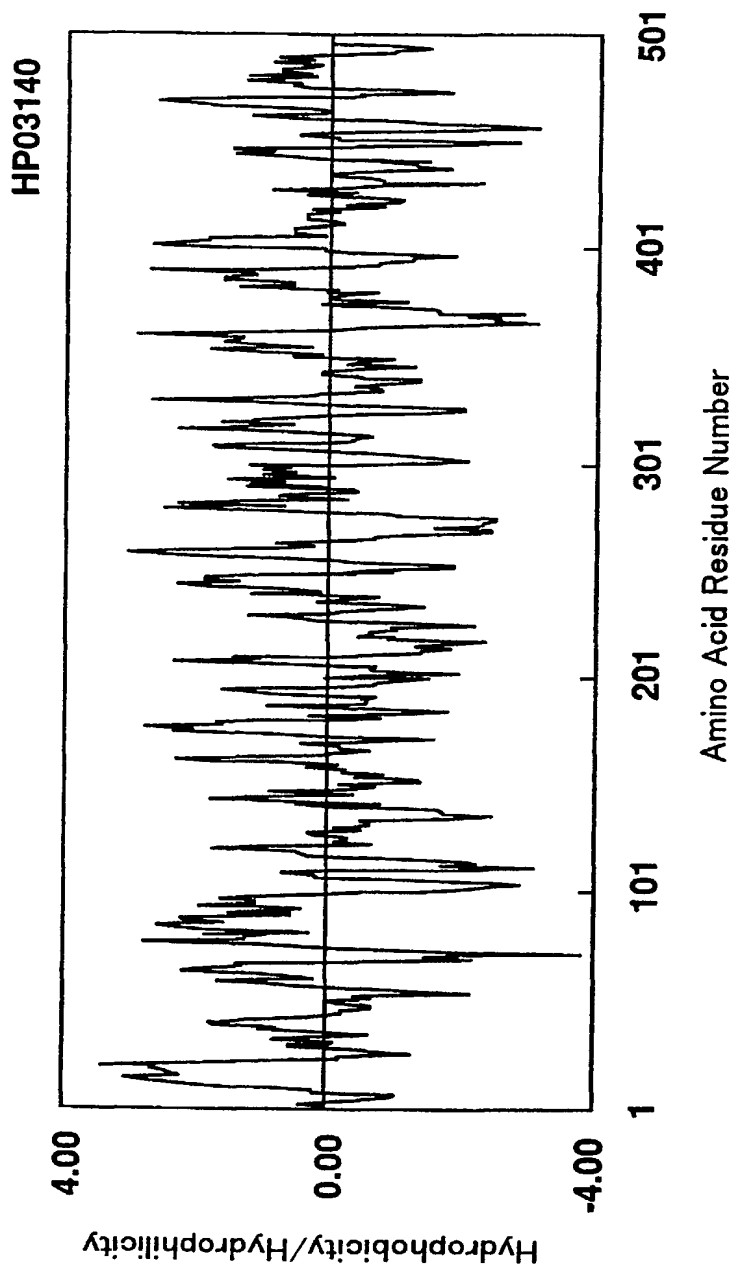
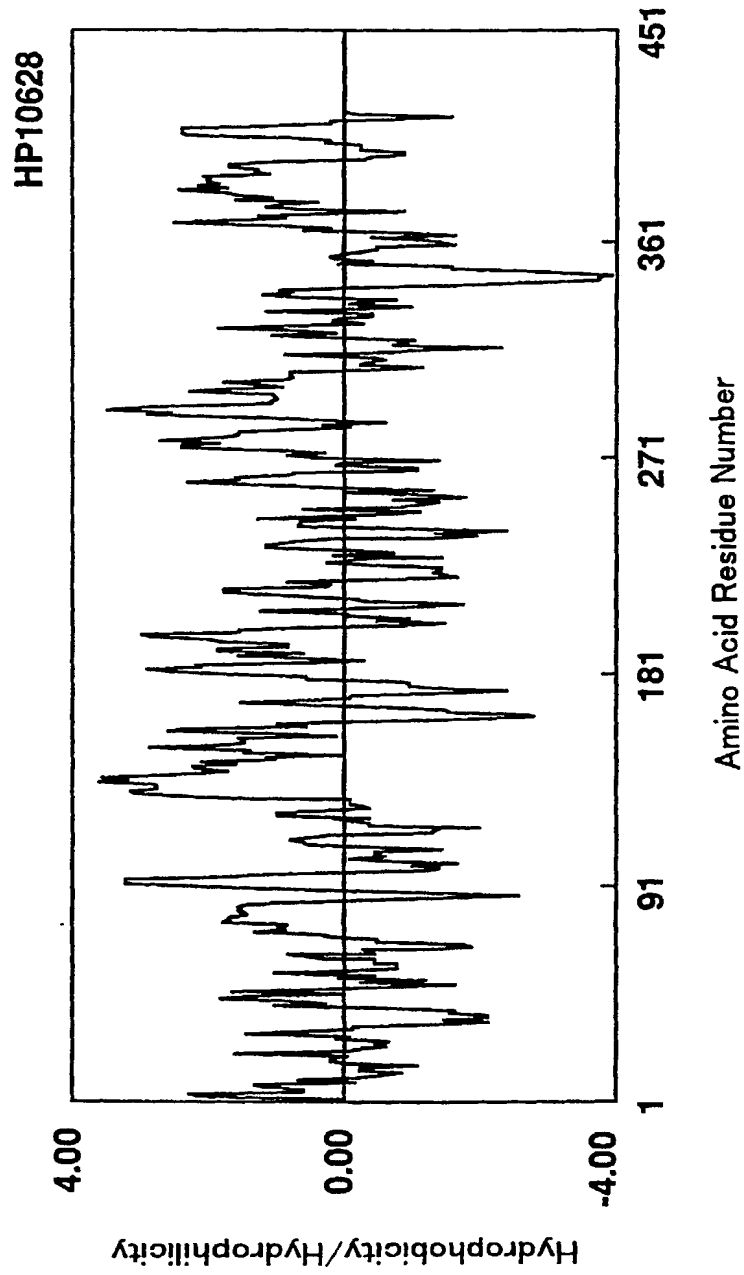


Fig.23



24/50

Fig.24

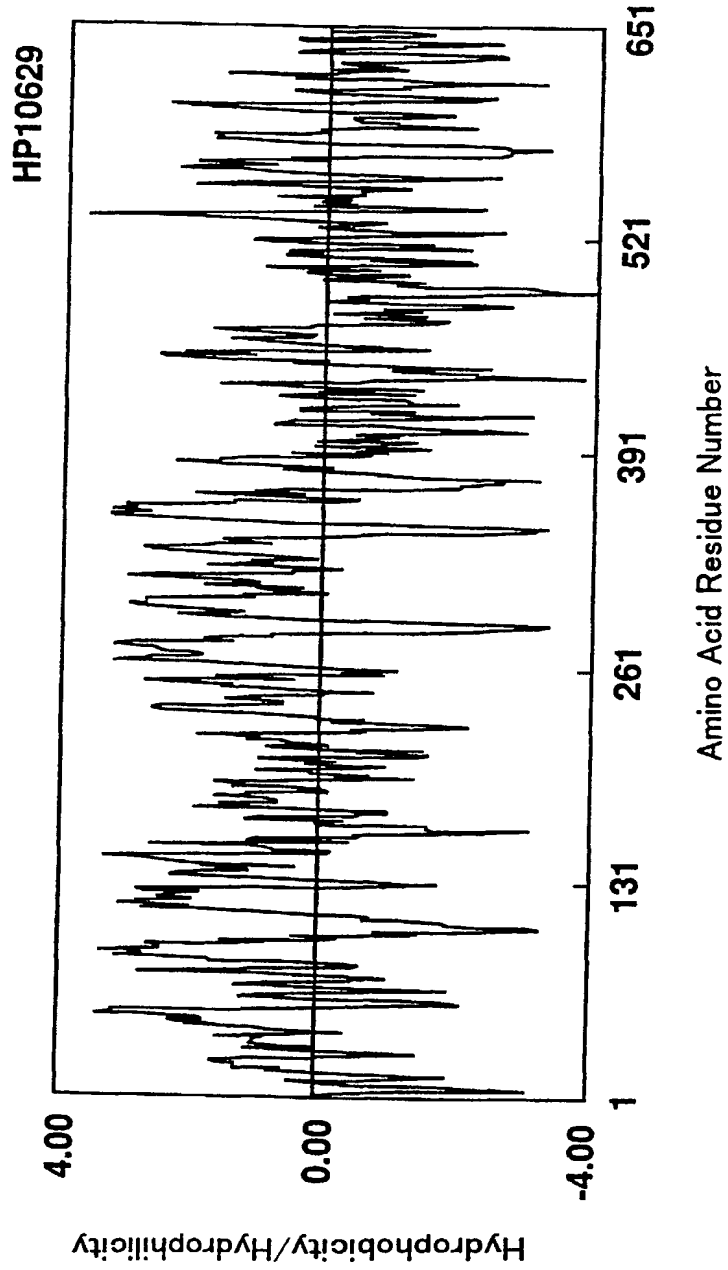
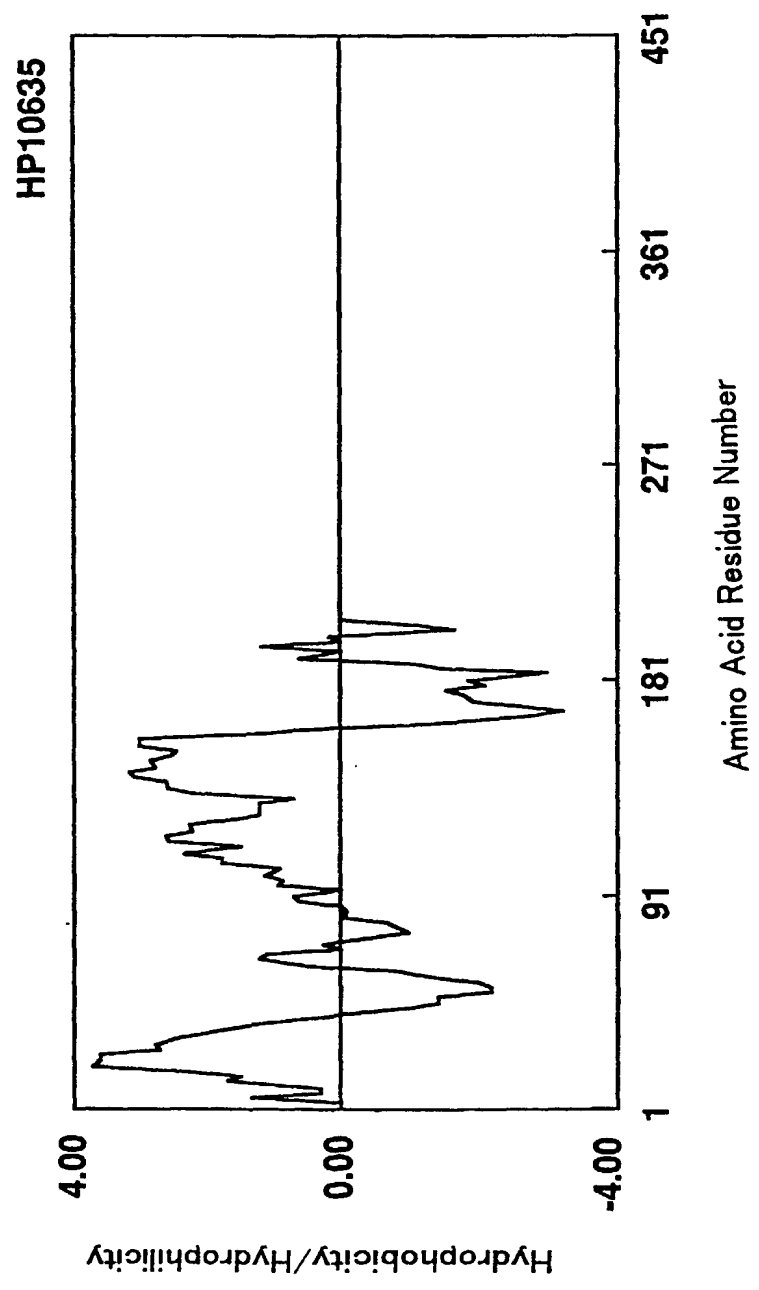
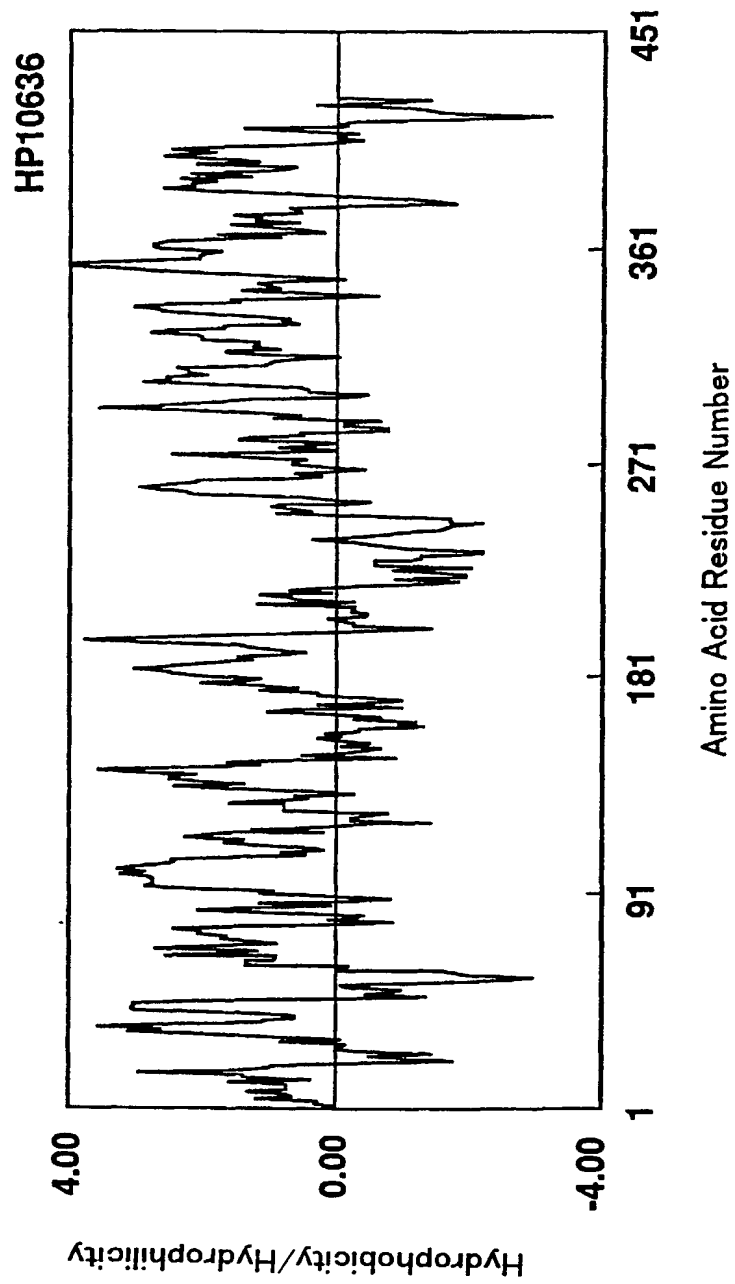


Fig.25



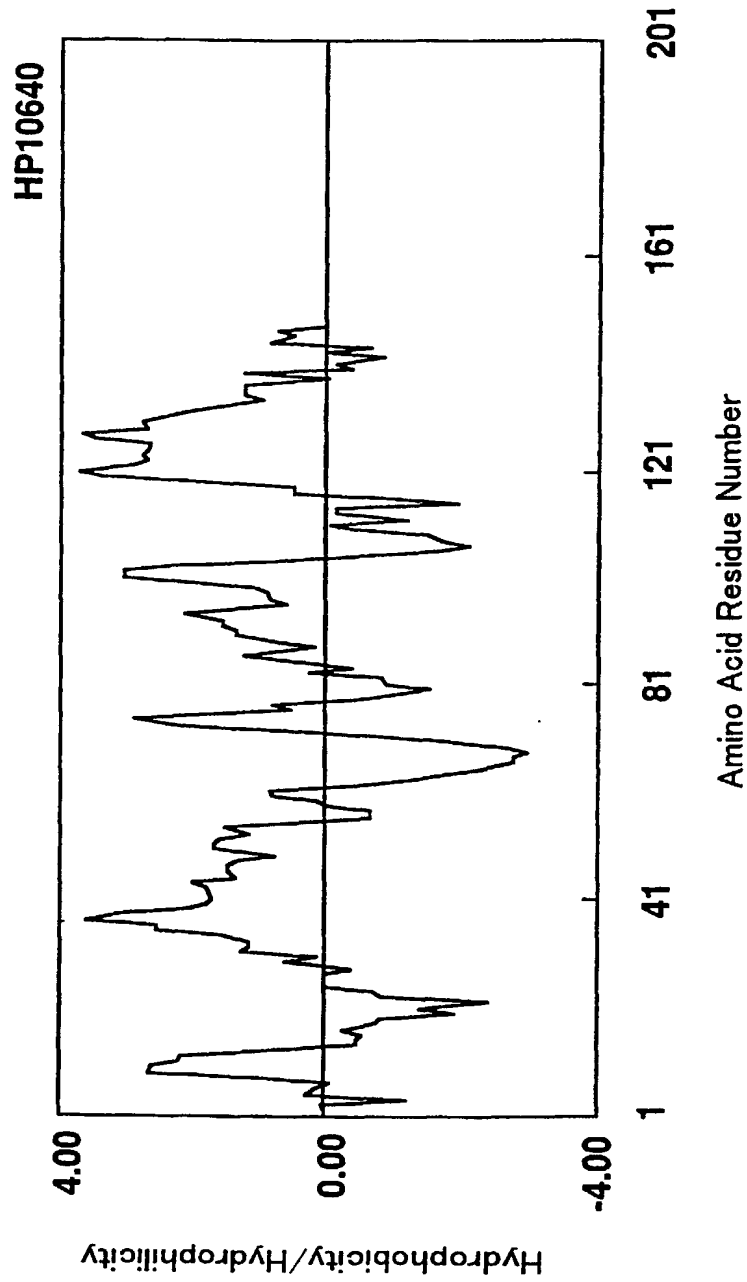
26/50

Fig.26



27/50

Fig.27



28/50

Fig.28

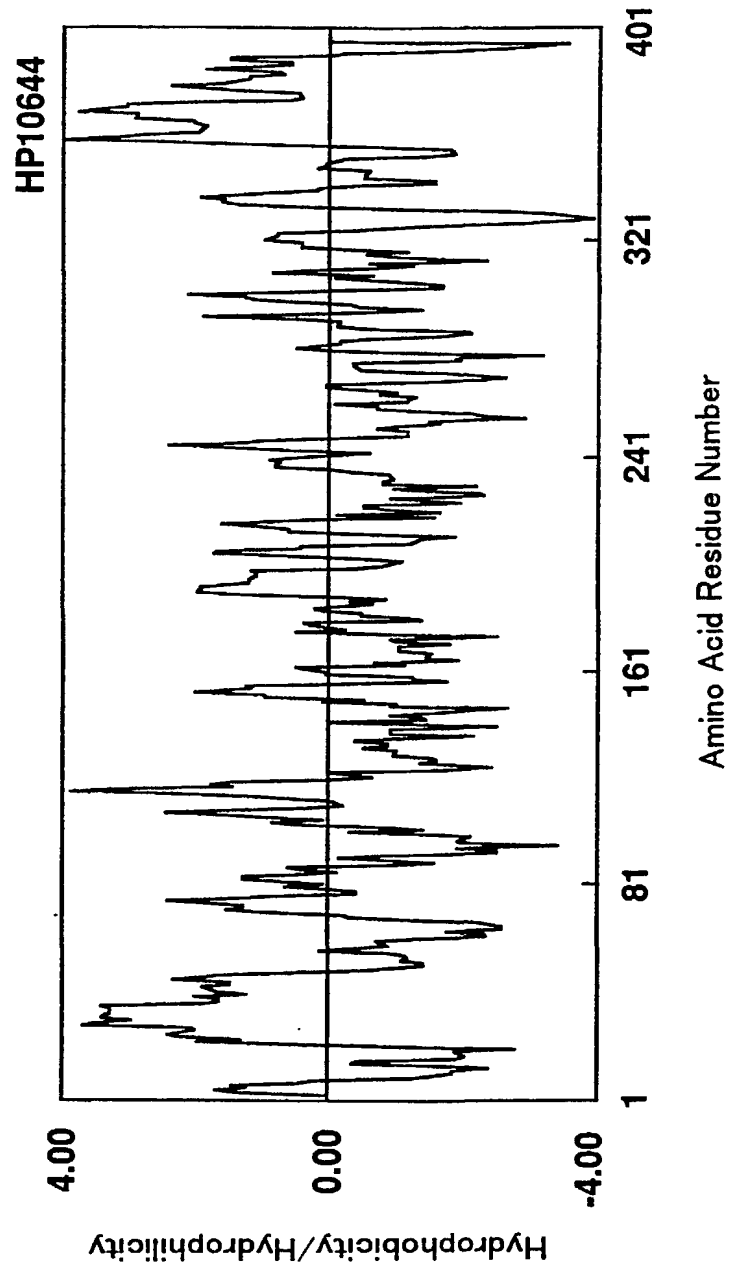
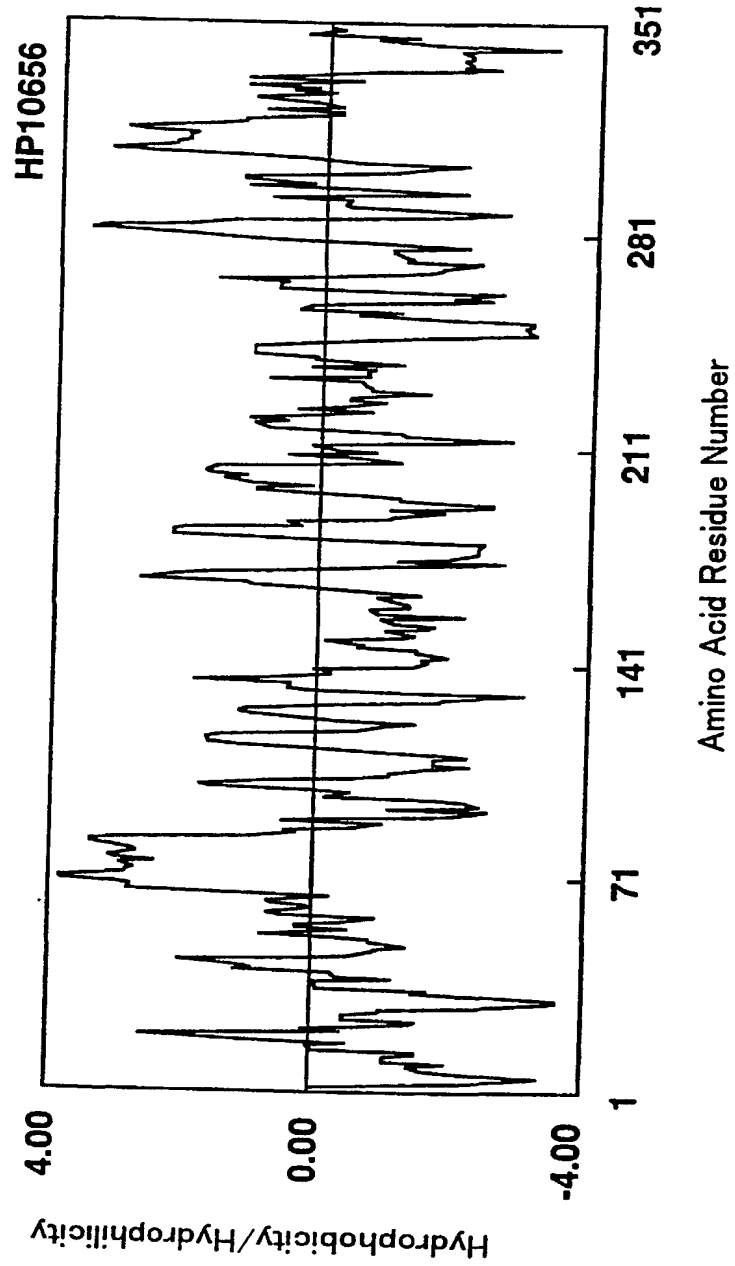
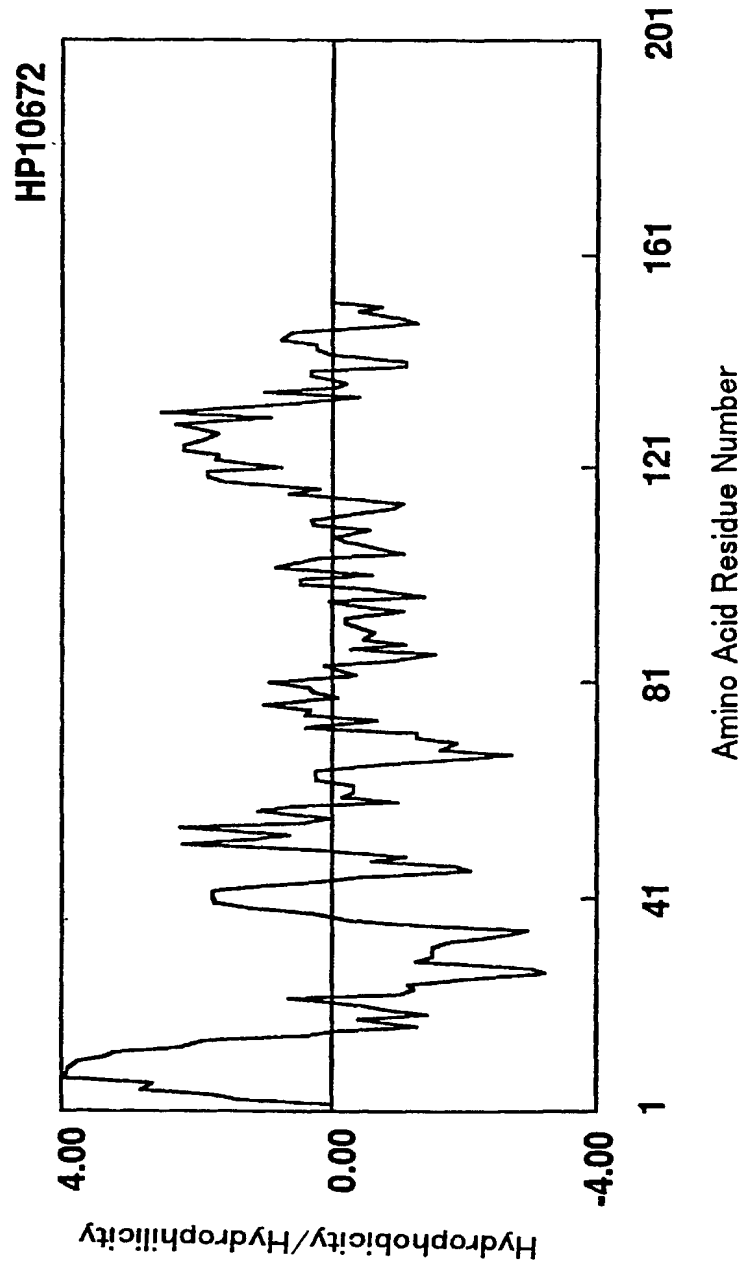


Fig.29

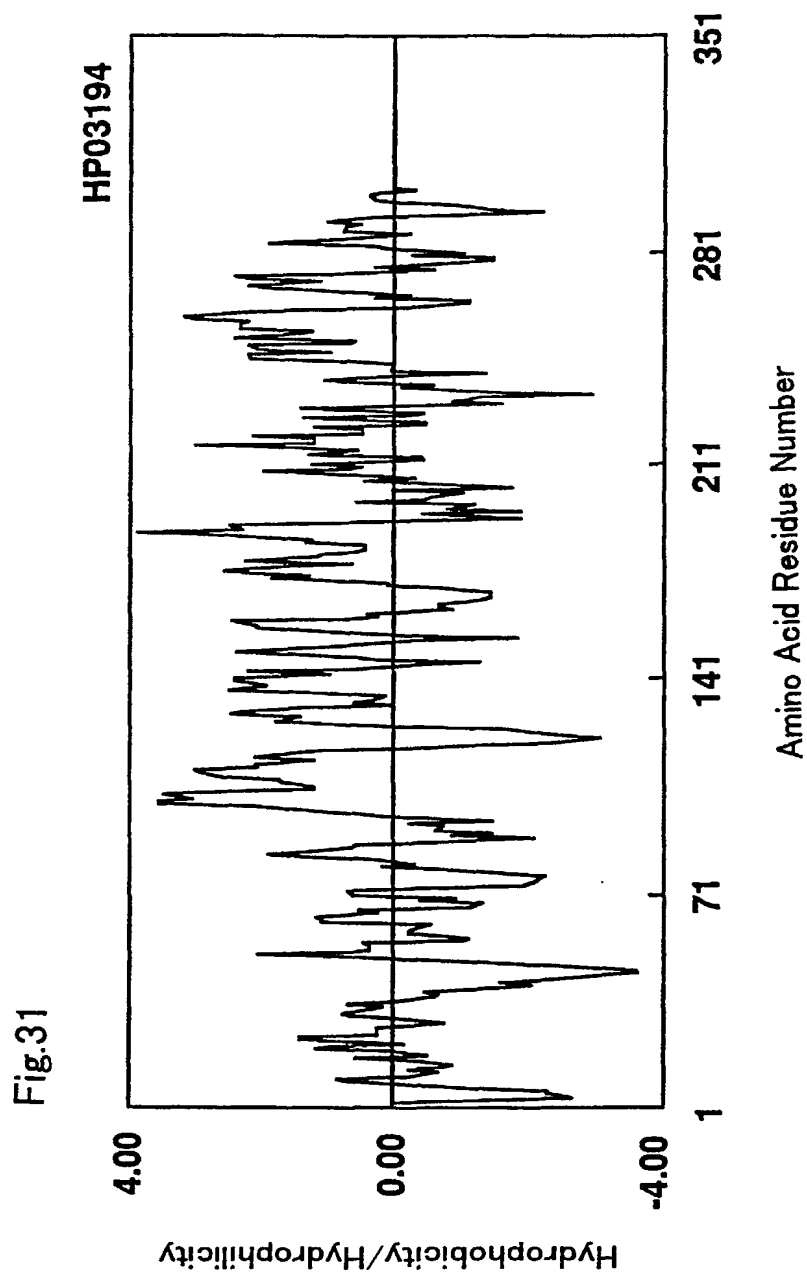


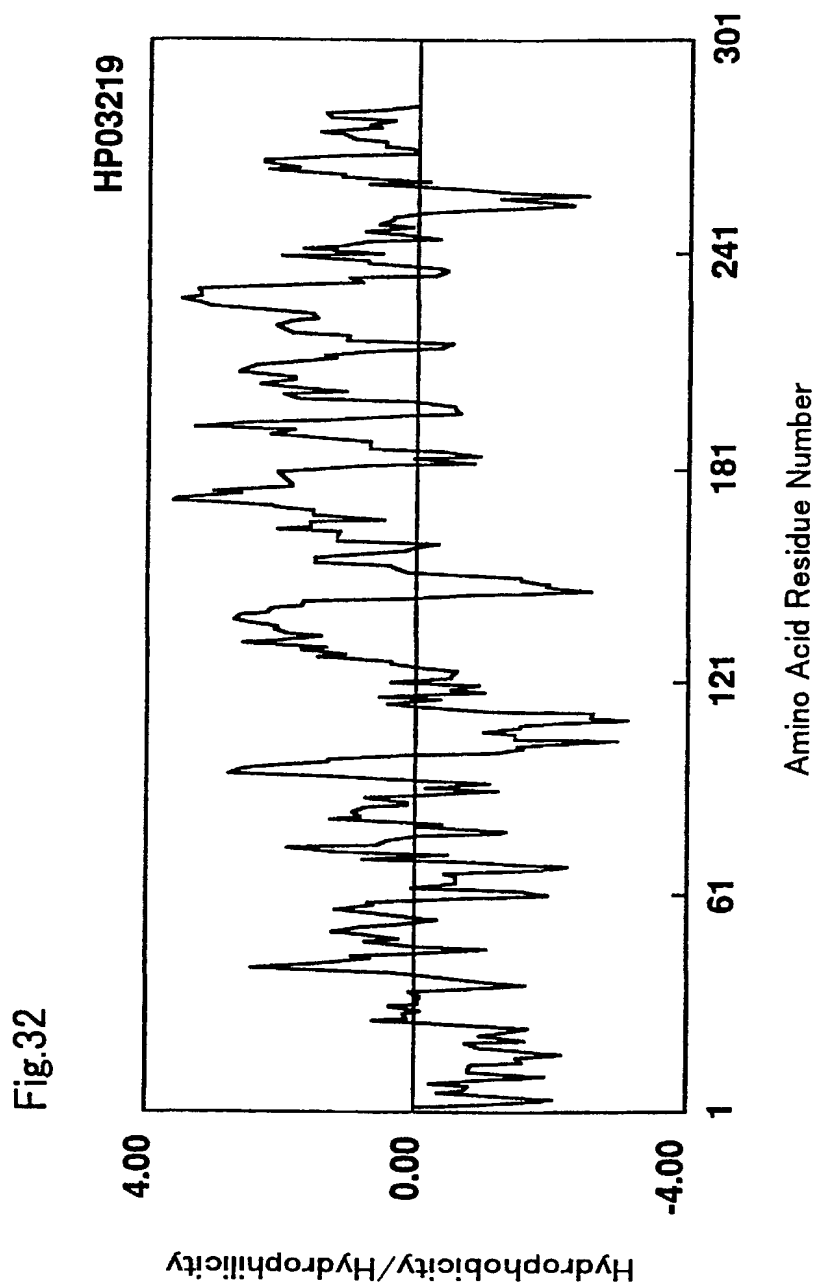
30/50

Fig.30

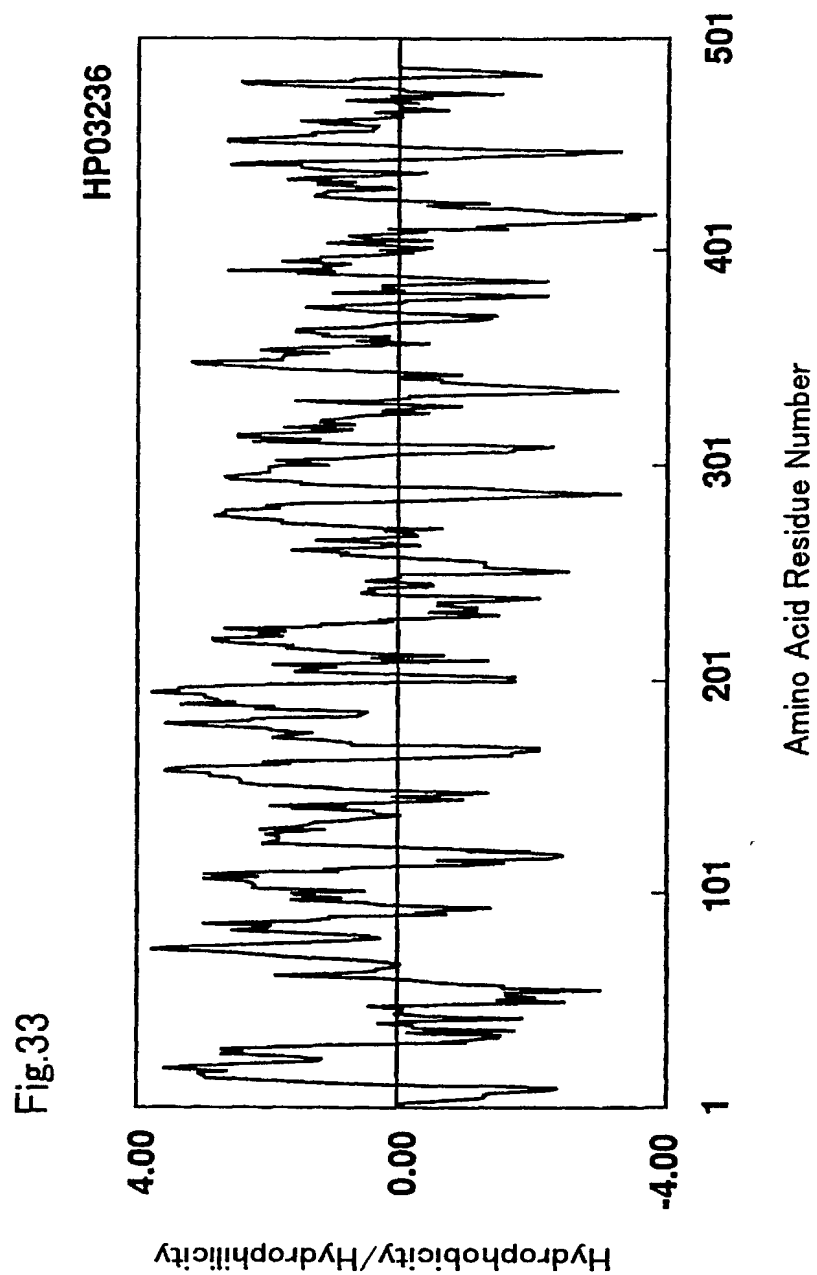


31/50

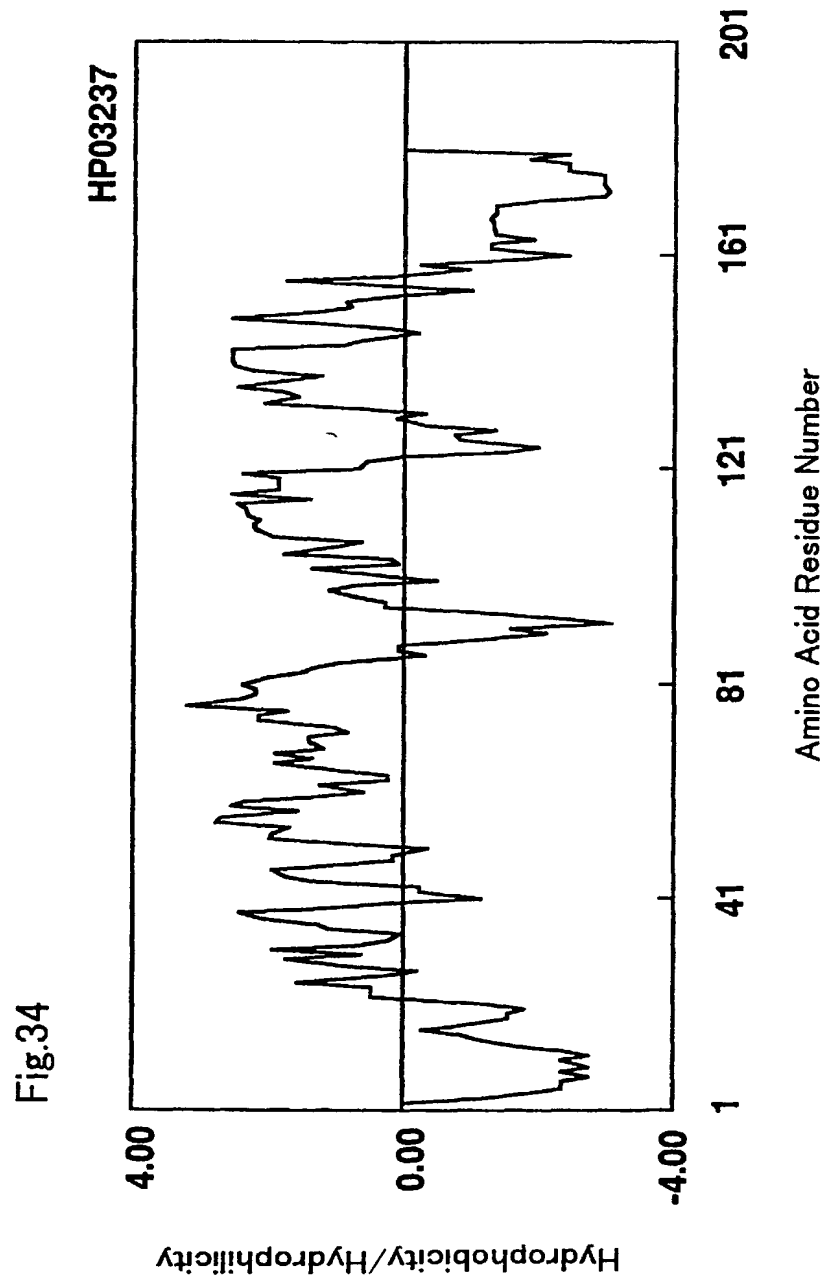




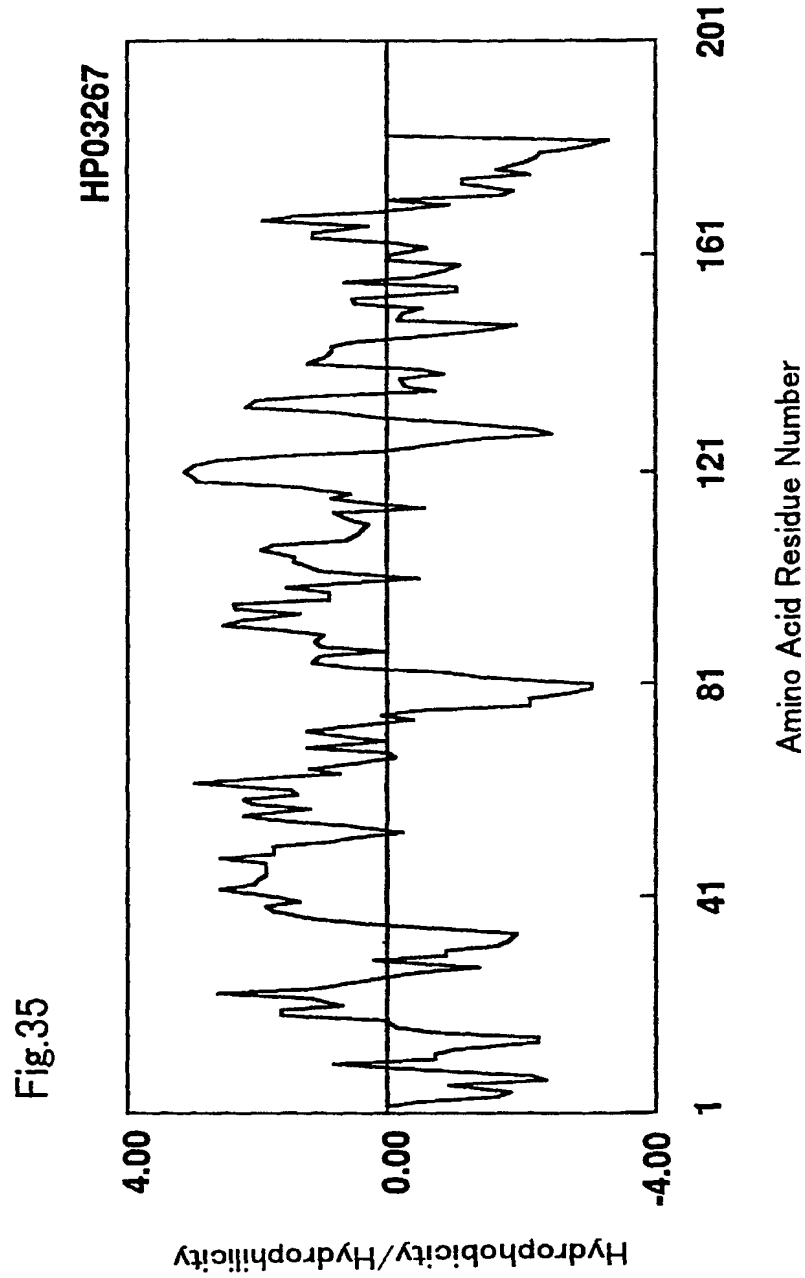
33/50



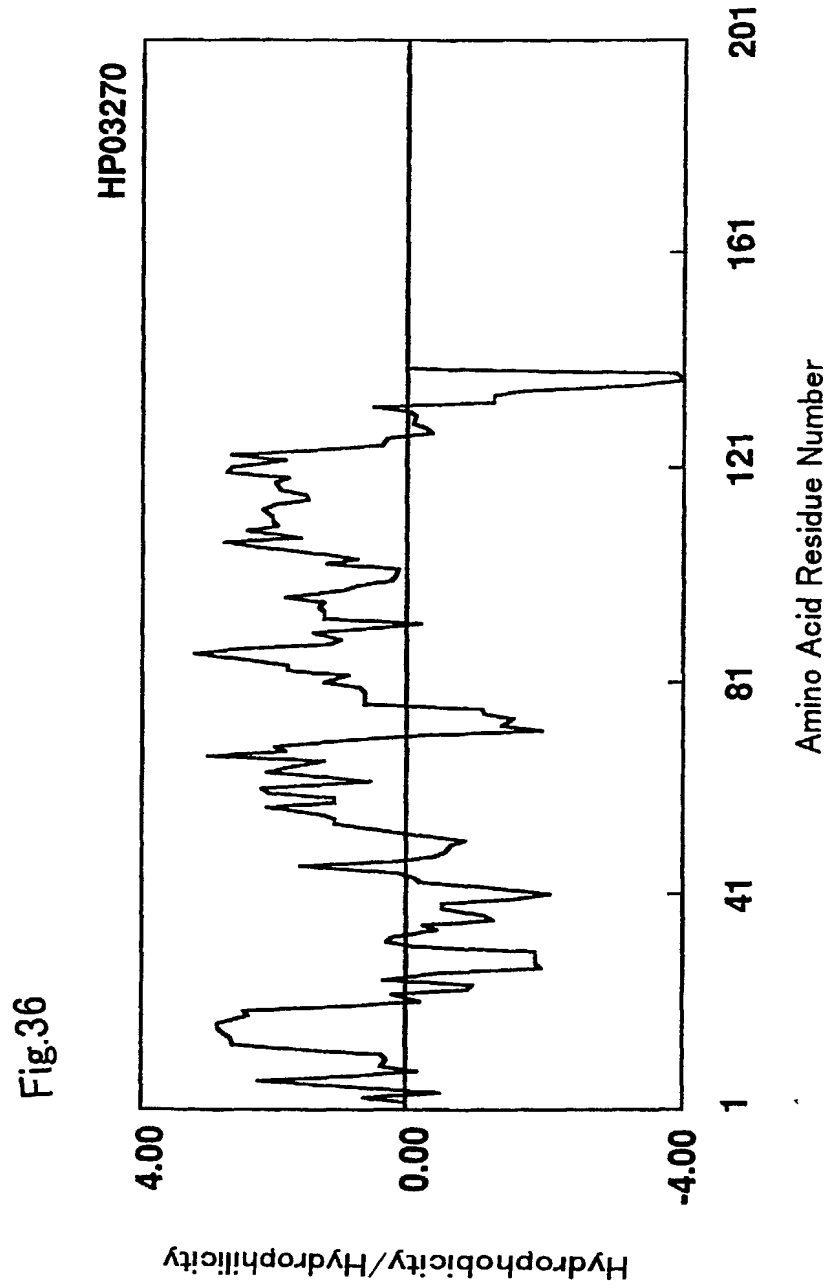
34/50



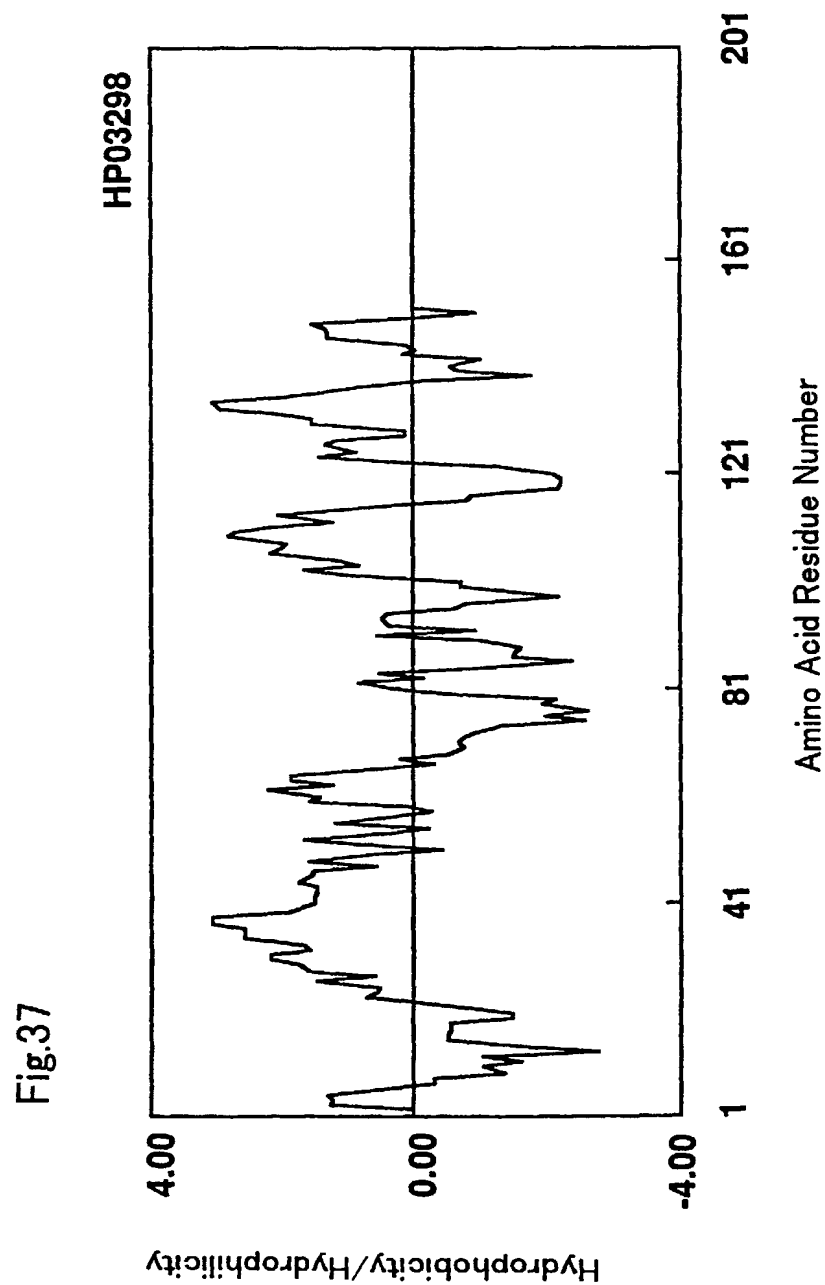
35/50



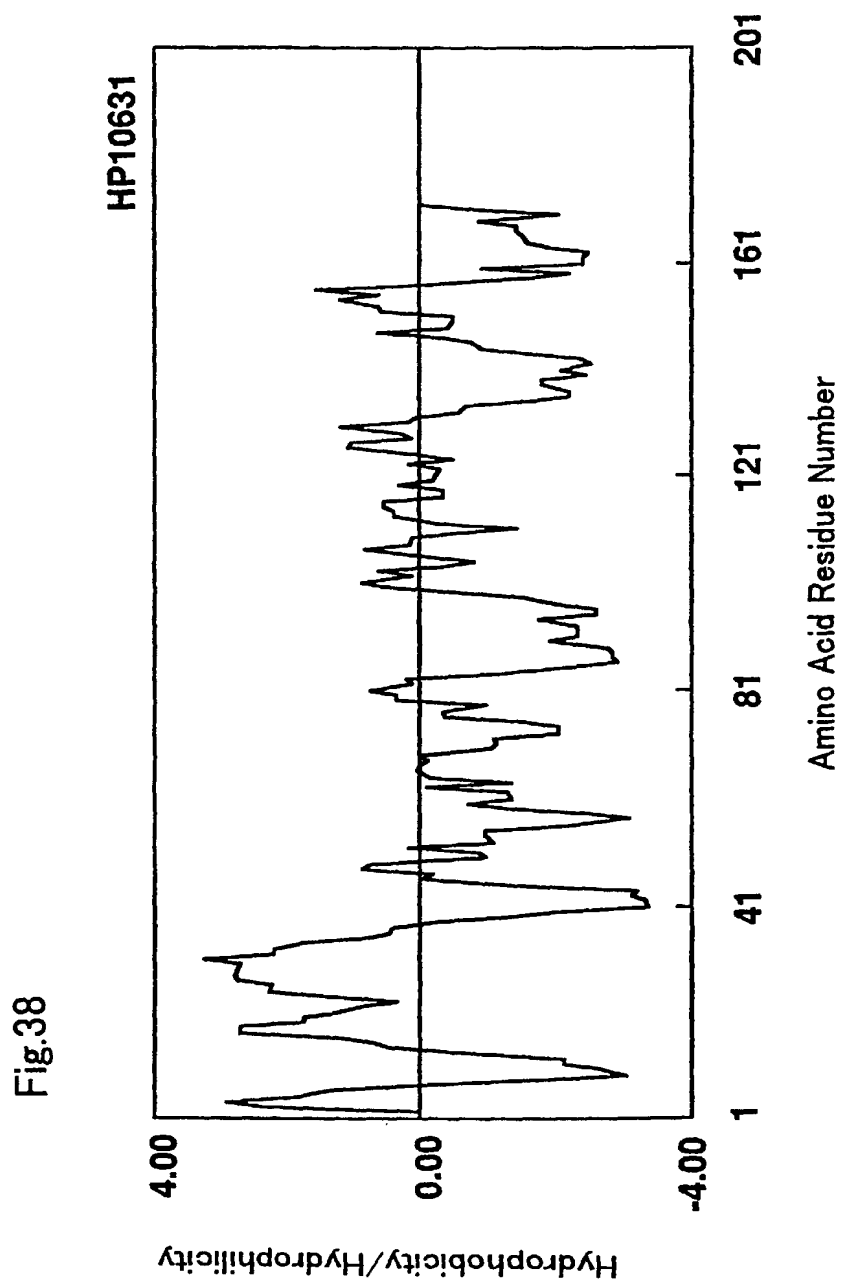
36/50



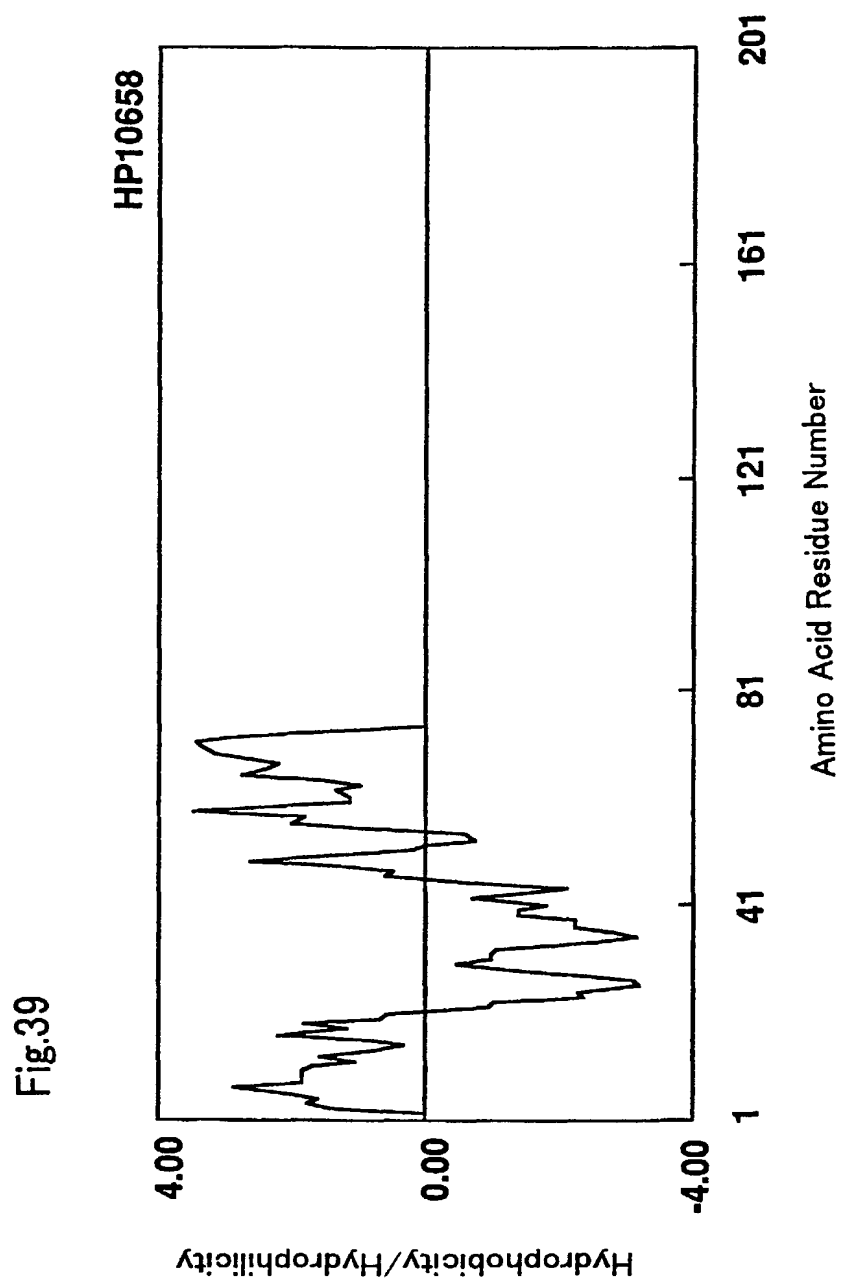
37/50

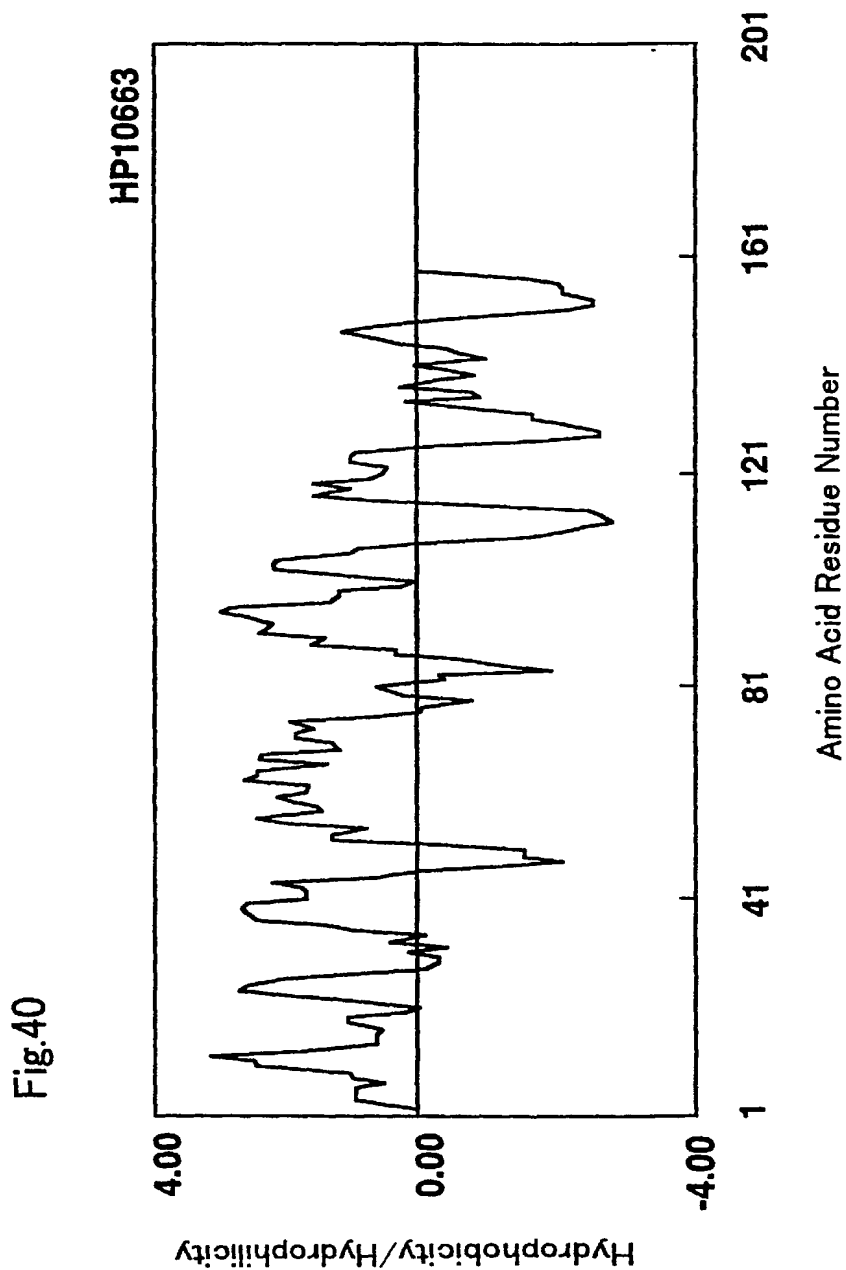


38/50



39/50





41/50

Fig.41

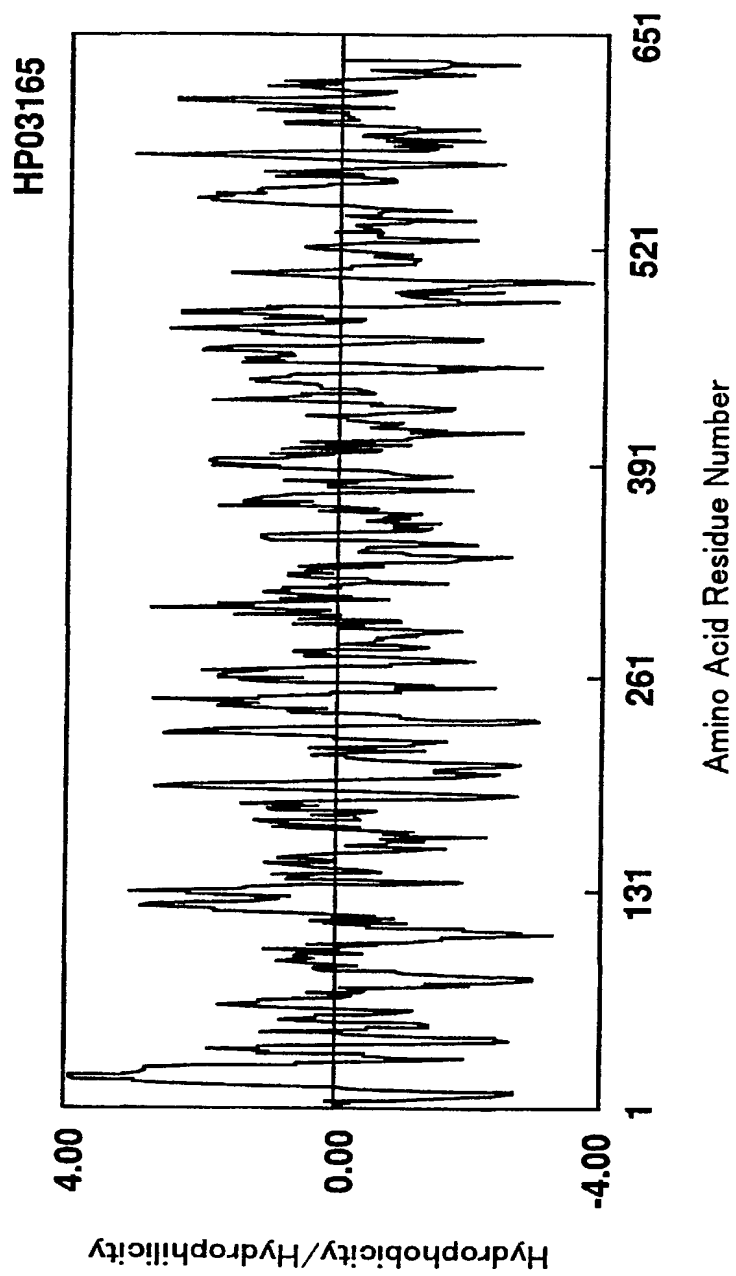


Fig.42

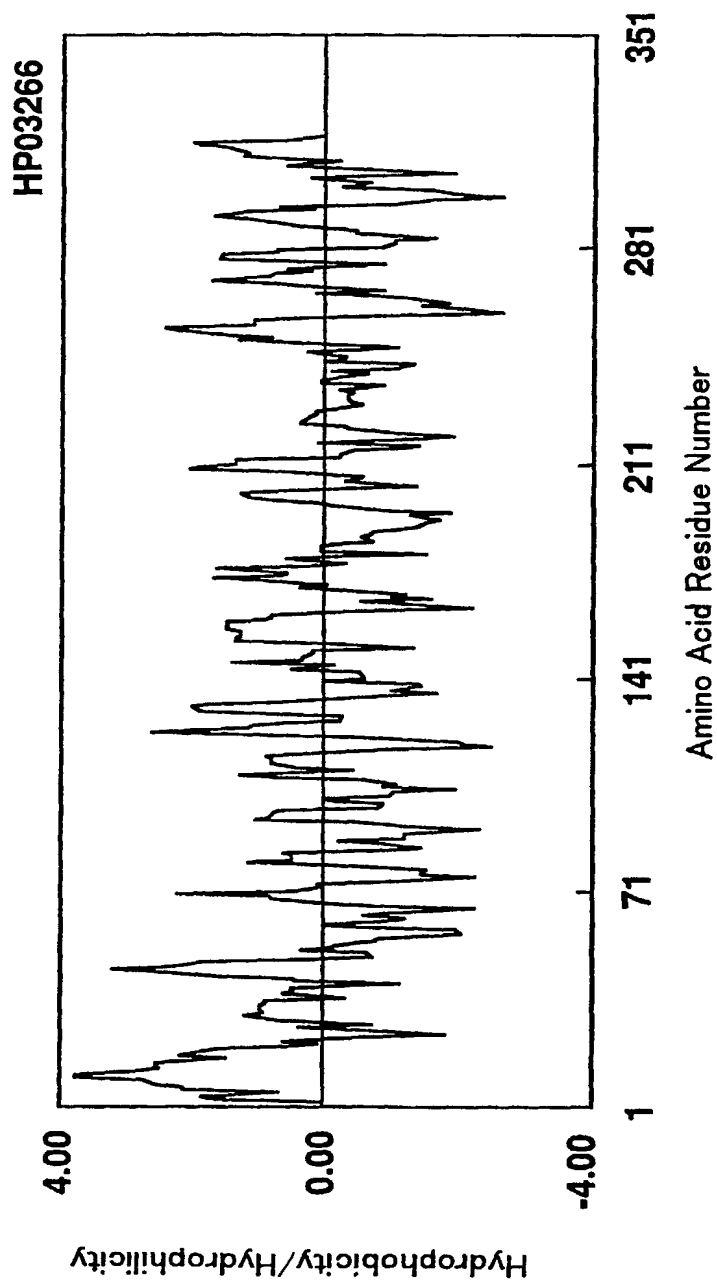


Fig.43

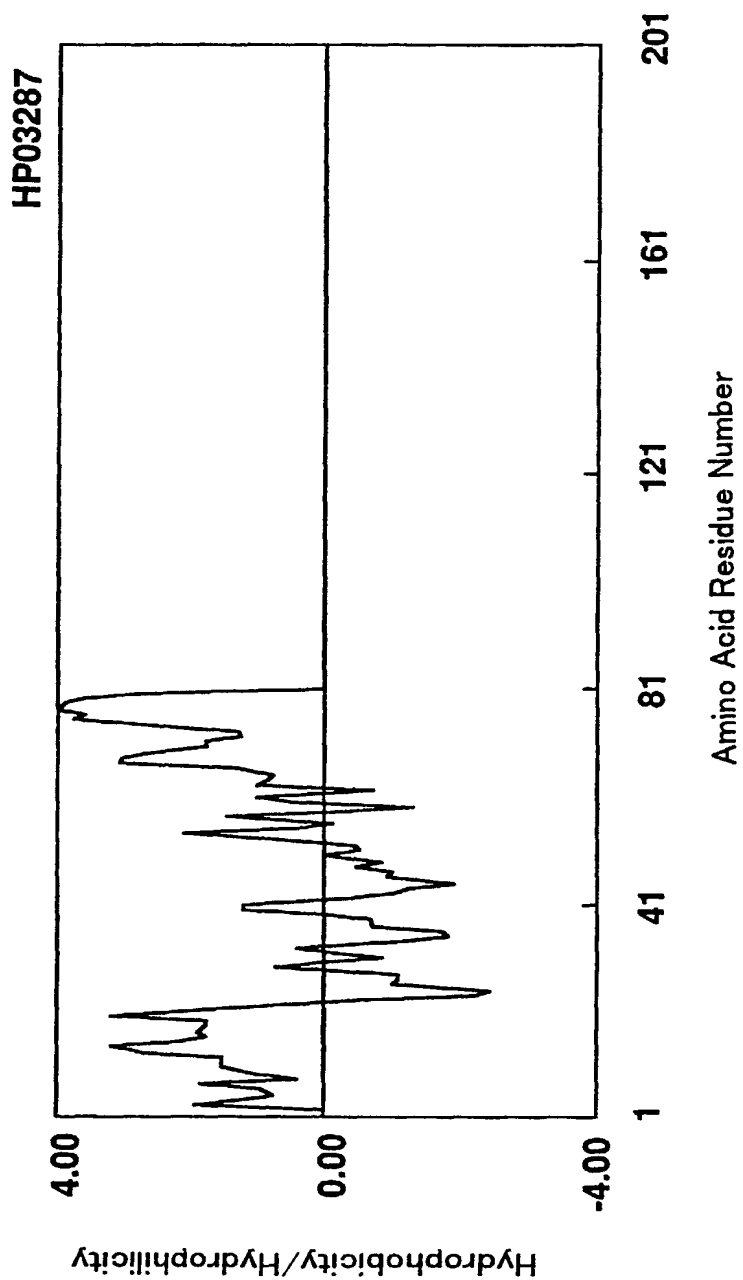
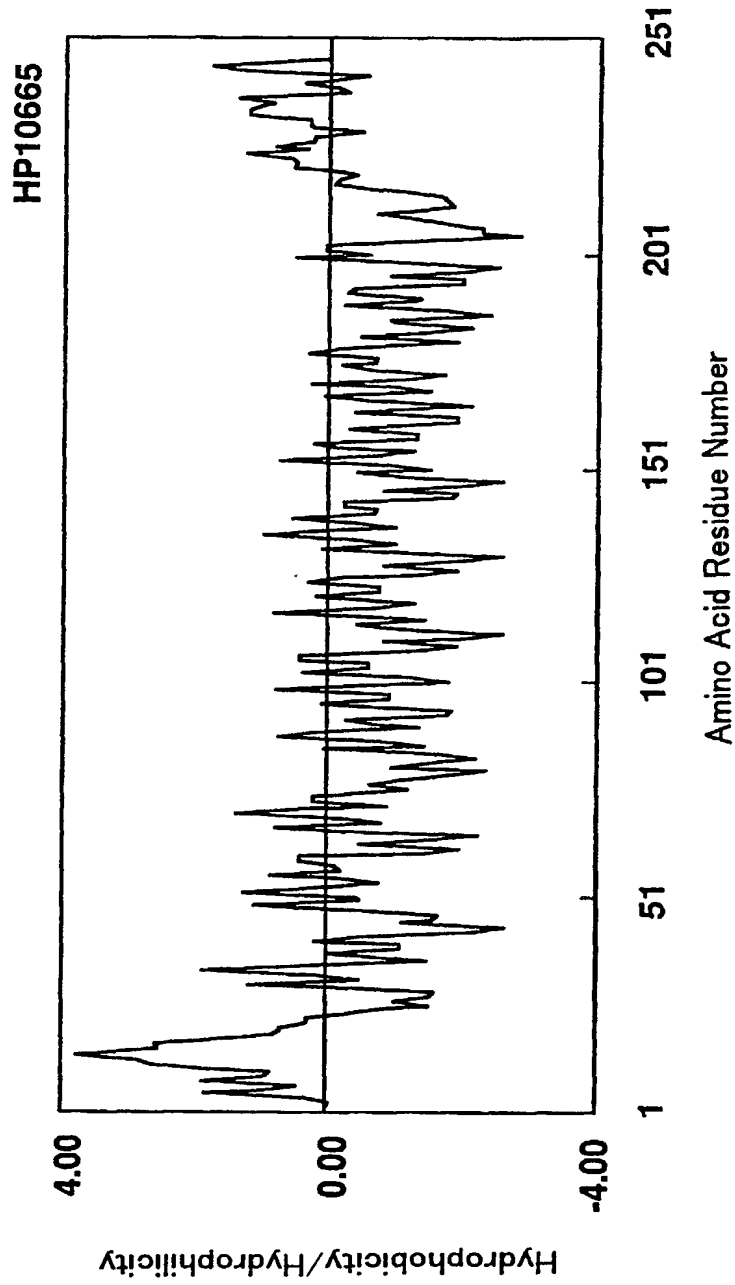
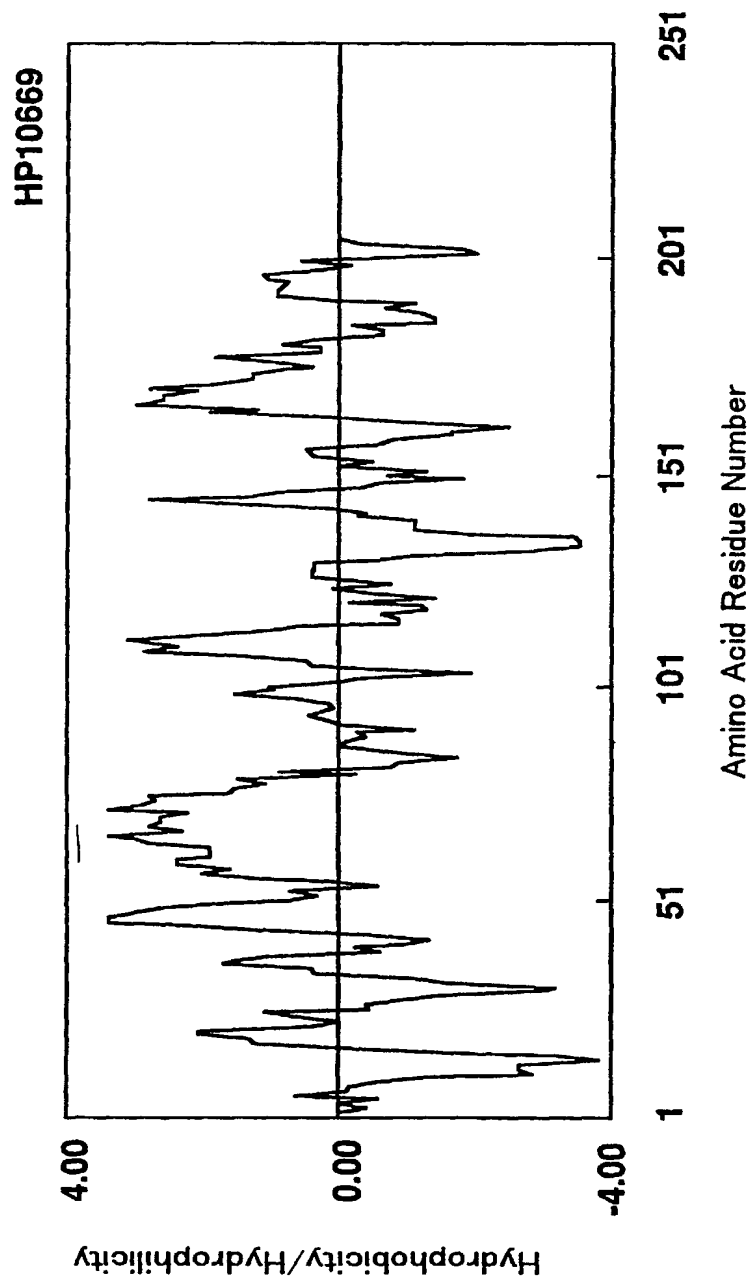


Fig.44



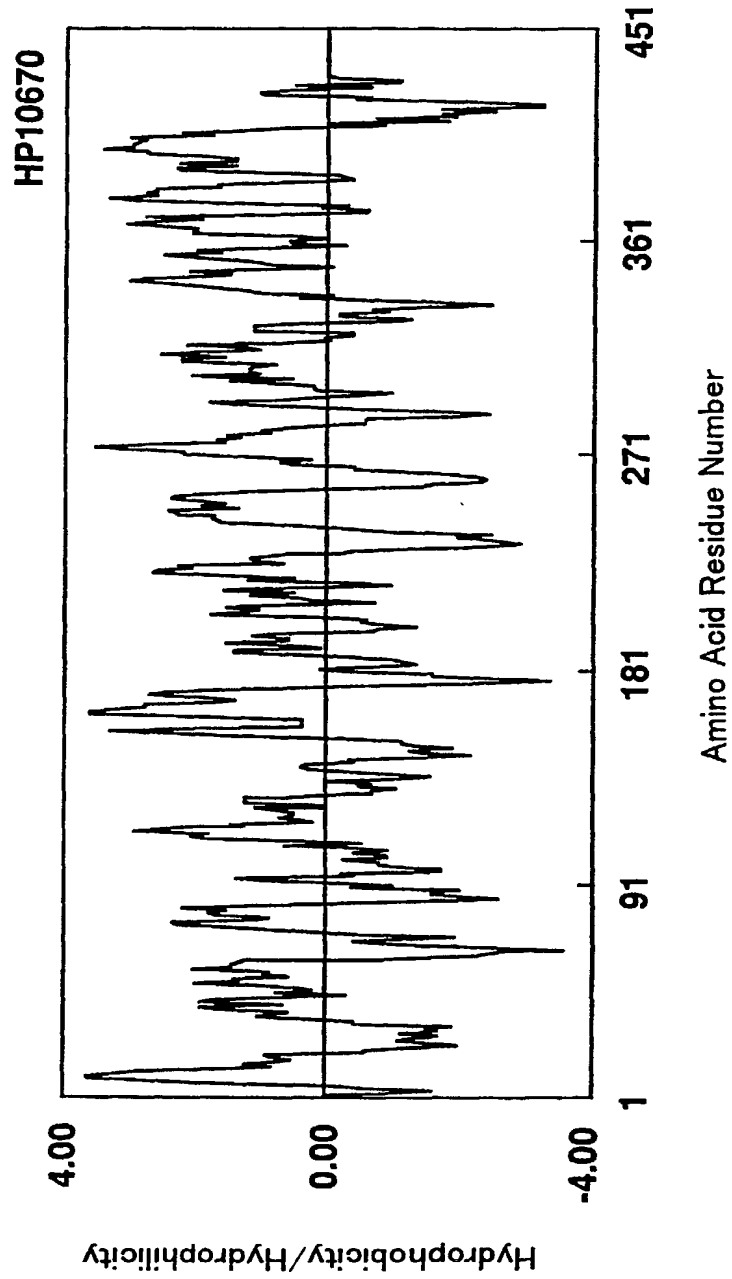
45/50

Fig.45



46/50

Fig.46



47/50

Fig.47

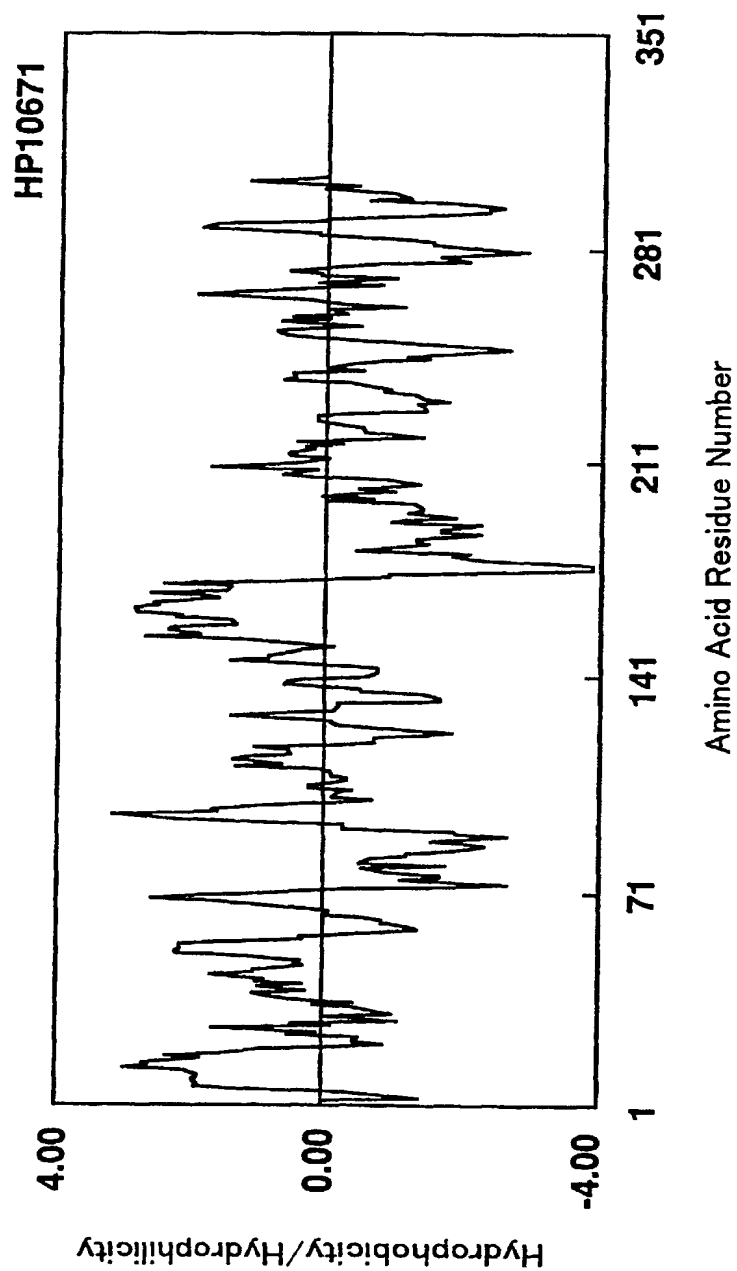


Fig.48

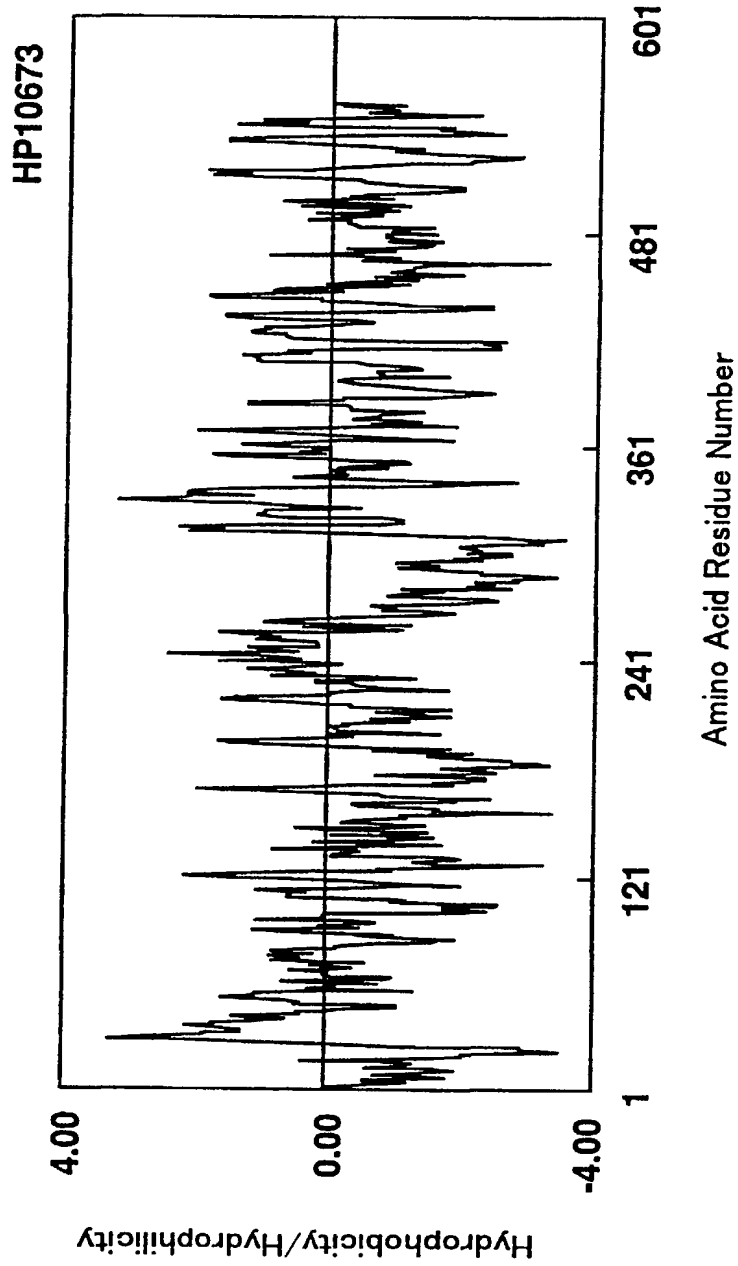


Fig.49

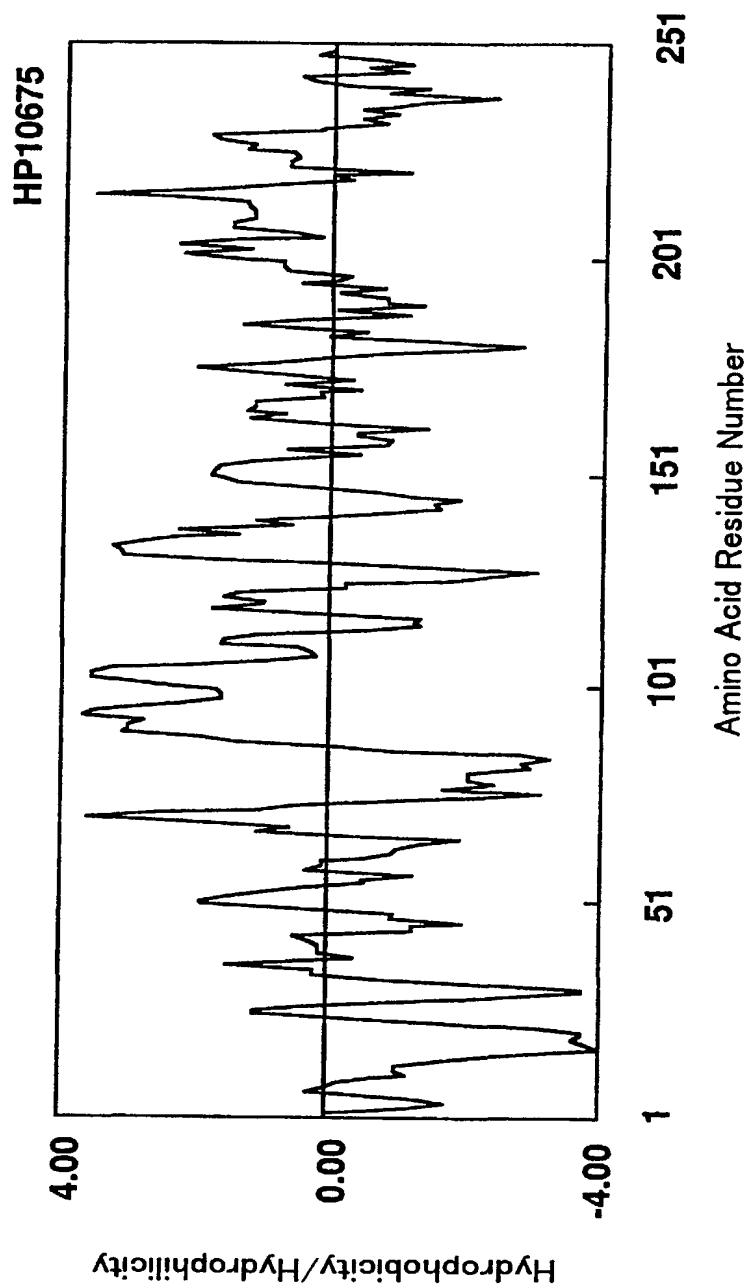
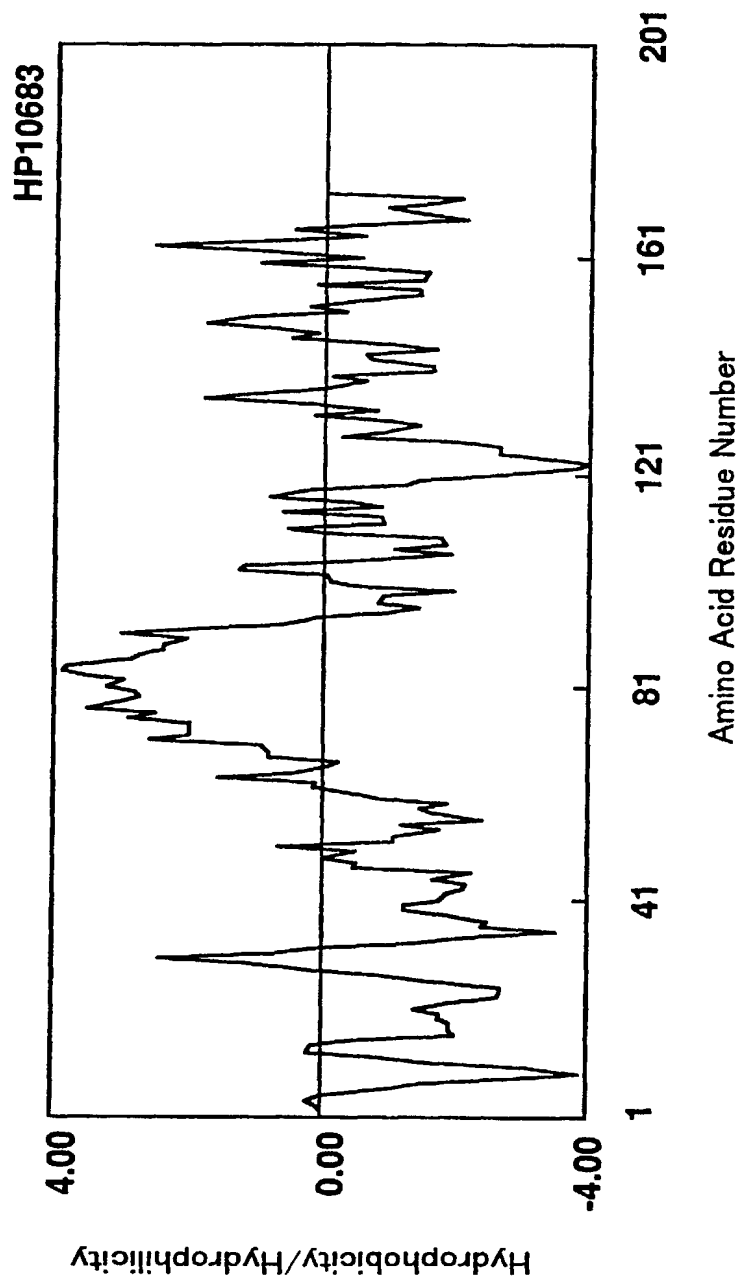


Fig.50



**DECLARATION, PETITION AND POWER OF ATTORNEY
FOR PATENT APPLICATION**

(Check one):

- ☐ Declaration Submitted with Initial Filing
☒ Declaration Submitted after Initial Filing

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS
AND DNAs ENCODING THESE PROTEINS**

the specification of which (check one):

- ☐ is attached hereto.

OR

- ☒ was filed on May 17, 2001 as U.S. Application Number
09/856,231

- ☐ and was amended by PCT Article 19 Amendment on _____
(if applicable),

- ☐ and was amended by PCT Article 34 Amendment on _____
(if applicable).

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I hereby state that I have reviewed and understood the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

PRIORITY CLAIM

(Check one):

- ☐ no such applications have been filed.
- ☒ such applications have been filed as follows:

1) FOREIGN PRIORITY CLAIM: I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate or §365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application Number(s)	Country	Foreign Filing Date (dd/mm/yyyy)	Priority - Not Claimed	Certified Copy Attached	
				Yes	No
JP-326255/1998	JP	17 November 1998 (17.11.1998)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
JP-364315/1998	JP	12 December 1998 (12.12.1998)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
JP-069811/1999	JP	16 March 1999 (16.03.1999)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
JP-119299/1999	JP	27 April 1999 (27.04.1999)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
JP-138169/1999	JP	19 May 1999 (19.05.1999)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

☐ Additional foreign application numbers are listed on a supplemental priority sheet attached hereto.

2) PROVISIONAL PRIORITY CLAIM: I hereby claim the benefit under Title 35, United States Code §119(e) of any United States provisional application(s) listed below.

Provisional Application Number(s)	Filing Date (dd/mm/yyyy)

☐ Additional provisional application numbers are listed on a supplemental priority sheet attached hereto.

3) U.S./PCT PRIORITY CLAIM: I hereby claim the benefit under Title 35, United States Code, §120 of any United States application or §365(c) of any PCT international application designating the United States of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

U.S. Parent Application Number	PCT Parent Number	Parent Filing Date (dd/mm/yyyy)	Parent Patent Number (if applicable)
	PCT/JP99/06412	17 November 1999	

☐ Additional U.S. or PCT international application numbers are listed on a supplemental priority sheet attached hereto.

As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Megan E. Williams	Reg. No. <u>43,270</u>
Nicholas P. Triano III	Reg. No. <u>36,397</u>
Jeremiah Lynch	Reg. No. <u>17,425</u>
David J. Rikkers	Reg. No. <u>43,882</u>
Maria C. Laccotripe	Limited Recognition Under 37 C.F.R. § 10 9(b)
Debra J. Milasincic	Reg. No. <u>46,931</u>
David R. Burns	Reg. No. <u>46,590</u>
Sean D. Detweiler	Reg. No. <u>42,482</u>
Peter S. Stecher	Reg. No. <u>47,259</u>
Cynthia L. Kanik	Reg. No. <u>37,320</u>
Theodore R. West	Reg. No. <u>47,202</u>
Shayne Y. Huff	Reg. No. <u>44,784</u>

M. Andrea Ryan	Reg. No. <u>28,469</u>
Elizabeth A. Hurley	Reg. No. <u>41,859</u>
Gavin T. Bogle	Limited Recognition
	Under 37 C.F.R. § 10.9(b)

Elizabeth M. Barnhard Reg. No. 31,088
Alan M. Gordon Reg. No. 30,637

Steven R. Eck Reg. No. 36,126
Michael R. Nagy Reg. No. 33,432

Send Correspondence to:

Direct Telephone Calls to:

Amy E. Mandragouras , (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1-00

Full name of first inventor Seishi Kato	
Inventor's signature <i>Seishi Kato</i>	Date Aug. 16, 2001
Residence 3-46-50, Naka-cho, Meuro-ku, Tokyo 153-0065, Japan	
Citizenship Japan	
Post Office Address (if different)	

2-00

Full name of second inventor Tomoko Kimura	
Inventor's signature <i>Tomoko Kimura</i>	Date Aug. 20, 2001
Residence 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037, Japan	
Citizenship Japan	
Post Office Address (if different)	

Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Thr Glu

WO 00/29448

PCT/JP99/06412

3/233

Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg			
305	310	315	320
Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe			
325	330	335	
Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu			
340	345	350	
Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala			
355	360	365	
Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys			
370	375	380	
Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu			
385	390	395	400
Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser			
405	410	415	
Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly			
420	425	430	
Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His			
435	440	445	
Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala			
450	455	460	
Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly			
465	470	475	480
Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe			
485	490	495	
Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser			
500	505	510	
Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu			
515	520	525	
Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr			
530	535	540	
Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu Gln Ala			
545	550	555	560
Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys Lys Ser			
565	570	575	
Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro			

Met	His	Pro	Ala	Ala	Phe	Pro	Leu	Pro	Val	Val	Val	Ala	Ala	Val	Leu
1				5					10					15	
Trp	Gly	Ala	Ala	Pro	Thr	Arg	Gly	Leu	Ile	Arg	Ala	Thr	Ser	Asp	His
			20					25					30		
Asn	Ala	Ser	Met	Asp	Phe	Ala	Asp	Leu	Pro	Ala	Leu	Phe	Gly	Ala	Thr
		35					40					45			
Leu	Ser	Gln	Glu	Gly	Leu	Gln	Gly	Phe	Leu	Val	Glu	Ala	His	Pro	Asp
	50					55					60				
Asn	Ala	Cys	Ser	Pro	Ile	Ala	Pro	Pro	Pro	Pro	Ala	Pro	Val	Asn	Gly
65					70				75					80	
Ser	Val	Phe	Ile	Ala	Leu	Leu	Arg	Arg	Phe	Asp	Cys	Asn	Phe	Asp	Leu
			85					90					95		
Lys	Val	Leu	Asn	Ala	Gln	Lys	Ala	Gly	Tyr	Gly	Ala	Ala	Val	Val	His
		100					105					110			
Asn	Val	Asn	Ser	Asn	Glu	Leu	Leu	Asn	Met	Val	Trp	Asn	Ser	Glu	Glu
	115					120				125					
Ile	Gln	Gln	Gln	Ile	Trp	Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Arg	Ser
	130				135				140						
Ser	Glu	Tyr	Leu	Arg	Ala	Leu	Phe	Val	Tyr	Glu	Lys	Gly	Ala	Arg	Val
145				150				155					160		

WO 00/29448

PCT/JP99/06412

5/233

Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr Leu Ile Pro
165 170 175
Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly Ala Val Met
180 185 190
Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg Asn Arg Leu
195 200 205
Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr Gln Lys Gly
210 215 220
Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly
225 230 235 240
Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His Ser Arg Cys
245 250 255
Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro Ile Cys Lys
260 265 270
Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu Glu Thr
275 280 285
Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp His Pro Ala
290 295 300
Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu Pro Thr Ser
305 310 315 320
Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly Pro Ser Thr
325 330 335
Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu Val
340 345 350

<210> 3

<211> 206

<212> PRT

<213> Homo sapiens

<400> 3

Met Gly Leu Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala
1 5 10 15
Val Val Tyr Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val
20 25 30
Phe Leu Leu Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn

Met	Arg	Ala	Ala	Arg	Ala	Ala	Pro	Leu	Leu	Gln	Leu	Leu	Leu	Leu	Leu
1				5					10					15	
Gly	Pro	Trp	Leu	Glu	Ala	Ala	Gly	Val	Ala	Glu	Ser	Pro	Leu	Pro	Ala
			20					25					30		
Val	Val	Leu	Ala	Ile	Leu	Ala	Arg	Asn	Ala	Glu	His	Ser	Leu	Pro	His
			35				40					45			
Tyr	Leu	Gly	Ala	Leu	Glu	Arg	Leu	Asp	Tyr	Pro	Arg	Ala	Arg	Met	Ala
	50					55				60					
Leu	Trp	Cys	Ala	Thr	Asp	His	Asn	Val	Asp	Asn	Thr	Thr	Glu	Met	Leu

WO 00/29448

PCT/JP99/06412

8/233

65	70	75	80
Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp			
	85	90	95
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys			
	100	105	110
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu			
	115	120	125
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala			
	130	135	140
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met			
	145	150	155
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr			
	165	170	175
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg			
	180	185	190
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe			
	195	200	205
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu			
	210	215	220
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp			
	225	230	235
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly			
	245	250	255
Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val			
	260	265	270
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile			
	275	280	285
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser			
	290	295	300
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp			
	305	310	315
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg			
	325	330	335
Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp			
	340	345	350

WO 00/29448

PCT/JP99/06412

9/233

Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
355 360 365
Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
370 375 380
Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
385 390 395 400
Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
405 410 415
Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
420 425 430
Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
435 440 445
Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
450 455 460
Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
465 470 475 480
Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
485 490 495
Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
500 505 510
Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
515 520 525
Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
530 535 540
Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
545 550 555 560
Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Arg
565 570 575
Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln Pro Arg
580 585 590
Asp Glu Leu
595

<210> 6

<211> 264

Met	Val	Ala	Ser	Ala	Lys	Met	Gly	Arg	Ala	Gly	Thr	Met	Ala	Val	Ala
1				5					10					15	
Ala	Glu	Leu	Arg	Glu	Leu	Cys	Pro	Gly	Val	Asn	Asn	Gln	Pro	Tyr	Leu
			20					25					30		
Cys	Glu	Ser	Gly	His	Cys	Cys	Gly	Glu	Thr	Gly	Cys	Cys	Thr	Tyr	Tyr
		35					40					45			
Tyr	Glu	Leu	Trp	Trp	Phe	Trp	Leu	Leu	Trp	Thr	Val	Leu	Ile	Leu	Phe
	50					55					60				
Ser	Cys	Cys	Cys	Ala	Phe	Arg	His	Arg	Arg	Ala	Lys	Leu	Arg	Leu	Gln
65					70					75					80
Gln	Gln	Gln	Arg	Gln	Arg	Glu	Ile	Asn	Leu	Leu	Ala	Tyr	His	Gly	Ala
			85					90						95	
Cys	His	Gly	Ala	Gly	Pro	Phe	Pro	Thr	Gly	Ser	Leu	Leu	Asp	Leu	Arg
		100						105					110		
Phe	Leu	Ser	Thr	Phe	Lys	Pro	Pro	Ala	Tyr	Glu	Asp	Val	Val	His	Arg
	115						120					125			
Pro	Gly	Thr	Pro	Pro	Pro	Pro	Tyr	Thr	Val	Ala	Pro	Gly	Arg	Pro	Leu
	130					135					140				
Thr	Ala	Ser	Ser	Glu	Gln	Thr	Cys	Cys	Ser	Ser	Ser	Ser	Ser	Cys	Pro
145				150					155					160	
Ala	His	Phe	Glu	Gly	Thr	Asn	Val	Glu	Gly	Val	Ser	Ser	His	Gln	Ser
		165						170					175		
Ala	Pro	Pro	His	Gln	Glu	Gly	Glu	Pro	Gly	Ala	Gly	Val	Thr	Pro	Ala
	180						185					190			
Ser	Thr	Pro	Pro	Ser	Cys	Arg	Tyr	Arg	Arg	Leu	Thr	Gly	Asp	Ser	Gly
	195					200						205			
Ile	Glu	Leu	Cys	Pro	Cys	Pro	Ala	Ser	Gly	Glu	Gly	Glu	Pro	Val	Lys
	210					215					220				
Glu	Val	Arg	Val	Ser	Ala	Thr	Leu	Pro	Asp	Leu	Glu	Asp	Tyr	Ser	Pro
225				230					235					240	
Cys	Ala	Leu	Pro	Pro	Glu	Ser	Val	Pro	Gln	Ile	Phe	Pro	Met	Gly	Leu
		245						250						255	

WO 00/29448

PCT/JP99/06412

11/233

Ser Ser Ser Glu Gly Asp Ile Pro

260

<210> 7

<211> 343

<212> PRT

<213> Homo sapiens

<400> 7

Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp

1 5 10 15

Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu

20 25 30

Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr

35 40 45

Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala

50 55 60

Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala

65 70 75 80

Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp

85 90 95

Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val

100 105 110

Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala

115 120 125

Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu

130 135 140

Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr

145 150 155 160

Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr

165 170 175

Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp

180 185 190

Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu

195 200 205

Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu

WO 00/29448

PCT/JP99/06412

12/233

210	215	220
Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr		
225	230	235 240
Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr		
245	250	255
Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu		
260	265	270
Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe		
275	280	285
Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu		
290	295	300
Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly		
305	310	315 320
Asn Phe Phe Thr Thr Leu Arg Val Val His His Lys Phe His Ser Gln		
325	330	335
Arg His Gly Ser Lys Lys Asp		
340		

<210> 8

<211> 244

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu Thr
1 5 10 15
Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys
20 25 30
Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro Lys Ser Asn
35 40 45
Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly
50 55 60
Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu Glu Leu Gly Cys Gly
65 70 75 80
Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
85 90 95

WO 00/29448

PCT/JP99/06412

13/233

Leu Asp Pro Asn Pro His Phe Glu Lys Phe Leu Thr Lys Ser Met Ala
100 105 110
Glu Asn Arg His Leu Gln Tyr Glu Arg Phe Val Val Ala Pro Gly Glu
115 120 125
Asp Met Arg Gln Leu Ala Asp Gly Ser Met Asp Val Val Val Cys Thr
130 135 140
Leu Val Leu Cys Ser Val Gln Ser Pro Arg Lys Val Leu Gln Glu Val
145 150 155 160
Arg Arg Val Leu Arg Pro Gly Gly Val Leu Phe Phe Trp Glu His Val
165 170 175
Ala Glu Pro Tyr Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu
180 185 190
Pro Thr Trp Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr
195 200 205
Trp Lys Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg
210 215 220
Gln Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
225 230 235 240
Lys Ala Val Lys

<210> 9

<211> 303

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Leu Lys Leu Lys Asn Val Phe Leu Ala Tyr Phe Leu Val Ser
1 5 10 15
Ile Ala Gly Leu Leu Tyr Ala Leu Val Gln Leu Gly Gln Pro Cys Asp
20 25 30
Cys Leu Pro Pro Leu Arg Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp
35 40 45
Leu Arg Ile Ser Gln Leu Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala
50 55 60
Pro Ala Gln Pro Pro Glu Pro Glu Ala Leu Pro Thr Ile Tyr Val Val

```
<210> 10
<211> 160
<212> PRT
<213> Homo sapiens
<400> 10
```

WO 00/29448

PCT/JP99/06412

15/233

Met	Asp	Lys	Leu	Lys	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	Arg
1				5					10					15	
Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp	Ser	Thr
			20					25					30		
Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile	Leu	Cys	Ser
		35					40					45			
Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys	Gly	Leu	His	Leu
		50				55					60				
Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala	Ser	Ile	Gly	Ser	Thr
	65				70					75				80	
Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Arg	Met	Phe	Glu	Pro
			85					90				95			
Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val	Leu	Leu	Cys	Phe	Ala	Leu	Thr
		100						105				110			
Leu	Cys	Ser	Ala	Phe	Trp	Trp	His	Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe
		115					120					125			
Cys	Ile	Leu	Gln	Ser	Leu	Ala	Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile
		130					135					140			
Pro	Phe	Ala	Arg	Asp	Ala	Val	Lys	Lys	Cys	Phe	Ala	Val	Cys	Leu	Ala
	145					150				155				160	

<210> 11

<211> 1941

<212> DNA

<213> Homo sapiens

<400> 11

atggctgagg	aggaggcgcc	taagaagtcc	cgggccgccg	gcggtggcgc	gagctgggaa	60
ctttgtgccg	gggcgtctc	ggcccggtg	acggaggagg	gcagcgggga	cgccggtggc	120
cgccgccgcc	cgccagttga	ccccggcga	ttggcgcgcc	agctgctgct	gctgctttgg	180
ctgctggagg	ctccgctgct	gctgggggtc	cgggcccgag	cgccggggcca	ggggccaggc	240
caggggcccc	ggccggggca	gcaaccgccg	ccgccgcctc	agcagcaaca	gagcgggcag	300
cagtacaacg	gcgagcgggg	catctccgtc	ccggaccaacg	gotattgcca	gcccctctcc	360
atcccgcgtg	gcacggacat	cgcgtaacaac	cagaccatca	tgcccaacct	gctggggccac	420
acgaaccagg	aggacgcggg	cctggagggtg	caccagttct	accctctagt	gaaagtgcag	480
tgttccgctg	agctcaagtt	cttcctgtgc	tccatgtaacg	cgcccggtg	caccgtgcta	540

WO 00/29448

PCT/JP99/06412

16/233

gagcaggcgc tgcgcgcctg ccgctccctg tgcgagcgcg cgcgcagggg ctgcgaggcg	600
ctcatgaaca agttcggctt ccagtggcca gacacgctca agtgtgagaa gttcccgggtg	660
cacggcgccg gcgagctgtg cgtgggccag aacacgtccg acaagggcac cccgacgccc	720
tcgtgcttc cagagttctg gaccagcaac cctcagcacg gcggcggagg gcaccgtggc	780
ggcttcccgg ggggcgcggg cgcgtcggag cgaggcaagt tctcctgcc gcgcgcctc	840
aaggtgccct cctacctcaa ctaccacttc ctgggggaga aggactgcgg cgcaccttgt	900
gagccgacca aggtgtatgg gctcatgtac ttcggggccg aggagctgcg cttctcgcgc	960
acctggattg gcatttggtc agtgctgtgc tgcgcctcca cgtcttcac ggtgcttacg	1020
tacctgggtg acatgcggcg cttcagctac ccggagcggc ccatcatctt cttgtccggc	1080
tgttacacgg ccgtggccgt ggcctacatc gccggcttcc tcctggaaga ccgagtgggtg	1140
tgtaatgaca agttcgccga ggacggggca cgcactgtgg cgcagggcac caagaaggag	1200
ggctgcacca tcctcttcat gatgctctac ttcttcagca tggccagctc catctgggtg	1260
gtgatcctgt cgtcacctg gttcctggcg gctggcatga agtggggcca cgaggccatc	1320
gaagccaact cacagtattt tcacctggcc gcctgggctg tgccggccat caagaccatc	1380
accatcctgg cgtggggcca ggtggacggc gatgtgctga gcggagtgtg cttcgtgggg	1440
cttaacaacg tggacgcgt gcgtggcttc gtgtgggcgc cctctctcgt gtacctgttt	1500
atcggcacgt cctttctgct ggccggcttt gtgtcgtct tcccatccg caccatcatg	1560
aagcacgatg gcaccaagac cgagaagctg gagaagctca tgggtgcgcat tggcgtcttc	1620
agcgtgctgt aactgtgcc agccaccatc gtcatgcct gctacttcta cgagcaggcc	1680
ttccgggacc agtgggaacg cagctgggtg gccagagct gcaagagcta cgtatcccc	1740
tgcctcacc tcaggcggg cggaggcgcc ccgcgcacc cggccatgag cccggacttc	1800
acggtcttca tgattaagta ccttatgacg ctgatcgtgg gcatcacgtc gggtctctgg	1860
atctggctcg gcaagacct caactcctgg aggaagttct acacgaggct caccaacagc	1920
aaacaagggg agactacagt c	1941

<210> 12

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 12

atgcacctg cagccttccc gcttctgtg gttgtggccg ctgtgctgtg gggagcggcc	60
cggacccggg ggctcattcg agcgacctcg gaccacaatg ccagcatgga ctttgcagac	120
cttccagctc tgtttggggc taccttgagc caggagggcc tccaggggtt ccttgtggag	180
gctcaccacg acaatgcctg cagccccatt gccccaccac cccagcccc ggtaaatggg	240
tcagtcttta ttgcgtgct tcgaagattc gactgcaact ttgacctcaa ggtcctaaat	300

WO 00/29448

PCT/JP99/06412

17/233

gcccagaagg ctggatatgg tgccgctgta gtacacaatg tgaattccaa tgaacttctg	360
aacatggtgt ggaatagtga ggaaatccag cagcagatct ggatcccgtc tgtattttatt	420
ggggagagaa gctccgagta cctgcgtgcc ctctttgtct acgagaaggg ggctcgggtg	480
cttctgggtc cagacaatac cttccccttg ggctattacc tcatcccttt cacagggatt	540
gtgggactgc tggttttggc catgggagca gtaatgatac ctcgttgtat ccagcacccg	600
aaacggctcc agcggaatcg acttaccaaa gagcaactga aacagattcc tacacatgac	660
tatcagaagg gagaccagta tgatgtctgt gccatttgcc tggatgaata tgaggatggg	720
gacaagctgc gggactccc ctgtgctcat gcctaccaca gccgctgcgt ggacccctgg	780
ctcactcaga cccggaagac ctgccccatt tgcaagcagc ctgttcacgc gggtcctggg	840
gacgaagacc aagaggaaga aactcaaggg caagaggagg gtgatgaagg ggagccaagg	900
gaccaccctg cctcagaaag gaccccaactt ttgggttcta gcccactct tcccacctcc	960
tttggttcct tagccccagc tccccttgtt ttctctgggc cttcaacaga tccccactg	1020
tcccctccct cttcccctgt tatcctggtc	1050

<210> 13

<211> 618

<212> DNA

<213> Homo sapiens

<400> 13

atggggctgg gtcagcccca ggcctggttg ctgggtctgc ccacagctgt ggtctatggc	60
tccctggctc tcttcaccac catcctgcac aatgtottcc tgcttacta tgtggacacc	120
tttgtctcag tgtacaagat caacaaaatg gccttctggg tcggagagac agtggttctc	180
ctctggaaca gcctcaatga cccctctctc ggttggtctc gtgaccggca gttcctcagc	240
tcccagcccc ggggaagaga tctaccctgg cttggcttgg ttggccctc tggactgtgg	300
actgcaaaca ccctctgctg cttctggaag attcctttgc cccatccctg cttgagcccg	360
tcatcaccac caaccttgag aagtgggcat cccataccct ttggccatca gcccaacagg	420
ctaataaggg ggtggaaatt ggggcagagg aggagagtgt acccactggt caggcgccgg	480
gctctcctca agggctgtgg tgctggcccg ggtgcaggcc ctgggctggc atgggcccgt	540
gctggcgtg tcgttctctg cgttctgggt gccctgggce ccagctggcc tgcagttctt	600
gctgtgcctg tgctctta	618

<210> 14

<211> 639

<212> DNA

<213> Homo sapiens

WO 00/29448

PCT/JP99/06412

18/233

<400> 14

atgcactatt atagatactc taacgccaaag gtcagctgct ggtacaagta cctccttttc	60
agctacaaca tcattctctg gttggtctga gttgtcttcc ttggagtcgg gctgtgggca	120
tggagcgaaa aggggtgtgct gtccgacctc accaaagtga cccggatgca tggaatcgac	180
cctgtggtgc tggtcctgat ggtgggctg gtgatgttca ccctggggtt cgccggctgc	240
gtgggggctc tgcgggagaa tatctgcttg ctcaacttta accagtgtg tggcgcatat	300
ggccctgaag actgggacct caacgtctac ttcaattgca gcggtgccag ctacagccga	360
gagaagtgcg ggggtccctt ctctgctgc gtgccagatc ctgcgcaaaa agttgtgaac	420
acacagtgtg gatatgatgt caggattcag ctgaagagca agtgggatga gtccatcttc	480
acgaaaggct gcatccaggc gctggaaagc tggtcccgcc ggaacattta cattgtggct	540
ggcgtcttca tcgccatctc gctgttgag atatttgga tcttcttggc aaggacgctg	600
atctcagaca tcgaggcagt gaaggccggc catcacttc	639

<210> 15

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 15

atgcgcgctg cccgcgccgc gccgtgctc cagctgctgc tcctgctggg gccgtggctg	60
gaggctgcgg gcgttgcgga gtgcgcgctg cccgcctggg tccttgccat cctggccgc	120
aatgcgaac actcgtgcc ccaactcctg ggcgtctgg agcggtgga ctacccccgg	180
gccaggatgg ccctctggtg tgccacggac cacaatgtgg acaacaccac agagatgctg	240
caggagtggc tggcggctgt gggcgatgac tatgctgctg tggctctggag gcctgagggc	300
gagcccaggt tctacccaga tgaagagggc cccaagcact ggaccaaaga aaggcaccag	360
tttctgatgg agctgaagca ggaagccctc acctttgcca ggaactgggg ggccgactat	420
atcctgtttg cagacacaga caacattctg accaacaatc agactctgcg gcttctcatg	480
gggcaggggc ttccagtggg ggccccaatg ctggactccc agacctacta ctccaacttc	540
tgggtgtggga tcacccccca gggctactac cgccgcacag ccgagtactt cccaccaag	600
aaccgccagc gccggggctg cttccgtgct cccatggtcc actccacctt ccttgcatcc	660
ctgggggctg aaggggcaga ccagcttget ttctaccgc caccatccaa ctacacttgg	720
cctttcgacg acatcatcgt cttcgctat gcctgccagg ctgctggggg ctccgtccac	780
gtgtgcaatg agcaccgtta tgggtacatg aatgtgccgg tgaaatccca ccaggggctg	840
gaagacgaga gggctcaact catccacctg atcttagaag cactagtgga cggccccgc	900
atgcaggcct cagctcatgt gactcgccc tctaagaggc ccagcaagat agggtttgac	960
gagggtctttg tcatcagcct ggctcgagg cctgaccgtc gggaacgcat gctcgctcg	1020

WO 00/29448

PCT/JP99/06412

19/233

ctctgggaga	tggagatctc	tgggaggggtg	gtggacgctg	tggatggctg	gatgctcaac	1080
agcagtgcc	tcaggaacct	cggcgtagac	ctgctcccg	gctaccagga	cccttactcg	1140
ggccgcactc	tgaccaagg	cgaggtgggc	tgttctctca	gccattactc	catctgggaa	1200
gaggtggtt	ccaggggcct	ggcccggtc	ctggtgtttg	aggatgacgt	gcgttttgag	1260
agcaacttca	gggggcggct	ggagcggtg	atggaggatg	tggaggcaga	gaaactgtct	1320
tgggacctga	tctacctcg	acggaagcag	gtgaaccctg	agaaggagac	ggcgtggag	1380
gggtgcctg	gcctggtgt	ggctgggtac	tcctactgga	cgctggccta	tgcctgcgt	1440
ctggcggtg	cccgcaagct	gctggcctca	cagcctctgc	gccgcctgct	ggcgtggac	1500
gagttcctgc	ccatcatgtt	cgaccagcac	cccaacgagc	agtacaaggc	acacttctgg	1560
ccacgggacc	tgggtgcctt	ctccgcccag	cccctgctcg	ctgcccctac	ccactatgcc	1620
ggggacgccg	agtggctcag	tgacacggag	acatcctctc	catgggatga	tgacagcggc	1680
cgctcatca	gctggagcgg	ctcccaaaag	accctgcgca	gccccgcct	ggacctgact	1740
ggcagcagcg	ggcacagcct	ccaacccccag	ccccgagatg	agctc		1785

<210> 16

<211> 792

<212> DNA

<213> Homo sapiens

<400> 16

atggtggcct	cagcgaagat	gggcccggca	gggaccatgg	cggtggcagc	agagcttcga	60
gagctgtgcc	caggagtga	caaccagccc	tacctctgtg	agagtggcca	ctgctgcggg	120
gagactggct	gctgcacct	ctactatgag	ctctgggtgt	tctggctgct	ctggactgtc	180
ctcactctct	ttagctgctg	ttgcgccttc	cgccacgcag	gagctaaact	caggctgcaa	240
caacagcagc	ggcagcgtga	aatcaacttg	ttggcctatc	atggggcatg	ccatggggct	300
ggtcctttcc	ctaccggttc	actgcttgac	cttcgcttcc	tcagcacctt	caagccccca	360
gcctacgagg	atgtggttca	ccgcccaggc	acacaccccc	ccccttatac	tgtggcccca	420
ggccgcccct	tgactgcttc	cagtgaacaa	acctgctgtt	cctcctcctc	cagctgccct	480
gccacttttg	aaggaacaaa	tgtggaaggt	gtttcctccc	accagagtgc	cccccccat	540
caggaggggtg	agcccggggc	aggggtgacc	cctgcctcca	cacccccctc	ctgcgctat	600
cgccgtttaa	ctggcgactc	cgggtattgag	ctctgccctt	gtcctgcctc	cggtgaggg	660
gagccagtca	aggaggtgag	ggttagtgcc	acctgccag	atctggagga	ctactccccg	720
tgtgcactac	ccccagagtc	tgtaccgcag	atctttccca	tggggctgtc	ttccagtga	780
ggggacatcc	ca					792

<210> 17

WO 00/29448

PCT/JP99/06412

20/233

<211> 1029

<212> DNA

<213> Homo sapiens

<400> 17

atgcagcccc	cgcccccg	cccgcctggc	gactgcctgc	gggactggga	ggatctacag	60
caggacttcc	agaacatcca	ggagacccat	cggtctctacc	gcctgaagct	ggaggagctg	120
accaaacttc	agaacaattg	caccagctcc	atcacgcggc	agaagaagcg	gctccaggag	180
ctggccctcg	ccctgaagaa	atgcaaacc	tccctcccag	cagaggccga	gggggcccga	240
caggagctgg	agaaccagat	gaaagagcgc	caaggcctct	tctttgacat	ggaggcctat	300
ttgcctaaga	agaatggatt	gtacctgagc	ctggttctgg	ggaacgtcaa	cgtcacgctc	360
ctgagcaagc	aggctaagtt	tgcctacaag	gacgagtatg	agaagttcaa	gctctacctc	420
accateatcc	tcctctcat	ctccttcaact	tgcgccttcc	tgtctaaactc	caggggtgaca	480
gatgctgct	tcaacttcct	gctgggtctgg	tactactgca	cctgaccat	cggggagagc	540
atcctcatca	acaacggctc	ccggatcaaa	ggctgggtggg	tgttccatca	ctacgtgtcc	600
acottcctgt	cgggagtcac	gctgacgtgg	ccgacgggc	tcattgtacca	gaaattccgg	660
aaccaattcc	tctccttttc	catgtaccag	agcttcgtgc	agtttctcca	gtactactac	720
cagagcggct	gcctctaccg	cctgcgggcg	ctgggcgagc	ggcacaccat	ggacctcact	780
gtggagggct	tccagtcctg	gatgtggcgg	ggcctcacct	tcctgctgcc	ttttcttttc	840
tttggaact	tctggcagct	ttttaacgcg	ctgacgttgt	tcaacctggc	ccaggaccct	900
cagtgcagg	agtggcagg	gcttatgtgc	ggctttccct	tcctcctcct	tttctcggc	960
aatttcttca	ccacctgag	ggttgtgcac	cacaagtttc	acagtcagcg	gcacggggagc	1020
aagaaggat						1029

<210> 18

<211> 732

<212> DNA

<213> Homo sapiens

<400> 18

atggacatcc	tggctcccact	cctgcagctg	ctggtgctgc	ttcttaccct	gcccctgcac	60
ctcatggctc	tgtctgggctg	ctggcagccc	ctgtgcaaaa	gtacttccc	ctacctgatg	120
gccgtgctga	ctcccaagag	caaccgcaag	atggagagca	agaaacggga	gctcttcagc	180
cagataaagg	ggcttacagg	agcctccggg	aaagtggccc	tactggagct	gggctgcgga	240
accggagcca	actttcagtt	ctacccaccg	ggctgcaggg	tcacctgcct	agacccaaat	300
ccccactttg	agaagttcct	gacaaagagc	atggttgaga	acaggcacct	ccaatatgag	360
cgggtttgtg	tggctcctgg	agaggacatg	agacagctgg	ctgatggctc	catggatgtg	420

WO 00/29448

PCT/JP99/06412

21/233

gtggtctgca ctctggtgct gtgctctgtg cagagcccaa ggaaggtcct gcaggaggtc	480
eggagagtac tgagaccggg aggtgtgctc tttttctggg agcatgtggc agaaccatat	540
ggaagctggg ccttcatgtg gcagcaagtt ttcgagccca cctggaaaca cattggggat	600
ggctgctgcc tcaccagaga gacctggaag gatcttgaga acgcccagtt ctccgaaatc	660
caaatggaac gacagccccc tcccttgaag tggctacctg ttgggccccca catcatggga	720
aaggctgtca aa	732

<210> 19

<211> 909

<212> DNA

<213> Homo sapiens

<400> 19

atgaagctga agctgaagaa cgtgtttctc gcctacttcc tgggtgtcgat cgccggcctc	60
ctctacgcgc tgggtacagct cggccagcca tgtgactgcc ttcctcccct gcgggcagca	120
gccgagcagc tacggcagaa ggatctgagg atttcccagc tgcaagcggg actccgacgg	180
ccaccccctg cccctgccca gcccctgaa cccgaggccc tgctactat ctatgttgtt	240
acccccacct atgccaggcc cctgtgggtg cagtaccctc aggatgtgac taccttcaat	300
atagatgatc agtacttgct tggggatgcg ttgctgggtc accctgtatc agactctgga	360
gcccattggtg tccaggtcta tctgcctggc caaggggagg tgtggtatga cattcaaagc	420
taccagaagc atcatggtcc ccagaccctg tacctgcctg taactctaag cagtatccct	480
gtgttccagc gtggagggac aatcgtgcct cgatggatgc gagtgcggcg gtcttcagaa	540
tgtatgaagg atgaccccat cactctcttt gttgcaetta gccctcaggg tacagctcaa	600
ggagagctct ttotggatga tgggcacacg ttcaactatc agactcgcca agagttcctg	660
ctgcgtcgat tctcattctc tggcaacacc cttgtctcca gctcagcaga ccctgaagga	720
cacttttgaga caccaatctg gattgagcgg gtggtgataa taggggctgg aaagccagca	780
gctgtggtac tccagacaaa aggatctcca gaaagccgcc tgtccttcca gcatgacct	840
gagacctctg tgttggtcct gcgcaagcct ggcatcaatg tggcatctga ttggagtatt	900
cacctgca	909

<210> 20

<211> 480

<212> DNA

<213> Homo sapiens

<400> 20

atggacaagc tgaagaaggt gctgagcggg caggacacgg aggaccggag cggcctgtcc	60
---	----

WO 00/29448

PCT/JP99/06412

22/233

gaggttggtg aggcattctt attaatgttg agtaccagga taaaaggctt cattgcgtgt	120
tttgcctatag gaattctctg ctactgctg ggtactgttc tgctgtgggt gccaggaag	180
ggactacacc tcttcgcagt gttttatacc tttggtaata tcgcatcaat tgggagtacc	240
atcttctctca tgggaccagt gaaacagctg aagcgaatgt ttgagcctac tcgtttgatt	300
gcaactatca tgggtgctgt gtgttttgca cttaccctgt gttctgcctt ttggtggcat	360
aacaagggac ttgcatttat cttctgcatt ttgcagctct tggcattgac gtggtacagc	420
ctttccttca taccatttgc aagggatgct gtgaagaagt gttttgccgt gtgtcttgca	480

<210> 21

<211> 4485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (189)...(2132)

<400> 21

gaatcgcaag tttccgcggc ggccggcggt gcggtacgca gaacaggagc cgggggagcg	60
ggccgaaagc ggcttgggct cgacggaggg caccgcgca gaggtctccc tggccgcagg	120
gggagccgcc gccggccgtg cccctggcag cccagcggga gcggcgccaa gagaggagcc	180
gagaaagt atg gct gag gag gag gcg cct aag aag tcc cgg gcc gcc ggc	230
Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly	
1 5 10	
ggt ggc gcg agc tgg gaa ctt tgt gcc ggg gcg ctc tcg gcc cgg ctg	278
Gly Gly Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu	
15 20 25 30	
acg gag gag ggc agc ggg gac gcc ggt ggc cgc cgc cgc cca gtt	326
Thr Glu Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val	
35 40 45	
gac ccc cgg cga ttg gcg cgc cag ctg ctg ctg ctg ctt tgg ctg ctg	374
Asp Pro Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu	
50 55 60	
gag gct ccg ctg ctg ctg ggg gtc cgg gcc cag gcg gcg ggc cag ggg	422
Glu Ala Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly	
65 70 75	
cca ggc cag ggg ccc ggg ccg ggg cag caa ccg ccg ccg cct cag	470

Pro	Gly	Gln	Gly	Pro	Gly	Gln	Gln	Pro	Pro	Pro	Pro	Pro	Gln
80					85				90				
cag	caa	cag	agc	ggg	cag	cag	tac	aac	ggc	gag	cgg	ggc	atc tcc gtc
Gln	Gln	Gln	Ser	Gly	Gln	Gln	Tyr	Asn	Gly	Glu	Arg	Gly Ile Ser Val	518
95					100				105				110
ccg	gac	cac	ggc	tat	tgc	cag	ccc	atc	tcc	atc	ccg	ctg tgc acg gac	566
Pro	Asp	His	Gly	Tyr	Cys	Gln	Pro	Ile	Ser	Ile	Pro	Leu Cys Thr Asp	
				115					120			125	
atc	gcg	tac	aac	cag	acc	atc	atg	ccc	aac	ctg	ctg	ggc cac acg aac	614
Ile	Ala	Tyr	Asn	Gln	Thr	Ile	Met	Pro	Asn	Leu	Leu	Gly His Thr Asn	
				130					135			140	
cag	gag	gac	gcg	ggc	ctg	gag	gtg	cac	cag	ttc	tac	cct cta gtg aaa	662
Gln	Glu	Asp	Ala	Gly	Leu	Glu	Val	His	Gln	Phe	Tyr	Pro Leu Val Lys	
				145					150			155	
gtg	cag	tgt	tcc	gct	gag	ctc	aag	ttc	ttc	ctg	tgc	tcc atg tac gcg	710
Val	Gln	Cys	Ser	Ala	Glu	Leu	Lys	Phe	Phe	Leu	Cys	Ser Met Tyr Ala	
				160					165			170	
ccc	gtg	tgc	acc	gtg	cta	gag	cag	gcg	ctg	ccg	ccc	tgc cgc tcc ctg	758
Pro	Val	Cys	Thr	Val	Leu	Glu	Gln	Ala	Leu	Pro	Pro	Cys Arg Ser Leu	
175					180					185		190	
tgc	gag	cgc	gcg	cgc	cag	ggc	tgc	gag	gcg	ctc	atg	aac aag ttc ggc	806
Cys	Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Ala	Leu	Met	Asn Lys Phe Gly	
				195					200			205	
ttc	cag	tgg	cca	gac	acg	ctc	aag	tgt	gag	aag	ttc	ccg gtg cac ggc	854
Phe	Gln	Trp	Pro	Asp	Thr	Leu	Lys	Cys	Glu	Lys	Phe	Pro Val His Gly	
				210					215			220	
gcc	ggc	gag	ctg	tgc	gtg	ggc	cag	aac	acg	tcc	gac	aag ggc acc ccg	902
Ala	Gly	Glu	Leu	Cys	Val	Gly	Gln	Asn	Thr	Ser	Asp	Lys Gly Thr Pro	
				225					230			235	
acg	ccc	tcg	ctg	ctt	cca	gag	ttc	tgg	acc	age	aac	cct cag cac ggc	950
Thr	Pro	Ser	Leu	Leu	Pro	Glu	Phe	Trp	Thr	Ser	Asn	Pro Gln His Gly	
				240					245			250	
ggc	gga	ggg	cac	cgt	ggc	ggc	ttc	ccg	ggg	ggc	gcc	ggc gcg tcg gag	998
Gly	Gly	Gly	His	Arg	Gly	Gly	Phe	Pro	Gly	Gly	Ala	Gly Ala Ser Glu	
255					260					265		270	

WO 00/29448

PCT/JP99/06412

24/233

cga ggc aag ttc tcc tgc ccg cgc gcc ctc aag gtg ccc tcc tac ctc	1046
Arg Gly Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu	
275 280 285	
aac tac cac ttc ctg ggg gag aag gac tgc ggc gca cct tgt gag ccg	1094
Asn Tyr His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro	
290 295 300	
acc aag gtg tat ggg ctc atg tac ttc ggg ccc gag gag ctg cgc ttc	1142
Thr Lys Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe	
305 310 315	
tcg cgc acc tgg att ggc att tgg tca gtg ctg tgc tgc gcc tcc acg	1190
Ser Arg Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr	
320 325 330	
ctc ttc acg gtg ctt acg tac ctg gtg gac atg cgg cgc ttc agc tac	1238
Leu Phe Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr	
335 340 345 350	
ccg gag cgg ccc atc atc ttc ttg tcc ggc tgt tac acg gcc gtg gcc	1286
Pro Glu Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala	
355 360 365	
gtg gcc tac atc gcc ggc ttc ctc ctg gaa gac cga gtg gtg tgt aat	1334
Val Ala Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn	
370 375 380	
gac aag ttc gcc gag gac ggg gca cgc act gtg gcg cag ggc acc aag	1382
Asp Lys Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys	
385 390 395	
aag gag ggc tgc acc atc ctc ttc atg atg ctc tac ttc ttc agc atg	1430
Lys Glu Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met	
400 405 410	
gcc agc tcc atc tgg tgg gtg atc ctg tcg ctc acc tgg ttc ctg gcg	1478
Ala Ser Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala	
415 420 425 430	
gct ggc atg aag tgg ggc cac gag gcc atc gaa gcc aac tca cag tat	1526
Ala Gly Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr	
435 440 445	
ttt cac ctg gcc gcc tgg gct gtg ccg gcc atc aag acc atc acc atc	1574
Phe His Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile	

WO 00/29448

PCT/JP99/06412

25/233

450	455	460	
ctg gcg ctg ggc cag gtg gac ggc gat gtg ctg agc gga gtg tgc ttc			1622
Leu Ala Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe			
465	470	475	
gtg ggg ctt aac aac gtg gac gcg ctg cgt ggc ttc gtg ctg gcg ccc			1670
Val Gly Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro			
480	485	490	
ctc ttc gtg tac ctg ttt atc ggc acg tcc ttt ctg ctg gcc ggc ttt			1718
Leu Phe Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe			
495	500	505	510
gtg tcg ctc ttc cgc atc cgc acc atc atg aag cac gat ggc acc aag			1766
Val Ser Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys			
515	520	525	
acc gag aag ctg gag aag ctc atg gtg cgc att ggc gtc ttc agc gtg			1814
Thr Glu Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val			
530	535	540	
ctg tac act gtg cca gcc acc atc gtc atc gcc tgc tac ttc tac gag			1862
Leu Tyr Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu			
545	550	555	
cag gcc ttc cgg gac cag tgg gaa cgc agc tgg gtg gcc cag agc tgc			1910
Gln Ala Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys			
560	565	570	
aag agc tac gct atc ccc tgc cct cac ctc cag gcg ggc gga ggc gcc			1958
Lys Ser Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala			
575	580	585	590
ccg ccg cac ccg ccc atg agc ccg gac ttc acg gtc ttc atg att aag			2006
Pro Pro His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys			
595	600	605	
tac ctt atg acg ctg atc gtg ggc atc acg tcg ggc ttc tgg atc tgg			2054
Tyr Leu Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp			
610	615	620	
tcc ggc aag acc ctc aac tcc tgg agg aag ttc tac acg agg ctc acc			2102
Ser Gly Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr			
625	630	635	
aac agc aaa caa ggg gag act aca gtc tgagaccg ggcacagccc a			2150

WO 00/29448

PCT/JP99/06412

26/233

Asn Ser Lys Gln Gly Glu Thr Thr Val

640	645	
tgcccaggcc	tgggccgggg	cgcagcgatc ccccaaagcc agcgccgtgg agttcgtgcc 2210
aatcctgaca	tctcgagggt	tcctcactag acaactctct ttcgcaggct cctttgaaca 2270
actcagctcc	tgcaaaagct	tccgtccctg aggcaaaagg acacgagggc ccgactgcca 2330
gagggaggat	ggacagacct	cttgccctca cactctggta ccaggactgt tcgcttttat 2390
gattgtaaat	agcctgtgta	agatttttgt aagtatatatt gtatttaaata gacgaccgat 2450
caecgcgtttt	tctttttcaa	aagtttttaa ttatttaggg cggtttaacc atttgaggct 2510
tttccttctt	gcccttttcg	gagtattgca aaggagctaa aactggtgtg caaccgcaca 2570
gcgtccttgg	tcgtcctcgc	gcgcctctcc ctaccacggg tgctcgggac ggctggggcg 2630
cagctccggg	gcgagttcag	cactgcgggg tgcgactagg gctgcgtgc cagggtcact 2690
tcccgctccc	tccttttgcc	ccctcccccct ccttctgtcc cctcccttcc tttcctggct 2750
tgaggtaggg	gctcttaagg	tacagaactc cacaacacct ccaaactcgg aggagggccc 2810
ccatacatta	caattcctcc	cttgctcggc ggtggattgc gaaggcccg ccttcgact 2870
tcctgaagct	ggatttttaa	ctgtccagaa ctttcctcca acttcattgg ggcccacggg 2930
tgtgggcgct	ggcagctcca	gcctccctcc acgggtcacct tcaacgcccc gacactccct 2990
tctcccacct	tagttgggta	cagggtgagt gagataacca atgccaaact ttttgaagtc 3050
taatttttga	ggggtgagct	catttcattc tctagtgtct aaaacctggg atgggtttgg 3110
ccagcgtcat	ggaaagatgt	ggttaactgag atttgggaag aagcatgaag ctttgtgtgg 3170
gttggaagag	actgaagata	tgggttataa aatgttaatt ctaattgcac acggatgcct 3230
ggcaaccttg	cctttgagaa	tgagacagcc tgcgcttaga ttttacgggt ctgtaaaatg 3290
gaaatgttga	ggtcacctgg	aaagctttgt taaggagttg atgtttgctt tccttaacaa 3350
gacagcaaaa	cgtaaacaga	aattgaaaac ttgaaggata tttcagtgtc atggacttcc 3410
tcaaaatgaa	gtgctatttt	cttattttta atcaaataac tagacatata tcagaaaactt 3470
taaaatgtaa	aagttgtaca	ctttcaacat tttattacga ttattattca gcagcacatt 3530
ctgagggggg	aacaattcac	accaccaata ataacctggg aagatttcag gaggtaaaga 3590
aggtggaata	attgacgggg	agatagcgcc tgaaataaac aaaatatggg catgcatgct 3650
aaagggaaaa	tgtgtgcagg	tctactgcac taaatcctgt gtgctcctct tttggattta 3710
cagaaatgtg	tcaaatgtaa	atctttcaaa gccatttaaa aatatcact ttagttctct 3770
gtgaagaaga	ggagaaaagc	aatcctcctg attgtattgt tttaaaactt aagaatttat 3830
caaaatgccg	gtacttagga	cctaaattta tctatgtctg tcatacgcta aaatgatatt 3890
ggtctttgaa	tttggatata	atttattctg ttcactatca caaaatcacc tatatttata 3950
gaggaataga	agttttatata	tatataatac catattttta atttcacaaa taaaaaatcc 4010
aaagttttgt	acaaaatttat	atggattttg tgccctgaaaa taatagagct tgagctgtct 4070
gaactatttt	acatttttatg	gtgtctcata gccaatccca cagtgtaaaa attcaggaat 4130

WO 00/29448

PCT/JP99/06412

27/233

tcaatgaaaa aagtctaccc ttaaaccctc agatcagtct ttccaaagaa ttactctgtt 4190
 tgcattgttg tgattgacat ttgtgaagtc ccaagaaaag atctgttttc atgacagtag 4250
 aaaatagaag ttgcaaatt atttctttac tcaaagagga ttaaaagaga actctaattt 4310
 taatattaaa gctttctttt ctttcagggg ataaatttac atgacttttt atattatgga 4370
 gggtttatttt taaatcatca cttttctcat attttttaga ggtattgtct tatctcttcc 4430
 ataatcttgg atattacaaa accctaaata ggcaatcaat aaatggttaa ctggc 4485

<210> 22

<211> 1509

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (253)...(1305)

<400> 22

ttttccgcgt tttatccccg taccagaaaa ggatacattt agtgcctccc acccagctcc 60
 actaaacggg ttggatatct cattctttga gttggtgttc cttccccggc gccccatgt 120
 agctgggaag tgggacctgg ggggtggttg acccctggga tccataagga ggggcaggga 180
 gggcgagaaa ctccgcttct gctccttget accaggacgc ggggcctcct cagcctcttt 240
 cctcccgctg cc atg cac cct gca gcc ttc ccg ctt cct gtg gtt gtg gcc 291

Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala

1

5

10

gct gtg ctg tgg gga gcg gcc ccg acc cgg ggg ctc att cga gcg acc 339
 Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr

15

20

25

tcg gac cac aat gcc agc atg gac ttt gca gac ctt cca gct ctg ttt 387
 Ser Asp His Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe

30

35

40

45

ggg gct acc ttg agc cag gag ggc ctc cag ggg ttc ctt gtg gag gct 435
 Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala

50

55

60

cac cca gac aat gcc tgc agc ccc att gcc cca cca ccc cca gcc ccg 483
 His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro

65

70

75

gtc aat ggg tca gtc ttt att gcg ctg ctt cga aga ttc gac tgc aac 531

Val	Asn	Gly	Ser	Val	Phe	Ile	Ala	Leu	Leu	Arg	Arg	Phe	Asp	Cys	Asn	
80						85						90				
ttt	gac	ctc	aag	gtc	cta	aat	gcc	cag	aag	gct	gga	tat	ggg	gcc	gct	579
Phe	Asp	Leu	Lys	Val	Leu	Asn	Ala	Gln	Lys	Ala	Gly	Tyr	Gly	Ala	Ala	
95						100						105				
gta	gta	cac	aat	gtg	aat	tcc	aat	gaa	ctt	ctg	aac	atg	gtg	tgg	aat	627
Val	Val	His	Asn	Val	Asn	Ser	Asn	Glu	Leu	Leu	Asn	Met	Val	Trp	Asn	
110						115						120			125	
agt	gag	gaa	atc	cag	cag	cag	atc	tgg	atc	cgg	tct	gta	ttt	att	ggg	675
Ser	Glu	Glu	Ile	Gln	Gln	Gln	Ile	Trp	Ile	Pro	Ser	Val	Phe	Ile	Gly	
			130						135						140	
gag	aga	agc	tcc	gag	tac	ctg	cgt	gcc	ctc	ttt	gtc	tac	gag	aag	ggg	723
Glu	Arg	Ser	Ser	Glu	Tyr	Leu	Arg	Ala	Leu	Phe	Val	Tyr	Glu	Lys	Gly	
145						150						155				
gct	cgg	gtg	ctt	ctg	gtt	cca	gac	aat	acc	ttc	ccc	ttg	ggc	tat	tac	771
Ala	Arg	Val	Leu	Leu	Val	Pro	Asp	Asn	Thr	Phe	Pro	Leu	Gly	Tyr	Tyr	
160						165						170				
ctc	atc	cct	ttc	aca	ggg	att	gtg	gga	ctg	ctg	gtt	ttg	gcc	atg	gga	819
Leu	Ile	Pro	Phe	Thr	Gly	Ile	Val	Gly	Leu	Leu	Val	Leu	Ala	Met	Gly	
175						180						185				
gca	gta	atg	ata	gct	cgt	tgt	atc	cag	cac	cgg	aaa	cgg	ctc	cag	cgg	867
Ala	Val	Met	Ile	Ala	Arg	Cys	Ile	Gln	His	Arg	Lys	Arg	Leu	Gln	Arg	
190						195						200			205	
aat	cga	ctt	acc	aaa	gag	caa	ctg	aaa	cag	att	cct	aca	cat	gac	tat	915
Asn	Arg	Leu	Thr	Lys	Glu	Gln	Leu	Lys	Gln	Ile	Pro	Thr	His	Asp	Tyr	
			210						215						220	
cag	aag	gga	gac	cag	tat	gat	gtc	tgt	gcc	att	tgc	ctg	gat	gaa	tat	963
Gln	Lys	Gly	Asp	Gln	Tyr	Asp	Val	Cys	Ala	Ile	Cys	Leu	Asp	Glu	Tyr	
225						230						235				
gag	gat	ggg	gac	aag	ctg	cgg	gta	ctc	ccc	tgt	gct	cat	gcc	tac	cac	1011
Glu	Asp	Gly	Asp	Lys	Leu	Arg	Val	Leu	Pro	Cys	Ala	His	Ala	Tyr	His	
240						245						250				
agc	cgc	tgc	gtg	gac	ccc	tgg	ctc	act	cag	acc	cgg	aag	acc	tgc	ccc	1059
Ser	Arg	Cys	Val	Asp	Pro	Trp	Leu	Thr	Gln	Thr	Arg	Lys	Thr	Cys	Pro	
255						260						265				

WO 00/29448

PCT/JP99/06412

29/233

att tgc aag cag cct gtt cat cgg ggt cct ggg gac gaa gac caa gag 1107
 Ile Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu
 270 275 280 285
 gaa gaa act caa ggg caa gag gag ggt gat gaa ggg gag cca agg gac 1155
 Glu Glu Thr Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp
 290 295 300
 cac cct gcc tca gaa agg acc cca ctt ttg ggt tct agc ccc act ctt 1203
 His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu
 305 310 315
 ccc acc tcc ttt ggt tcc tta gcc cca gct ccc ctt gtt ttt cct ggg 1251
 Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly
 320 325 330
 cct tca aca gat ccc cca ctg tcc cct ccc tct tcc cct gtt atc ctg 1299
 Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu
 335 340 345
 gtc taataacccc ccacacatac acctctggtg acctatttgc acagaccg 1350
 Val
 350
 togttttccc tccagtcttc tgagggatag gggacattcc atcccaagct tctcccttac 1410
 ccacacctat ctttttgagg ggctttgggg tggggctggg gcaagcagag ggactgggtc 1470
 ttcacttctt gggetaataa aattgtttct ttgtggact 1509

<210> 23

<211> 3059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (230)...(850)

<400> 23

cctggctccc gccagcctg ggattaggct tcgccggeta cgattgcggc ccccatcttc 60
 tgacttttcc togtgtgacc catcttttca aattccotta cctgaggaag gagcccgatt 120
 acaaggatat ttacctgctc ctacctgat ctagggaacga ggatgggaag accgcctgtg 180
 gccatgagcc ctccccgggtg ctccctggggc taaggctggg gctgcagcc atg ggg ctg 238
 Met Gly Leu

ggg	cag	ccc	cag	gcc	ggc	ttg	ctg	ggg	ctg	ccc	aca	gct	gtg	gtc	tat	286
Gly	Gln	Pro	Gln	Ala	Trp	Leu	Leu	Gly	Leu	Pro	Thr	Ala	Val	Val	Tyr	
5						10					15					
ggc	tcc	ctg	gct	ctc	ttc	acc	acc	atc	ctg	cac	aat	gtc	ttc	ctg	ctc	334
Gly	Ser	Leu	Ala	Leu	Phe	Thr	Thr	Ile	Leu	His	Asn	Val	Phe	Leu	Leu	
20					25				30			35				
tac	tat	gtg	gac	acc	ttt	gtc	tca	gtg	tac	aag	atc	aac	aaa	atg	gcc	382
Tyr	Tyr	Val	Asp	Thr	Phe	Val	Ser	Val	Tyr	Lys	Ile	Asn	Lys	Met	Ala	
				40				45				50				
ttc	tgg	gtc	gga	gag	aca	gtg	ttt	ctc	ctc	tgg	aac	agc	ctc	aat	gac	430
Phe	Trp	Val	Gly	Glu	Thr	Val	Phe	Leu	Leu	Trp	Asn	Ser	Leu	Asn	Asp	
			55				60				65					
ccc	ctc	ttc	ggg	tgg	ctc	agt	gac	cgg	cag	ttc	ctc	agc	tcc	cag	ccc	478
Pro	Leu	Phe	Gly	Trp	Leu	Ser	Asp	Arg	Gln	Phe	Leu	Ser	Ser	Gln	Pro	
	70				75				80							
cgg	gga	aga	gat	cta	ccc	tgg	ctt	ggc	ttg	gtt	ggc	ccc	tct	gga	ctg	526
Arg	Gly	Arg	Asp	Leu	Pro	Trp	Leu	Gly	Leu	Val	Gly	Pro	Ser	Gly	Leu	
85				90				95								
tgg	act	gca	aac	acc	ctc	tgc	tgc	ttc	tgg	aag	att	cct	ttg	ccc	cat	574
Trp	Thr	Ala	Asn	Thr	Leu	Cys	Cys	Phe	Trp	Lys	Ile	Pro	Leu	Pro	His	
100				105				110				115				
ccc	tgc	ttg	agc	ccg	tca	tca	ccc	cca	acc	ttg	aga	agt	ggg	cat	ccc	622
Pro	Cys	Leu	Ser	Pro	Ser	Ser	Pro	Pro	Thr	Leu	Arg	Ser	Gly	His	Pro	
			120				125				130					
ata	ccc	ttt	ggc	cat	cag	ccc	aac	agg	cta	ata	agg	ggg	tgg	aaa	ttg	670
Ile	Pro	Phe	Gly	His	Gln	Pro	Asn	Arg	Leu	Ile	Arg	Gly	Trp	Lys	Leu	
		135			140			145								
ggg	cag	agg	agg	aga	gtg	tac	cca	ctg	gtc	agg	cgc	cgg	gct	ctc	ctc	718
Gly	Gln	Arg	Arg	Arg	Val	Tyr	Pro	Leu	Val	Arg	Arg	Arg	Ala	Leu	Leu	
	150			155				160								
aag	ggc	tgt	ggg	gct	ggc	ccg	ggg	gca	ggc	cct	ggg	ctg	gca	tgg	gcc	766
Lys	Gly	Cys	Gly	Ala	Gly	Pro	Gly	Ala	Gly	Pro	Gly	Leu	Ala	Trp	Ala	
	165			170				175								
gct	gct	ggc	gct	gtc	gtt	cct	ggc	gtt	ctg	ggg	gcc	ctg	ggc	ccc	agc	814

WO 00/29448

PCT/JP99/06412

31/233

Ala Ala Gly Ala Val Val Pro Gly Val Leu Gly Ala Leu Gly Pro Ser	
180	185
190	195
tgg cct gca gtt ctt gct gtg cct gtg cct cta tgatggcttc ctg	860
Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu	
200	205
acgctcgtgg acctgcacca ccattgccttg ctggccgacc tggccctctc agcccacgac	920
cgcaccccacc tcaacttcta ctgctccctc ttcagcgcgg ccggtccct ctctgtcttt	980
gcatactatg ccttttgga caaggaggat ttctctctc tccgccttt ctgctgaca	1040
ctggctgtca gctctgggct gggtttctg ggggccacac agctgctgag gcggcgggtt	1100
gaggcggccc gaaaggacc aggtgtctca ggcctggttg tggatagcgg cctgtgtgga	1160
gaggagctgc ttgtaggcag tgaggaggcg gacagcatca ccttgggccc gtatctccgg	1220
cagctggcac gccatcggaa ctctctgttg ttctgtagca tggacctggg gcaggctctc	1280
cactgccact tcaacagcaa ctcttccct ctcttccctg agcatctgtt gtccgacct	1340
atctcccttt ccacgggctc catctgttg ggcctctct atgtcgtcc ccatctcaac	1400
aacctctact tcctgtccct gtgcgggcgc tggggcgtct acgcggtgg gcgggggctc	1460
ttctgtctca agctgggact tagcctgtc atgttgttg ccggcccga ccacctcagc	1520
ctgtgtgccc tcttcattgc cagcaacgc gtcttcactg agggcacctg taagctgtg	1580
accttggtag tcaactgacct ggtagacgag gacctggtgc tgaaccaccg caagcaggca	1640
gcctcggcac tctcttttg catggttgcc ttggtgacca agccaggcca gaccttgcc	1700
ccgtgctgg gcacctggt gctctgtttc tacacaggtc atgacctct ccagcagtc	1760
ctcataaccc ctgtggggag tgcccatccc tggccagagc cccagctcc agccctgca	1820
caggccccga cgtccgcca gggtgcttc tacctgctgg tctggtgccc catcactgt	1880
gctctgtgc agctcttcac ctggtcccag ttcacgtgc atgggagacg cctgcacatg	1940
gtcaaggccc agcgcagaa cctgtcacag gcccacccc tggatgttaa gatggtgtga	2000
gagctgtggc aaggtcacc cactgaggat gctgctggca gcctggggaa ggagccagtt	2060
ttttttggt ttttttttaa ggatttcata gtttttttt ttttttttg gagatgttg	2120
ccaaaaaat ggatctgttg cagtgtgca atctgggctc actgaaacca ccaccaggt	2180
tcaagcaatt atcctgcctc agcttcccga gtaggtggga ttataggagc gtgccacct	2240
gcccggtac tttttgtatt tttagtagag acagggtttc atcatgttg ccaggctagt	2300
ctcaaacccc tgacctagg tgatcagccc gcctcggcct cccagagtgc tgggattaca	2360
ggcgtgagcc actgtggcca acctaat ttt tgtattatt agtagagaca gggtttcacc	2420
acattggcca ggtggtctc gaactcctga cctcaagtga tctgcctgcc ttggtctccc	2480
aaagtgtgg gaatacaggc atgagccacc gcactcggcc aggagctagt tttaccagca	2540
tcctgtcca ctgcctcct ctagtgcagc ctggaagaca tggcagcggg tagctcctgg	2600
ggctgagcca gaagcatcac tgcagtgaat gtctctgctt acctgtctgg ctcagcttgg	2660

90

WO 00/29448

PCT/JP99/06412

33/233

cag tgc tgt ggc gca tat ggc cct gaa gac tgg gac ctc aac gtc tac	398
Gln Cys Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr	
95 100 105 110	
ttc aat tgc agc ggt gcc agc tac agc cga gag aag tgc ggg gtc ccc	446
Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro	
115 120 125	
ttc tcc tgc tgc gtg cca gat cct gcg caa aaa gtt gtg aac aca cag	494
Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln	
130 135 140	
tgt gga tat gat gtc agg att cag ctg aag agc aag tgg gat gag tcc	542
Cys Gly Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser	
145 150 155	
atc ttc acg aaa ggc tgc atc cag gcg ctg gaa agc tgg ctc ccg cgg	590
Ile Phe Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg	
160 165 170	
aac att tac att gtg gct ggc gtc ttc atc gcc atc tcg ctg ttg cag	638
Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln	
175 180 185 190	
ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag gca	686
Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala	
195 200 205	
gtg aag gcc ggc cat cac ttc tgaggagcag agttgaggga gccgagctga gcc	740
Val Lys Ala Gly His His Phe	
210	
acgctgggag gccagagcct ttctctgcca tcagccctac gtccagaggg agaggagccg	800
acacccccag agccagtgcc ccatcttaag catcagcgtg acgtgacctc tctgtttctg	860
cttgctggtg ctgaagacca aggggtcccc ttgttacctg cccaaacttg tgactgcac	920
cctctggagt ctacccagag acagagaatg tgtctttatg tgggagtggg gactctgaaa	980
gacagagagg gctcctgtgg ctgccaggag ggcttgactc agacccctg cagctcaagc	1040
atgtctgcag gacaccctgg tccccctctcc actggcatcc agacatctgc tttgggtcat	1100
ccacatctgt ggggtggccg tgggttagagg gaccacagg cgtggacagg gcactctct	1160
ccatcaagca aagcagcatg ggggcctgcc cgtaacggga ggcggacgtg gccccgctgg	1220
gcctctgagt gccagcgcag tctgctggga catgcacata tcaggggttg tttgcaggat	1280
cctcagccat gttcaagtga agtaagcctg agccagtgcg tggactggtg ccacgggagt	1340
gccttgtcca ctgtccccct gtgtccacca gctattctcc tggcgccgga actgcctctg	1400

WO 00/29448

PCT/JP99/06412

34/233

```

gtcttgatag cattaagccc tgatggcgcc ggtggcgcg tgggcatggt tcttactga 1460
gagccggctc tccttttctt aaagtgtgta aatagtttat ttataggggt aagaatgttc 1520
tcacaccatt tcacttcctc ttctctcct ccagcattct cctctgagca gccttagata 1580
gtgtccatgg ctggagccga ccctttgagt ccctttgagt gtcttaagaa ccagcccaca 1640
acagcctctc tttctcctcc acatactgca gcctccctcc atgcatccca catacaagca 1700
ctccccact cccagcgtg gcctcactgt cttctggtct tgggtgctact gaaattgtca 1760
cccagaattt gaatcctgac cctccccact gcaagcccag ggagccccag cccaagatgg 1820
ccagcctgaa actgttggcc agggctcctc ttgtggccat gtaccaggg ctggctggcc 1880
tgccatttgc ctctccccg agacagccgt tcttctgcaa ccacaccccg tgcctagcca 1940
caaccccagg ctgcagctgc tcagaagctc caggcatttt gtttctggtg accgccccta 2000
atgggatatc ggtgatcact ggtccaccct tcctgtcagg gcttttctgg ggctgctctt 2060
ggaaatgaag tcttaagtac tgaataactc ccctggggat agctggggca tttgtctagc 2120
tgggctactt tctaactt tgccatagct cagaccactt ctcacgttc agggatggac 2180
tgcaacctta atttacttgc cggagtgtac attctagtgt ggtgtatact ggtggctgtt 2240
gatgatgatt tttttttttt ttttttacac aattctctgt agactaggag aagaatgctt 2300
gtgtttttcg gaagtgtgat gcttctcttt gactgccaaa ctcttttatg gaatatatct 2360
ttatatt 2367

```

<210> 25

<211> 2355

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)...(1807)

<400> 25

```

agccgcccaa gcgcccgc atg cgc gct gcc cgc gcc gcg ccg ctg ctc cag 52
Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln
1 5 10
ctg ctg ctc ctg ctg ggg ccg tgg ctg gag gct gcg ggc gtt gcg gag 100
Leu Leu Leu Leu Leu Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu
15 20 25
tcg ccg ctg ccc gcc gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa 148
Ser Pro Leu Pro Ala Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu
30 35 40

```

WO 00/29448

PCT/JP99/06412

35/233

cac tgc ctg ccc cac tac ctg ggc gct ctg gag cgg ctg gac tac ccc	196
His Ser Leu Pro His Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro	
45 50 55	
cgg gcc agg atg gcc ctc tgg tgt gcc acg gac cac aat gtg gac aac	244
Arg Ala Arg Met Ala Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn	
60 65 70 75	
acc aca gag atg ctg cag gag tgg ctg gcg gct gtg ggc gat gac tat	292
Thr Thr Glu Met Leu Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr	
80 85 90	
gct gct gtg gtc tgg agg cct gag ggc gag ccc agg ttc tac cca gat	340
Ala Ala Val Val Trp Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp	
95 100 105	
gaa gag ggt ccc aag cac tgg acc aaa gaa agg cac cag ttt ctg atg	388
Glu Glu Gly Pro Lys His Trp Thr Lys Glu Arg His Gln Phe Leu Met	
110 115 120	
gag ctg aag cag gaa gcc ctc acc ttt gcc agg aac tgg ggg gcc gac	436
Glu Leu Lys Gln Glu Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp	
125 130 135	
tat atc ctg ttt gca gac aca gac aac att ctg acc aac aat cag act	484
Tyr Ile Leu Phe Ala Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr	
140 145 150 155	
ctg cgg ctt ctc atg ggg cag ggg ctt cca gtg gtg gcc cca atg ctg	532
Leu Arg Leu Leu Met Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu	
160 165 170	
gac tcc cag acc tac tac tcc aac ttc tgg tgt ggg atc acc ccc cag	580
Asp Ser Gln Thr Tyr Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln	
175 180 185	
ggc tac tac cgc cgc aca gcc gag tac ttc ccc acc aag aac cgc cag	628
Gly Tyr Tyr Arg Arg Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln	
190 195 200	
cgc cgg ggc tgc ttc cgt gtc ccc atg gtc cac tcc acc ttc ctt gca	676
Arg Arg Gly Cys Phe Arg Val Pro Met Val His Ser Thr Phe Leu Ala	
205 210 215	
tcc ctg cgg gct gaa ggg gca gac cag ctt gct ttc tac ccg cca cat	724
Ser Leu Arg Ala Glu Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His	

WO 00/29448

PCT/JP99/06412

36/233

220	225	230	235	
ccc aac tac act tgg cct ttc gac gac atc atc gtc ttc gcc tat gcc				772
Pro Asn Tyr Thr Trp Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala				
	240	245	250	
tgc cag gct gct ggg gtc tcc gtc cac gtg tgc aat gag cac cgt tat				820
Cys Gln Ala Ala Gly Val Ser Val His Val Cys Asn Glu His Arg Tyr				
	255	260	265	
ggg tac atg aat gtg ccg gtg aaa tcc cac cag ggg ctg gaa gac gag				868
Gly Tyr Met Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu				
	270	275	280	
agg gtc aac ttc atc cac ctg atc tta gaa gca cta gtg gac ggc ccc				916
Arg Val Asn Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro				
	285	290	295	
cgc atg cag gcc tca gct cat gtg act cgg ccc tct aag agg ccc agc				964
Arg Met Gln Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser				
300	305	310	315	
aag ata ggg ttt gac gag gtc ttt gtc atc agc ctg gct cgc agg cct				1012
Lys Ile Gly Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro				
	320	325	330	
gac cgt cgg gaa cgc atg ctc gcc tcg ctc tgg gag atg gag atc tct				1060
Asp Arg Arg Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser				
	335	340	345	
ggg agg gtg gtg gac gct gtg gat ggc tgg atg ctc aac agc agt gcc				1108
Gly Arg Val Val Asp Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala				
	350	355	360	
atc agg aac ctc ggc gta gac ctg ctc ccg ggc tac cag gac cct tac				1156
Ile Arg Asn Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr				
	365	370	375	
tcg ggc cgc act ctg acc aag ggc gag gtg ggc tgc ttc ctc agc cat				1204
Ser Gly Arg Thr Leu Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His				
380	385	390	395	
tac tcc atc tgg gaa gag gtg gtt gcc agg ggc ctg gcc cgg gtc ctg				1252
Tyr Ser Ile Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu				
	400	405	410	
gtg ttt gag gat gac gtg cgc ttt gag agc aac ttc agg ggg cgg ctg				1300

WO 00/29448

PCT/JP99/06412

37/233

Val Phe Glu Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu	
415 420 425	
gag cgg ctg atg gag gat gtg gag gca gag aaa ctg tct tgg gac ctg	1348
Glu Arg Leu Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu	
430 435 440	
atc tac ctc gga cgg aag cag gtg aac cct gag aag gag acg gcc gtg	1396
Ile Tyr Leu Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val	
445 450 455	
gag ggg ctg ccg ggc ctg gtg gtg gct ggg tac tcc tac tgg acg ctg	1444
Glu Gly Leu Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu	
460 465 470 475	
gcc tat gcc ctg cgt ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag	1492
Ala Tyr Ala Leu Arg Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln	
480 485 490	
cct ctg cgc cgc atg ctg ccc gtg gac gag ttc ctg ccc atc atg ttc	1540
Pro Leu Arg Arg Met Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe	
495 500 505	
gac cag cac ccc aac gag cag tac aag gca cac ttc tgg cca cgg gac	1588
Asp Gln His Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp	
510 515 520	
ctg gtg gcc ttc tcc gcc cag ccc ctg ctc gct gcc cct acc cac tat	1636
Leu Val Ala Phe Ser Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr	
525 530 535	
gcc ggg gac gcc gag tgg ctc agt gac acg gag aca tcc tct cca tgg	1684
Ala Gly Asp Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp	
540 545 550 555	
gat gat gac agc ggc cgc ctc atc agc tgg agc ggc tcc caa aag acc	1732
Asp Asp Asp Ser Gly Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr	
560 565 570	
ctg cgc agc ccc cgc ctg gac ctg act ggc agc agc ggg cac agc ctc	1780
Leu Arg Ser Pro Arg Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu	
575 580 585	
caa ccc cag ccc cga gat gag ctc taggtccagg tgatgactgc aaagca	1830
Gln Pro Gln Pro Arg Asp Glu Leu	
590 595	

WO 00/29448

PCT/JP99/06412

38/233

gtgtccagga gcaggccact actgccaga gagcagagga ggaggttgtt ggcagggact 1890
gcagatcctg tcagacctgg ccaccacctt gggcatggcc actctgccct ctggacctgt 1950
ctttcatcgg gagaaaccac tcagagatgg atcccattcc ctaaaggtct cacagcaaaag 2010
gagcaggact cccaggcccc tgtaccctgc ctggcctgat tcagggcctt gtggccccc 2070
gcttctgttt caagctgggc agaccccagg atcccttccc tccctaagga ctcagctgag 2130
gggcccctct gccccttct acctccacct cagcaccctc ccccagcttg atgtttgggt 2190
ctccccagca cctcctccc tggccggtgc aaagtacagg gaggtaaagc aggacccttg 2250
cagacatgtt gccagcaca cagtaggccc tcaataaaag ccatttgac tttaaatata 2310
tatatgtatg tatatatatg tatatatata tatatatata tatgt 2355

<210> 26

<211> 1024

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27)...(821)

<400> 26

cggatggaag ctccggccgc ggagtg atg gtg gcc tca gcg aag atg ggc cgg 53
Met Val Ala Ser Ala Lys Met Gly Arg
1 5
gca ggg acc atg gcg gtg gca gca gag ctt cga gag ctg tgc cca gga 101
Ala Gly Thr Met Ala Val Ala Ala Glu Leu Arg Glu Leu Cys Pro Gly
10 15 20 25
gtg aac aac cag ccc tac ctc tgt gag agt ggt cac tgc tgc ggg gag 149
Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His Cys Cys Gly Glu
30 35 40
act ggc tgc tgc acc tac tac tat gag ctc tgg tgg ttc tgg ctg ctc 197
Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Leu
45 50 55
tgg act gtc ctc atc ctc ttt agc tgc tgt tgc gcc ttc cgc cac cga 245
Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala Phe Arg His Arg
60 65 70
cga gct aaa ctc agg ctg caa caa cag cag cgg cag cgt gaa atc aac 293
Arg Ala Lys Leu Arg Leu Gln Gln Gln Gln Arg Gln Arg Glu Ile Asn

WO 00/29448

PCT/JP99/06412

39/233

75	80	85	
ttg ttg gcc tat cat ggg gca tgc cat ggg gct ggt cct ttc cct acc			341
Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly Pro Phe Pro Thr			
90	95	100	105
ggg tca ctg ctt gac ctt cgc ttc ctc agc acc ttc aag ccc cca gcc			389
Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala			
110	115	120	
tac gag gat gtg gtt cac cgc cca ggc aca cca ccc ccc cct tat act			437
Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro Pro Pro Tyr Thr			
125	130	135	
gtg gcc cca ggc cgc ccc ttg act gct tcc agt gaa caa acc tgc tgt			485
Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu Gln Thr Cys Cys			
140	145	150	
tcc tcc tca tcc agc tgc cct gcc cac ttt gaa gga aca aat gtg gaa			533
Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly Thr Asn Val Glu			
155	160	165	
ggg gtt tcc tcc cac cag agt gcc ccc ccc cat cag gag ggt gag ccc			581
Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln Glu Gly Glu Pro			
170	175	180	185
ggg gca ggg gtg acc cct gcc tcc aca ccc ccc tcc tgc cgc tat cgc			629
Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser Cys Arg Tyr Arg			
190	195	200	
cgt tta act ggc gac tcc ggt att gag ctc tgc cct tgt cct gcc tcc			677
Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro Cys Pro Ala Ser			
205	210	215	
ggg gag ggt gag cca gtc aag gag gtg agg gtt agt gcc acc ctg cca			725
Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser Ala Thr Leu Pro			
220	225	230	
gat ctg gag gac tac tcc ccg tgt gca cta ccc cca gag tct gta ccg			773
Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro Glu Ser Val Pro			
235	240	245	
cag atc ttt ccc atg ggg ctg tct tcc agt gaa ggg gac atc cca			818
Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Glu Gly Asp Ile Pro			
250	255	260	
ta agtagttttg agaggggtgga tgggttactt gccaccaga aacagcccta			870

WO 00/29448

PCT/JP99/06412

40/233

gtcccaactc cttgcgttcc tttggccct cctgcctac ctagaatctg cctgaaaggg 930
ctggagaggg gcagtattgg gggactgtgc tagctttacc cccgcaggac atacacagga 990
gcctttgatc tcattaaaga gatgtgaacc agct 1024

<210> 27

<211> 1237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24)...(1055)

<400> 27

tactggctac tggcgctgca gcc atg cag ccc ccg ccc ccg ggc ccg ctg ggc 53
Met Gln Pro Pro Pro Pro Gly Pro Leu Gly
1 5 10
gac tgc ctg cgg gac tgg gag gat cta cag cag gac ttc cag aac atc 101
Asp Cys Leu Arg Asp Trp Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile
15 20 25
cag gag acc cat cgg ctc tac cgc ctg aag ctg gag gag ctg acc aaa 149
Gln Glu Thr His Arg Leu Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys
30 35 40
ctt cag aac aat tgc acc agc tcc atc acg cgg cag aag aag cgg ctc 197
Leu Gln Asn Asn Cys Thr Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu
45 50 55
cag gag ctg gcc ctc gcc ctg aag aaa tgc aaa ccc tcc ctc cca gca 245
Gln Glu Leu Ala Leu Ala Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala
60 65 70
gag gcc gag ggg gcc gca cag gag ctg gag aac cag atg aaa gag cgc 293
Glu Ala Glu Gly Ala Ala Gln Glu Leu Glu Asn Gln Met Lys Glu Arg
75 80 85 90
caa ggc ctc ttc ttt gac atg gag gcc tat ttg cct aag aag aat gga 341
Gln Gly Leu Phe Phe Asp Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly
95 100 105
ttg tac ctg agc ctg gtt ctg ggg aac gtc aac gtc acg ctc ctg agc 389
Leu Tyr Leu Ser Leu Val Leu Gly Asn Val Asn Val Thr Leu Leu Ser

	110	115	120	
aag cag gct aag ttt gcc tac aag gac gag tat gag aag ttc aag ctc				437
Lys Gln Ala Lys Phe Ala Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu				
125	130	135		
tac ctc acc atc atc ctc atc ctc atc tcc ttc act tgc cgc ttc ctg				485
Tyr Leu Thr Ile Ile Leu Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu				
140	145	150		
ctc aac tcc agg gtg aca gat gct gcc ttc aac ttc ctg ctg gtc tgg				533
Leu Asn Ser Arg Val Thr Asp Ala Ala Phe Asn Phe Leu Leu Val Trp				
155	160	165	170	
tac tac tgc acc ctg acc atc cgg gag agc atc ctc atc aac aac ggc				581
Tyr Tyr Cys Thr Leu Thr Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly				
175	180	185		
tcc cgg atc aaa ggc tgg tgg gtg ttc cat cac tac gtg tcc acc ttc				629
Ser Arg Ile Lys Gly Trp Trp Val Phe His His Tyr Val Ser Thr Phe				
190	195	200		
ctg tcg gga gtc atg ctg acg tgg ccc gac ggt ctc atg tac cag aaa				677
Leu Ser Gly Val Met Leu Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys				
205	210	215		
ttc cgg aac caa ttc ctc tcc ttt tcc atg tac cag agc ttc gtg cag				725
Phe Arg Asn Gln Phe Leu Ser Phe Ser Met Tyr Gln Ser Phe Val Gln				
220	225	230		
ttt ctc cag tac tac tac cag agc ggc tgc ctc tac cgc ctg cgg gcg				773
Phe Leu Gln Tyr Tyr Tyr Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala				
235	240	245	250	
ctg ggc gag cgg cac acc atg gac ctc act gtg gag ggc ttc cag tcc				821
Leu Gly Glu Arg His Thr Met Asp Leu Thr Val Glu Gly Phe Gln Ser				
255	260	265		
tgg atg tgg cgg ggc ctc acc ttc ctg ctg cct ttt ctt ttc ttt gga				869
Trp Met Trp Arg Gly Leu Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly				
270	275	280		
cac ttc tgg cag ctt ttt aac gcg ctg acg ttg ttc aac ctg gcc cag				917
His Phe Trp Gln Leu Phe Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln				
285	290	295		
gac cct cag tgc aag gag tgg cag gtg ctt atg tgc gcc ttt ccc ttc				965

agtgcgccag	cggaagcaca	gtcagagct	ggtctgcc	atg	gac	atc	ctg	gtc	cca	56						
					Met	Asp	Ile	Leu	Val	Pro						
				1					5							
ctc	ctg	cag	ctg	ctg	gtg	ctg	ctt	ctt	acc	ctg	ccc	ctg	cac	ctc	atg	104
Leu	Leu	Gln	Leu	Leu	Val	Leu	Leu	Leu	Thr	Leu	Pro	Leu	His	Leu	Met	
		10						15					20			
gct	ctg	ctg	ggc	tgc	tgg	cag	ccc	ctg	tgc	aaa	agc	tac	ttc	ccc	tac	152
Ala	Leu	Leu	Gly	Cys	Trp	Gln	Pro	Leu	Cys	Lys	Ser	Tyr	Phe	Pro	Tyr	
		25						30					35			
ctg	atg	gcc	gtg	ctg	act	ccc	aag	agc	aac	cgc	aag	atg	gag	agc	aag	200
Leu	Met	Ala	Val	Leu	Thr	Pro	Lys	Ser	Asn	Arg	Lys	Met	Glu	Ser	Lys	
		40						45					50			
aaa	cgg	gag	ctc	ttc	agc	cag	ata	aag	ggg	ctt	aca	gga	gcc	tcc	ggg	248
Lys	Arg	Glu	Leu	Phe	Ser	Gln	Ile	Lys	Gly	Leu	Thr	Gly	Ala	Ser	Gly	
55					60					65					70	

WO 00/29448

PCT/JP99/06412

43/233

aaa gtg gcc cta ctg gag ctg ggc tgc gga acc gga gcc aac ttt cag	296
Lys Val Ala Leu Leu Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln	
75 80 85	
ttc tac cca ccg ggc tgc agg gtc acc tgc cta gac cca aat ccc cac	344
Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His	
90 95 100	
ttt gag aag ttc ctg aca aag agc atg gct gag aac agg cac ctc caa	392
Phe Glu Lys Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln	
105 110 115	
tat gag cgg ttt gtg gtg gct cct gga gag gac atg aga cag ctg gct	440
Tyr Glu Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala	
120 125 130	
gat ggc tcc atg gat gtg gtg gtc tgc act ctg gtg ctg tgc tct gtg	488
Asp Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val	
135 140 145 150	
cag agc cca agg aag gtc ctg cag gag gtc cgg aga gta ctg aga ccg	536
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg Pro	
155 160 165	
gga ggt gtg ctc ttt ttc tgg gag cat gtg gca gaa cca tat gga agc	584
Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr Gly Ser	
170 175 180	
tgg gcc ttc atg tgg cag caa gtt ttc gag ccc acc tgg aaa cac att	632
Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp Lys His Ile	
185 190 195	
ggg gat ggc tgc tgc ctc acc aga gag acc tgg aag gat ctt gag aac	680
Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys Asp Leu Glu Asn	
200 205 210	
gcc cag ttc tcc gaa atc caa atg gaa cga cag ccc cct ccc ttg aag	728
Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln Pro Pro Pro Leu Lys	
215 220 225 230	
tgg cta cct gtt ggg ccc cac atc atg gga aag gct gtc aaa taatcttcc	780
Trp Leu Pro Val Gly Pro His Ile Met Gly Lys Ala Val Lys	
235 240	
caagetccaa ggcactcatt tgetccttcc ccagctcca attagaacaa gccacccacc	840
agcctatcta tcttccactg agagggacct agcagaatga gagaagacat tcatgtacca	900

85

ccc	ctg	tgg	gtg	cag	tac	cct	cag	gat	gtg	act	acc	ttc	aat	ata	gat	343
Pro	Leu	Trp	Val	Gln	Tyr	Pro	Gln	Asp	Val	Thr	Thr	Phe	Asn	Ile	Asp	
90				95				100								
gat	cag	tac	ttg	ctt	ggg	gat	gcg	ttg	ctg	gtt	cac	cct	gta	tca	gac	391
Asp	Gln	Tyr	Leu	Leu	Gly	Asp	Ala	Leu	Leu	Val	His	Pro	Val	Ser	Asp	
105				110				115								
tct	gga	gcc	cat	ggg	gtc	cag	gtc	tat	ctg	cct	ggc	caa	ggg	gag	gtg	439
Ser	Gly	Ala	His	Gly	Val	Gln	Val	Tyr	Leu	Pro	Gly	Gln	Gly	Glu	Val	
120				125				130								
tgg	tat	gac	att	caa	agc	tac	cag	aag	cat	cat	ggg	ccc	cag	acc	ctg	487
Trp	Tyr	Asp	Ile	Gln	Ser	Tyr	Gln	Lys	His	His	Gly	Pro	Gln	Thr	Leu	
135				140				145				150				
tac	ctg	cct	gta	act	cta	agc	agt	atc	cct	gtg	ttc	cag	cgt	gga	ggg	535
Tyr	Leu	Pro	Val	Thr	Leu	Ser	Ser	Ile	Pro	Val	Phe	Gln	Arg	Gly	Gly	
155				160				165								
aca	atc	gtg	cct	cga	tgg	atg	cga	gtg	cgg	cgg	tct	tca	gaa	tgt	atg	583
Thr	Ile	Val	Pro	Arg	Trp	Met	Arg	Val	Arg	Arg	Ser	Ser	Glu	Cys	Met	
170				175				180								
aag	gat	gac	ccc	atc	act	ctc	ttt	gtt	gca	ctt	agc	cct	cag	ggg	aca	631
Lys	Asp	Asp	Pro	Ile	Thr	Leu	Phe	Val	Ala	Leu	Ser	Pro	Gln	Gly	Thr	
185				190				195								
gct	caa	gga	gag	ctc	ttt	ctg	gat	gat	ggg	cac	acg	ttc	aac	tat	cag	679
Ala	Gln	Gly	Glu	Leu	Phe	Leu	Asp	Asp	Gly	His	Thr	Phe	Asn	Tyr	Gln	
200				205				210								
act	cgc	caa	gag	ttc	ctg	ctg	cgt	cga	ttc	tca	ttc	tct	ggc	aac	acc	727
Thr	Arg	Gln	Glu	Phe	Leu	Leu	Arg	Arg	Phe	Ser	Phe	Ser	Gly	Asn	Thr	
215				220				225				230				
ctt	gtc	tcc	agc	tca	gca	gac	cct	gaa	gga	cac	ttt	gag	aca	cca	atc	775
Leu	Val	Ser	Ser	Ser	Ala	Asp	Pro	Glu	Gly	His	Phe	Glu	Thr	Pro	Ile	
235				240				245								
tgg	att	gag	cgg	gtg	gtg	ata	ata	ggg	gct	gga	aag	cca	gca	gct	gtg	823
Trp	Ile	Glu	Arg	Val	Val	Ile	Ile	Gly	Ala	Gly	Lys	Pro	Ala	Ala	Val	
250				255				260								
gta	ctc	cag	aca	aaa	gga	tct	cca	gaa	agc	cgc	ctg	tcc	ttc	cag	cat	871
Val	Leu	Gln	Thr	Lys	Gly	Ser	Pro	Glu	Ser	Arg	Leu	Ser	Phe	Gln	His	

WO 00/29448

PCT/JP99/06412

46/233

265	270	275	
gac cct gag acc tct gtg ttg gtc ctg cgc aag cct ggc atc aat gtg			919
Asp Pro Glu Thr Ser Val Leu Val Leu Arg Lys Pro Gly Ile Asn Val			
280	285	290	
gca tct gat tgg agt att cac ctg cga taacccaagg gatgttctgg gtta			970
Ala Ser Asp Trp Ser Ile His Leu Arg			
295	300		
gggggaggggaggagggagcat tagtgctgag agatattcctt tcttctgcct tggagttcgg			1030
ccctccccag acttcaactta tgctagtota agaccagat tctgccaaca tttgggcagg			1090
atgagaggggctgacctggg ctccaaattc ctcttgtgat ctctcacct ctccactcc			1150
attgatacca actctttccc ttcattcccc caacatcctg ttgctctaac tggagcacat			1210
tcaactacga acaccaggaa accacagggc ccttgctgcc ccttctcttt cccttattta			1270
ggagccctga actccccag agtctatcca ttcattgcctc ttgtatgttg atgccacttc			1330
ttggaagaag atgagggcaa tgagttaggg ctctctttcc ccttccctcc caccagattg			1390
ctctccccc tttcatttct tctccaggc tttactcccc tttttatgcc ccaccgatac			1450
actgggacca ccccttacc cggacaggat gaatggatca aaggagttag gttgctaaag			1510
aacatccttt tccctctcat tctacccttt tctctcccc gattccttgt agagctgctg			1570
caattcttag aggggcagtt ctacctctc tgtccctcgg cagaaagacg tttccacacc			1630
tcttagggga tgcgcattaa acttcttttg ccccttctt gtccctttg aggggcactt			1690
aagatggaga aatcagttgt ggtttcagtg aatcatgggc acctgtattt attgctagga			1750
gaagcctgag ggtgggggga gatgatcatg tgtgctcggg gttggctgga agccctgggt			1810
ggggggttg gggaggacta atggggagtc ggggaatatt tgtgggtatt tttttactt			1870
cctcttggtt cccagctgtg acacgttttg atcaaaggag aaacaataaa gggataaacc			1930
at			1932

<210> 30

<211> 1124

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73)...(555)

<400> 30

ggaagagccg tcaacttagc gagcgcaaca ggctgccgct gaggagctgg agctggtggg	60
gactggggccg ca atg gac aag ctg aag aag gtg ctg agc ggg cag gac acg	111

[illegible]

WO 00/29448

PCT/JP99/06412

48/233

agtggaaatct tcctcatgta cctgtttcct ctctggatgt tgtcccaactg aattcccatg 840
aatacaaacc tattcagcaa cagcacataa gccttgggtg caagtgattc ccaggtggca 900
aaaggcagcc ccatcagaga tcacgggagc aacagtaagg gacagagttt tgggggtccac 960
ttgtccctca gcatggaagc catcacctgt gtccctgcata gagtgagtct acttctactc 1020
tggcatctga gaacaagtga ctctgcttta gacaagcccc tggagagcct ggccatggag 1080
tgaggtagaa aagaagcact ttttggtggt atatgctgtt tctg 1124

<210> 31

<211> 1445

<212> PRT

<213> Homo sapiens

<400> 31

Met Gln Gly Pro Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys
1 5 10 15
Thr Ala Ala Leu Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala
20 25 30
Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
35 40 45
Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
50 55 60
Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
65 70 75 80
Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
85 90 95
Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
100 105 110
Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
115 120 125
Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
130 135 140
Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
145 150 155 160
Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
165 170 175
Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr

WO 00/29448

PCT/JP99/06412

50/233

Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
 465 470 475 480
 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
 485 490 495
 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
 500 505 510
 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
 515 520 525
 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
 530 535 540
 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
 545 550 555 560
 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
 565 570 575
 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
 580 585 590
 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
 595 600 605
 Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly
 610 615 620
 Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val
 625 630 635 640
 Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp
 645 650 655
 Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile
 660 665 670
 Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys
 675 680 685
 His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg
 690 695 700
 Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp
 705 710 715 720
 Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr
 725 730 735
 Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu

	740						745						750											
Asn	Leu	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Glu	Phe	Ala	Leu	Glu	Ile									
	755						760						765											
Thr	Ile	Phe	Asn	Tyr	Leu	Lys	Asp	Ala	Thr	Glu	Val	Lys	Val	Ile	Ile									
	770						775						780											
Glu	Lys	Ser	Asp	Lys	Phe	Asp	Ile	Leu	Met	Thr	Ser	Ser	Glu	Ile	Asn									
785							790						795						800					
Ala	Thr	Gly	His	Gln	Gln	Thr	Leu	Leu	Val	Pro	Ser	Glu	Asp	Gly	Ala									
	805						810						815											
Thr	Val	Leu	Phe	Pro	Ile	Arg	Pro	Thr	His	Leu	Gly	Glu	Ile	Pro	Ile									
	820						825						830											
Thr	Val	Thr	Ala	Leu	Ser	Pro	Thr	Ala	Ser	Asp	Ala	Ile	Thr	Gln	Met									
	835						840						845											
Ile	Leu	Val	Lys	Ala	Glu	Gly	Ile	Glu	Lys	Ser	Tyr	Ser	Gln	Ser	Ile									
	850						855						860											
Leu	Leu	Asp	Leu	Thr	Asp	Asn	Arg	Leu	Gln	Ser	Thr	Leu	Lys	Thr	Leu									
865							870						875						880					
Ser	Phe	Ser	Phe	Pro	Pro	Asn	Thr	Val	Thr	Gly	Ser	Glu	Arg	Val	Gln									
	885						890						895											
Ile	Thr	Ala	Ile	Gly	Asp	Val	Leu	Gly	Pro	Ser	Ile	Asn	Gly	Leu	Ala									
	900						905						910											
Ser	Leu	Ile	Arg	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	Asn									
	915						920						925											
Phe	Ala	Pro	Asn	Ile	Tyr	Ile	Leu	Asp	Tyr	Leu	Thr	Lys	Lys	Lys	Gln									
	930						935						940											
Leu	Thr	Asp	Asn	Leu	Lys	Glu	Lys	Ala	Leu	Ser	Phe	Met	Arg	Gln	Gly									
945							950						955						960					
Tyr	Gln	Arg	Glu	Leu	Leu	Tyr	Gln	Arg	Glu	Asp	Gly	Ser	Phe	Ser	Ala									
	965						970						975											
Phe	Gly	Asn	Tyr	Asp	Pro	Ser	Gly	Ser	Thr	Trp	Leu	Ser	Ala	Phe	Val									
	980						985						990											
Leu	Arg	Cys	Phe	Leu	Glu	Ala	Asp	Pro	Tyr	Ile	Asp	Ile	Asp	Gln	Asn									
	995						1000						1005											
Val	Leu	His	Arg	Thr	Tyr	Thr	Trp	Leu	Lys	Gly	His	Gln	Lys	Ser	Asn									
	1010						1015						1020											

Gly	Glu	Phe	Trp	Asp	Pro	Gly	Arg	Val	Ile	His	Ser	Glu	Leu	Gln	Gly
1025					1030					1035					1040
Gly	Asn	Lys	Ser	Pro	Val	Thr	Leu	Thr	Ala	Tyr	Ile	Val	Thr	Ser	Leu
				1045					1050					1055	
Leu	Gly	Tyr	Arg	Lys	Tyr	Gln	Pro	Asn	Ile	Asp	Val	Gln	Glu	Ser	Ile
			1060					1065					1070		
His	Phe	Leu	Glu	Ser	Glu	Phe	Ser	Arg	Gly	Ile	Ser	Asp	Asn	Tyr	Thr
			1075					1080				1085			
Leu	Ala	Leu	Ile	Thr	Tyr	Ala	Leu	Ser	Ser	Val	Gly	Ser	Pro	Lys	Ala
	1090					1095					1100				
Lys	Glu	Ala	Leu	Asn	Met	Leu	Thr	Trp	Arg	Ala	Glu	Gln	Glu	Gly	Gly
1105				1110						1115					1120
Met	Gln	Phe	Trp	Val	Ser	Ser	Glu	Ser	Lys	Leu	Ser	Asp	Ser	Trp	Gln
				1125					1130					1135	
Pro	Arg	Ser	Leu	Asp	Ile	Glu	Val	Ala	Ala	Tyr	Ala	Leu	Leu	Ser	His
			1140					1145					1150		
Phe	Leu	Gln	Phe	Gln	Thr	Ser	Glu	Gly	Ile	Pro	Ile	Met	Arg	Trp	Leu
	1155						1160					1165			
Ser	Arg	Gln	Arg	Asn	Ser	Leu	Gly	Gly	Phe	Ala	Ser	Thr	Gln	Asp	Thr
	1170					1175					1180				
Thr	Val	Ala	Leu	Lys	Ala	Leu	Ser	Glu	Phe	Ala	Ala	Leu	Met	Asn	Thr
1185				1190						1195					1200
Glu	Arg	Thr	Asn	Ile	Gln	Val	Thr	Val	Thr	Gly	Pro	Ser	Ser	Pro	Ser
				1205					1210					1215	
Pro	Val	Lys	Phe	Leu	Ile	Asp	Thr	His	Asn	Arg	Leu	Leu	Leu	Gln	Thr
			1220					1225					1230		
Ala	Glu	Leu	Ala	Val	Val	Gln	Pro	Thr	Ala	Val	Asn	Ile	Ser	Ala	Asn
	1235					1240					1245				
Gly	Phe	Gly	Phe	Ala	Ile	Cys	Gln	Leu	Asn	Val	Val	Tyr	Asn	Val	Lys
	1250					1255					1260				
Ala	Ser	Gly	Ser	Ser	Arg	Arg	Arg	Arg	Ser	Ile	Gln	Asn	Gln	Glu	Ala
1265				1270					1275					1280	
Phe	Asp	Leu	Asp	Val	Ala	Val	Lys	Glu	Asn	Lys	Asp	Asp	Leu	Asn	His
				1285					1290					1295	
Val	Asp	Leu	Asn	Val	Cys	Thr	Ser	Phe	Ser	Gly	Pro	Gly	Arg	Ser	Gly

WO 00/29448

PCT/JP99/06412

53/233

1300	1305	1310
Met Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser		
1315	1320	1325
Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His		
1330	1335	1340
Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys		
1345	1350	1355
Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp		
1365	1370	1375
Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val		
1380	1385	1390
Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser		
1395	1400	1405
Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His		
1410	1415	1420
His His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe		
1425	1430	1435
Met Glu Leu Trp Leu		1440
1445		

<210> 32

<211> 582

<212> PRT

<213> Homo sapiens

<400> 32

Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu		
1	5	10
Leu Gln Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly		
20	25	30
Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg		
35	40	45
Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe		
50	55	60
Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp		
65	70	75
		80

WO 00/29448

PCT/JP99/06412

54/233

Ser	Ser	Tyr	Asp	Arg	Asn	Thr	Leu	Val	Ala	Ile	Val	Val	Gly	Val	Gly
					85				90					95	
Arg	Leu	Ile	Thr	Gly	Met	Asp	Arg	Gly	Leu	Met	Gly	Met	Cys	Val	Asn
				100				105					110		
Glu	Arg	Arg	Arg	Leu	Ile	Val	Pro	Pro	His	Leu	Gly	Tyr	Gly	Ser	Ile
				115			120					125			
Gly	Leu	Ala	Gly	Leu	Ile	Pro	Pro	Asp	Ala	Thr	Leu	Tyr	Phe	Asp	Val
		130				135					140				
Val	Leu	Leu	Asp	Val	Trp	Asn	Lys	Glu	Asp	Thr	Val	Gln	Val	Ser	Thr
145						150				155				160	
Leu	Leu	Arg	Pro	Pro	His	Cys	Pro	Arg	Met	Val	Gln	Asp	Gly	Asp	Phe
					165				170					175	
Val	Arg	Tyr	His	Tyr	Asn	Gly	Thr	Leu	Leu	Asp	Gly	Thr	Ser	Phe	Asp
				180				185					190		
Thr	Ser	Tyr	Ser	Lys	Gly	Gly	Thr	Tyr	Asp	Thr	Tyr	Val	Gly	Ser	Gly
		195					200					205			
Trp	Leu	Ile	Lys	Gly	Met	Asp	Gln	Gly	Leu	Leu	Gly	Met	Cys	Pro	Gly
		210				215					220				
Glu	Arg	Arg	Lys	Ile	Ile	Ile	Pro	Pro	Phe	Leu	Ala	Tyr	Gly	Glu	Lys
225					230					235				240	
Gly	Tyr	Gly	Thr	Val	Ile	Pro	Pro	Gln	Ala	Ser	Leu	Val	Phe	His	Val
				245					250				255		
Leu	Leu	Ile	Asp	Val	His	Asn	Pro	Lys	Asp	Ala	Val	Gln	Leu	Glu	Thr
				260					265				270		
Leu	Glu	Leu	Pro	Pro	Gly	Cys	Val	Arg	Arg	Ala	Gly	Ala	Gly	Asp	Phe
			275				280					285			
Met	Arg	Tyr	His	Tyr	Asn	Gly	Ser	Leu	Met	Asp	Gly	Thr	Leu	Phe	Asp
		290					295					300			
Ser	Ser	Tyr	Ser	Arg	Asn	His	Thr	Tyr	Asn	Thr	Tyr	Ile	Gly	Gln	Gly
305					310					315				320	
Tyr	Ile	Ile	Pro	Gly	Met	Asp	Gln	Gly	Leu	Gln	Gly	Ala	Cys	Met	Gly
				325					330				335		
Glu	Arg	Arg	Arg	Ile	Thr	Ile	Pro	Pro	His	Leu	Ala	Tyr	Gly	Glu	Asn
				340					345				350		
Gly	Thr	Gly	Asp	Lys	Ile	Pro	Gly	Ser	Ala	Val	Leu	Ile	Phe	Asn	Val

WO 00/29448

PCT/JP99/06412

55/233

355	360	365
His Val Ile Asp Phe His Asn Pro Ala Asp Val Val Glu Ile Arg Thr		
370	375	380
Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu Thr Thr Lys Leu Gly Asp		
385	390	395
Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly Thr Gln Leu		
405	410	415
Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr Leu Gly Ala		
420	425	430
Asn Lys Val Ile Glu Gly Leu Asp Thr Gly Leu Gln Gly Met Cys Val		
435	440	445
Gly Glu Arg Arg Gln Leu Ile Val Pro Pro His Leu Ala His Gly Glu		
450	455	460
Ser Gly Ala Arg Gly Val Pro Gly Ser Ala Val Leu Leu Phe Glu Val		
465	470	475
Glu Leu Val Ser Arg Glu Asp Gly Leu Pro Thr Gly Tyr Leu Phe Val		
485	490	495
Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Met Asp Leu Asn		
500	505	510
Lys Asp Gly Glu Val Pro Pro Glu Glu Phe Ser Thr Phe Ile Lys Ala		
515	520	525
Gln Val Ser Glu Gly Lys Gly Arg Leu Met Pro Gly Gln Asp Pro Glu		
530	535	540
Lys Thr Ile Gly Asp Met Phe Gln Asn Gln Asp Arg Asn Gln Asp Gly		
545	550	555
Lys Ile Thr Val Asp Glu Leu Lys Leu Lys Ser Asp Glu Asp Glu Glu		
565	570	575
Arg Val His Glu Glu Leu		
580		

<210> 33

<211> 410

<212> PRT

<213> Homo sapiens

<400> 33

WO 00/29448

PCT/JP99/06412

56/233

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
1 5 10 15
Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
20 25 30
Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
35 40 45
Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
50 55 60
Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
65 70 75 80
Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
85 90 95
Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
100 105 110
Thr Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly
115 120 125
Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg
130 135 140
Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro
145 150 155 160
Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser
165 170 175
Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val
180 185 190
Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser
195 200 205
Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg
210 215 220
Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe
225 230 235 240
Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly
245 250 255
Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg
260 265 270
His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser

WO 00/29448

PCT/JP99/06412

57/233

275	280	285
Pro Gly Pro Ser Pro Asp Val	Gln Leu Ala Thr Leu Ala Gln Arg Val	
290	295	300
Lys Glu Val Leu Pro His Val	Pro Leu Gly Val Ile Gln Arg Asp Leu	
305	310	315
Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly		320
325	330	335
Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu		
340	345	350
Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly Pro Val Thr Pro		
355	360	365
Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu		
370	375	380
Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg		
385	390	395
Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp		400
405	410	

<210> 34

<211> 483

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro		
1	5	10
Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg		
20	25	30
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro		
35	40	45
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp		
50	55	60
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Cys Ile		
65	70	75
Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu Lys Asp Tyr Lys		
85	90	95

Gly	Pro	Asn	Pro	Arg	Glu	Leu	Leu	Glu	Pro	Leu	Phe	Lys	Gln	Ser	Ser	
			100					105					110			
Cys	Ser	Tyr	Arg	Ile	Glu	Ser	Tyr	Trp	Thr	Tyr	Glu	Val	Cys	His	Gly	
		115					120				125					
Lys	His	Ile	Arg	Gln	Tyr	His	Glu	Glu	Lys	Glu	Thr	Gly	Gln	Lys	Ile	
	130					135				140						
Asn	Ile	His	Glu	Tyr	Tyr	Leu	Gly	Asn	Met	Leu	Ala	Lys	Asn	Leu	Leu	
145					150					155					160	
Phe	Glu	Lys	Glu	Arg	Glu	Ala	Glu	Glu	Lys	Glu	Lys	Ser	Asn	Glu	Ile	
			165					170				175				
Pro	Thr	Lys	Asn	Ile	Glu	Gly	Gln	Met	Thr	Pro	Tyr	Tyr	Pro	Val	Gly	
		180					185			190						
Met	Gly	Asn	Gly	Thr	Pro	Cys	Ser	Leu	Lys	Gln	Asn	Arg	Pro	Arg	Ser	
	195					200				205						
Ser	Thr	Val	Met	Tyr	Ile	Cys	His	Pro	Glu	Ser	Lys	His	Glu	Ile	Leu	
	210					215				220						
Ser	Val	Ala	Glu	Val	Thr	Thr	Cys	Glu	Tyr	Glu	Val	Val	Ile	Leu	Thr	
225					230					235					240	
Pro	Leu	Leu	Cys	Ser	His	Pro	Lys	Tyr	Arg	Phe	Arg	Ala	Ser	Pro	Val	
			245					250				255				
Asn	Asp	Ile	Phe	Cys	Gln	Ser	Leu	Pro	Gly	Ser	Pro	Phe	Lys	Pro	Leu	
		260					265					270				
Thr	Leu	Arg	Gln	Leu	Glu	Gln	Gln	Glu	Glu	Ile	Leu	Arg	Val	Pro	Phe	
	275					280						285				
Arg	Arg	Asn	Lys	Glu	Glu	Asp	Leu	Gln	Ser	Thr	Lys	Glu	Glu	Arg	Phe	
	290					295				300						
Pro	Ala	Ile	His	Lys	Ser	Ile	Ala	Ile	Gly	Ser	Gln	Pro	Val	Leu	Thr	
305					310					315					320	
Val	Gly	Thr	Thr	His	Ile	Ser	Lys	Leu	Thr	Asp	Asp	Gln	Leu	Ile	Lys	
			325						330					335		
Glu	Phe	Leu	Ser	Gly	Ser	Tyr	Cys	Phe	Arg	Gly	Gly	Val	Gly	Trp	Trp	
	340						345					350				
Lys	Tyr	Glu	Phe	Cys	Tyr	Gly	Lys	His	Val	His	Gln	Tyr	His	Glu	Asp	
	355					360						365				
Lys	Asp	Ser	Gly	Lys	Thr	Ser	Val	Val	Val	Gly	Thr	Trp	Asn	Gln	Glu	

WO 00/29448

PCT/JP99/06412

59/233

370	375	380	
Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu			
385	390	395	400
Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly			
405	410	415	
Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val			
420	425	430	
Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr			
435	440	445	
Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro			
450	455	460	
Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser			
465	470	475	480
Leu Pro Asn			

<210> 35

<211> 607

<212> PRT

<213> Homo sapiens

<400> 35

Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly Gly Phe Gly Pro Phe			
1	5	10	15
Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro Arg Val Leu Leu Pro			
20	25	30	
Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala Val Pro Ala His Arg			
35	40	45	
Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser His Gln Asp Val Trp			
50	55	60	
Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly Thr Leu Ser Ser Cys			
65	70	75	80
Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn Thr Thr Leu Gly Glu			
85	90	95	
Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu Pro Ala Thr Val Pro			
100	105	110	

WO 00/29448

PCT/JP99/06412

60/233

Cys	Ser	Gln	Gly	Trp	Glu	Tyr	Asp	His	Ser	Glu	Phe	Ser	Ser	Thr	Ile
115							120					125			
Ala	Thr	Glu	Ser	Gln	Val	Gly	Ile	Tyr	Ile	Ile	His	Leu	Glu	Val	Glu
130						135					140				
Cys	Arg	Trp	Arg	Gln	Ser	Pro	Trp	Glu	Ala	Ala	Gly	Arg	Gly	Leu	Pro
145				150						155				160	
Trp	Glu	Glu	Ala	Glu	Ala	Ala	Gly	Leu	Gly	Arg	Asp	Lys	Val	Ser	Tyr
				165				170					175		
Ser	Pro	Ser	Trp	Arg	Glu	Ser	Leu	Gly	Gly	Leu	Leu	Ser	Gly	Met	Glu
				180				185					190		
Trp	Asp	Leu	Val	Cys	Glu	Gln	Lys	Gly	Leu	Asn	Arg	Ala	Ala	Ser	Thr
		195					200					205			
Phe	Phe	Phe	Ala	Gly	Val	Leu	Val	Gly	Ala	Val	Ala	Phe	Gly	Tyr	Leu
210						215					220				
Ser	Asp	Arg	Phe	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Val	Ala	Tyr	Val	Ser
225				230						235				240	
Thr	Leu	Val	Leu	Gly	Leu	Ala	Ser	Ala	Ala	Ser	Val	Ser	Tyr	Val	Met
				245					250				255		
Phe	Ala	Ile	Thr	Arg	Thr	Leu	Thr	Gly	Ser	Ala	Leu	Ala	Gly	Phe	Thr
		260						265					270		
Ile	Ile	Val	Met	Pro	Leu	Glu	Leu	Glu	Trp	Leu	Asp	Val	Glu	His	Arg
		275					280					285			
Thr	Val	Ala	Gly	Val	Leu	Ser	Ser	Thr	Phe	Trp	Thr	Gly	Gly	Val	Met
		290				295					300				
Leu	Leu	Ala	Leu	Val	Gly	Tyr	Leu	Ile	Arg	Asp	Trp	Arg	Trp	Leu	Leu
305				310					315					320	
Leu	Ala	Val	Thr	Leu	Pro	Cys	Ala	Pro	Gly	Ile	Leu	Ser	Leu	Trp	Trp
				325					330				335		
Val	Pro	Glu	Ser	Ala	Arg	Trp	Leu	Leu	Thr	Gln	Gly	His	Val	Lys	Glu
		340						345					350		
Ala	His	Arg	Tyr	Leu	Leu	His	Cys	Ala	Arg	Leu	Asn	Gly	Arg	Pro	Val
		355					360					365			
Cys	Glu	Asp	Ser	Phe	Ser	Gln	Glu	Ala	Val	Ser	Lys	Val	Ala	Ala	Gly
		370					375				380				
Glu	Arg	Val	Val	Arg	Arg	Pro	Ser	Tyr	Leu	Asp	Leu	Phe	Arg	Thr	Pro

WO 00/29448

PCT/JP99/06412

61/233

385	390	395	400
Arg Leu Arg His Ile Ser Leu Cys Cys Val Val Val Trp Phe Gly Val			
	405	410	415
Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val Ser Gly Leu Gly Leu			
	420	425	430
Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala Val Glu Leu Pro Ser			
	435	440	445
Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala Gly Arg Arg Leu Thr			
	450	455	460
Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala Phe Gly Thr Arg Leu			
465	470	475	480
Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr Val Leu Ala Val Met			
	485	490	495
Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr Ala Tyr Leu Phe Thr			
	500	505	510
Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr Gly Met Gly Leu Thr			
	515	520	525
Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala Pro Leu Ala Ala Leu			
	530	535	540
Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu Thr Tyr Gly Gly Ile			
545	550	555	560
Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu Pro Glu Thr Arg Gln			
	565	570	575
Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu Arg Lys Ser Ala Pro			
	580	585	590
Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys Gln Val Gln Asn			
	595	600	605

<210> 36

<211> 314

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala

1

5

10

15

WO 00/29448

PCT/JP99/06412

62/233

Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser	Gly	Pro
			20					25					30		
Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly	Glu	Asp	Ala
			35				40					45			
Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg	Leu	Trp	Asp	Ser
	50					55					60				
His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg	Trp	Ala	Leu	Thr	Ala
	65				70					75				80	
Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu	Ser	Asp	Pro	Ser	Gly	Trp
			85					90						95	
Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	Met	Pro	Ser	Phe	Trp	Ser	Leu
		100						105					110		
Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro
	115						120					125			
Arg	Tyr	Leu	Gly	Asn	Ser	Pro	Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser
	130					135						140			
Ala	Pro	Val	Thr	Tyr	Thr	Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala
	145					150				155				160	
Ser	Thr	Phe	Glu	Phe	Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp
			165					170						175	
Gly	Tyr	Ile	Lys	Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln
		180						185					190		
Glu	Val	Gln	Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe
	195						200					205			
Leu	Lys	Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala
	210					215						220			
Gly	Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly
	225					230				235				240	
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	Val
			245					250					255		
Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Thr
			260					265					270		
Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	Ala	Gln	Ser
	275						280						285		
Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	Phe	Phe	Pro	Leu

```

<210> 38
<211> 218
<212> PRT
<213> Homo sapiens
<400> 38
Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
 1             5             10             15
Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
          20             25             30
Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
          35             40             45
Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
      50             55             60

```

Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile	Ser
1				5					10					15	
Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser	Pro	Glu
			20					25					30		
Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile	Leu	Ala	Asn
		35					40					45			
Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe	Val	His	Lys	Thr
	50					55					60				
Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu	Asn	Ile	Phe	Asp	Gln

WO 00/29448

PCT/JP99/06412

65/233

65	70	75	80
Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu			
85	90	95	
Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu			
100	105	110	
Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu			
115	120	125	
Glu Glu Lys Ile Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln			
130	135	140	
Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu			
145	150	155	160
Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys			
165	170	175	
Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln			
180	185	190	
His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile			
195	200	205	
Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg			
210	215	220	
Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp			
225	230	235	240
Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr			
245	250	255	
Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val			
260	265	270	
Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg			
275	280	285	
Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr			
290	295	300	
Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile			
305	310	315	320
Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu			
325	330	335	
Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly			
340	345	350	

WO 00/29448

PCT/JP99/06412

66/233

Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
 355 360 365
 Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
 370 375 380
 Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
 385 390 395 400
 Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
 405 410 415
 Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
 420 425 430
 Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
 435 440 445
 Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 450 455 460

<210> 40

<211> 216

<212> PRT

<213> Homo sapiens

<400> 40

Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys Pro Leu Leu Leu
 1 5 10 15
 Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu Leu Gly Ile Lys
 20 25 30
 Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu Gly Gly Phe
 35 40 45
 Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu Trp Gly Leu Arg
 50 55 60
 Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly Pro Ser Gly Asn
 65 70 75 80
 Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr Glu Glu Ala Val
 85 90 95
 Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu Asp Gln Pro Pro
 100 105 110
 Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu Glu Glu Gln Pro

atgcagggcc	caccgctcct	gaccgcccgc	cacctcctct	gcgtgtgcac	cgccgcgctg	60
gccgtggctc	ccgggcctcg	gtttctggtg	acagccccag	ggatcatcag	gcccgaggga	120
aatgtgacta	ttgggggtgga	gttcttgga	cactgccctt	cacaggtgac	tgtgaaggcg	180
gagctgctca	agacagcatc	aaacctcact	gtctctgtcc	tggaagcaga	aggagtcttt	240
gaaaaaggct	cttttaagac	acttactctt	ccatcactac	ctctgaacag	tgcagatgag	300
atttatgagc	tacgtgtaac	cggacgtacc	caggatgaga	ttttattctc	taatagtacc	360
cgcttatcat	ttgagaccaa	gagaatatct	gtcttcattc	aaacagacaa	ggccttatac	420
aagccaaagc	aagaagtga	gtttcgcatt	gttacactct	tctcagattt	taagccttac	480
aaaacctctt	taaacattct	cattaaggac	cccaaataca	atttgatcca	acagtgggtg	540
tcacaacaaa	gtgatcttgg	agtcatttcc	aaaacttttc	agctatcttc	ccatccaata	600
cttggtgact	ggtctattca	agttcaagtg	aatgaccaga	catattatca	atcatttcag	660
gtttcagaat	atgtattacc	aaaatttgaa	gtgactttgc	agacaccatt	atattgttct	720
atgaattcta	agcattttaa	tggtaccatc	acggcaaagt	atacatatgg	gaagccagtg	780
aaaggagacg	taacgcttac	atttttacct	ttatcctttt	ggggaaagaa	gaaaaatatt	840
acaaaaacat	ttaagataaa	tggatctgca	aaactctctt	ttaatgatga	agagatgaaa	900
aatgtaatgg	attcttcaaa	tggactttct	gaataacctg	atctatcttt	ccctggacca	960

WO 00/29448

PCT/JP99/06412

68/233

gtagaaat	tttaaccacag	tacagagaat	ctaggtacag	gtttcaagaaa	tgttaagcact	1020
aatgtgtt	cttcaagcaaca	tgtattacat	cattgagtttt	ttgattatac	tactgtcttg	1080
aagccatct	ctcaacttcac	agccactgtg	aaggtaactc	gtgctgatgg	caaccaactg	1140
actcttgaag	aaagaagaaa	taatgtagtc	ataacagtga	cacagagaaa	ctatactgag	1200
tactggagcg	gatctaacag	tggaaatcag	aaaatggaag	ctgttcagaa	aataaattat	1260
actgtcccc	aaagtggaac	ttttaagatt	gaattcccaa	tcctggagga	ttccagtga	1320
ctacagttga	aggcctat	cttggtagt	aaaagtagca	tggcagttca	tagtctgttt	1380
aagtctccta	gtaagacata	catccaacta	aaaacaagag	atgaaaatat	aaaggtggga	1440
tcgcctttt	agttggtgt	tagtggcaac	aaacgattga	aggagttaag	ctatatggta	1500
gtatccaggg	gacagttggt	ggctgtagga	aaacaaaatt	caacaatgtt	ctctttaaca	1560
ccagaaaatt	cttggactcc	aaaagcctgt	gtaattgtgt	attatattga	agatgatggg	1620
gaaattataa	gtgatgttct	aaaaattcct	gttcagcttg	tttttaaaaa	taagataaag	1680
ctatattgga	gtaaagtga	agctgaacca	tctgagaaag	tctctcttag	gatctctgtg	1740
acacagcctg	actccatagt	tgggattgta	gctgttgaca	aaagtgtgaa	tctgatgaat	1800
gcctctaatt	atattacaat	ggaaaatgtg	gtccatgagt	tggaaacttta	taacacagga	1860
tattatttag	gcatgttcat	gaattctttt	gcagtctttc	aggaatgtgg	actctgggta	1920
ttgacagatg	caaacctcac	gaaggattat	attgatgggtg	tttatgacaa	tgcagaatat	1980
getgagaggt	ttatggagga	aatgaagga	catattgtag	atattcatga	cttttctttg	2040
ggtagcagtc	cacatgtccg	aaagcatttt	ccagagactt	ggatttggt	agacaccaac	2100
atgggttcca	ggattttacca	agaatttgaa	gtaactgtac	ctgattctat	cacttcttgg	2160
gtggctactg	gttttgtgat	ctctgaggac	ctgggtcttg	gactaacaac	tactccagtg	2220
gagctccaag	ccttccaacc	atttttcatt	tttttgaatc	ttccctactc	tgttatcaga	2280
ggtgaagaat	ttgcttttga	aataactata	ttcaattatt	tgaagatgc	cactgagggt	2340
aaggtaatca	ttgagaaaag	tgacaaat	gatattteta	tgaactcaag	tgaataaat	2400
gccacaggcc	accagcagac	ccttctggtt	cccagtgagg	atggggcaac	tgttcttttt	2460
cccatcaggc	caacacatct	gggagaaatt	cctatcacag	tcacagctct	ttcaccact	2520
gcttctgatg	ctatcaccca	gatgatttta	gtaaaggctg	aaggaataga	aaaatcatat	2580
tcacaatcca	tcttattaga	cttgactgac	aataggctac	agagtaccct	gaaaactttg	2640
agtttctcat	ttcctcctaa	tacagtgact	ggcagtga	gagttcagat	cactgcaatt	2700
ggagatgttc	ttggtccttc	catcaatggc	ttagcctcat	tgattcggat	gccttatggc	2760
tgtggtgaac	agaacatgat	aaattttgct	ccaaatat	acatttttga	ttatctgact	2820
aaaaagaaac	aactgacaga	taatttgaaa	gaaaaagctc	tttcatttat	gaggcaaggt	2880
taccagagag	aacttctcta	tcagagggaa	gatggctctt	tcagtgtttt	tgggaattat	2940
gacccttctg	ggagcacttg	gttgctcagct	tttgtttttaa	gatgtttcct	tgaagccgat	3000
ccttacatag	atattgatca	gaatgtgtta	cacagaacat	acacttggct	taaaggacat	3060

WO 00/29448

PCT/JP99/06412

69/233

cagaaatcca acggtgaatt ttgggatcca ggaagagtga ttcatagtga gcttcaaggt 3120
ggcaataaaa gtccagtaac acttacagcc tatattgtaa cttctctcct gggatataga 3180
aagtatcagc ctaacattga tgtgcaagag tctatccatt ttttggagtc tgaattcagt 3240
agaggaattt cagacaatta tactctagcc cttataaact atgcattgtc atcagtgggg 3300
agtcctaaag cgaaggaagc tttgaatatg ctgacttgga gagcagaaca agaaggtggc 3360
atgcaattct ggggtgcatc agagtccaaa ctttctgact cctggcagcc acgctccctg 3420
gatattgaag ttgcagccta tgcactgctc tcacacttct tacaatttca gacttctgag 3480
ggaatcccaa ttatgaggtg gctaagcagg caaagaaata gcttgggtgg ttttgcctct 3540
actcaggata ccactgtggc tttaaaggct ctgtctgaat ttgcagccct aatgaatata 3600
gaaaggacaa atatccaagt gaccgtgacg gggcctagct caccaagtc tgtaaagttt 3660
ctgattgaca cacacaaccg cttactcctt cagacagcag agcttgetgt ggtacagcca 3720
acggcagtta atatttccgc aaatggtttt ggatttgcta tttgtcagct caatgttgta 3780
tataatgtga aggcttcttg gtcttctaga agacgaagat ctatccaaaa tcaagaagcc 3840
tttgatttag atgttgetgt aaaagaaaat aaagatgatc tcaatcatgt ggatttgaat 3900
gtgtgtacaa gcttttcggg cccgggtagg agtggcatgg ctcttatgga agttaacct 3960
ttaagtggct ttatggtgcc ttcagaagca atttctctga gcgagacagt gaagaaagt 4020
gaatatgatc atggaaaact caacctctat ttagattctg taaatgaaac ccagttttgt 4080
gttaatatte ctgctgtgag aaactttaaa gtttcaaata cccaagatgc ttcagtgtcc 4140
atagtggatt actatgagcc aaggagacag gcggtgagaa gttacaactc tgaagtgaag 4200
ctgtcctcct gtgacctttg cagtgatgtc cagggtgcc gtccttgtga ggatggagct 4260
tcaggctccc atcatcactc ttcagtcatt tttattttct gtttcaagct tctgtacttt 4320
atggaacttt ggctg 4335

<210> 42

<211> 1746

<212> DNA

<213> Homo sapiens

<400> 42

atgttccccg cgggcccccc cagccacagc ctctccggc tccccctgt gcagttgctg 60
ctactgggtg tgcaggccgt ggggaggggg ctgggcggcg ccagcccgcc cgggggcccc 120
ctggaagatg tggtcacga gaggtaccac atccccagg cctgtccccg ggaagtgcag 180
atgggggatt ttgtgcgcta ccactacaac ggcacttttg aagatggcaa gaagtttgat 240
tcaagctatg atcgcaacac cttggtggcc atcgtgggtg gtgtggggcg cctcatcact 300
ggcatggacc gaggcctcat gggcatgtgt gtcaacgagc ggcgacgcct cattgtgcct 360
ccccacctgg gctatgggag catcggcctg gcggggctca ttccaccgga tgccacctc 420

atggagcttc	cctcagggcc	ggggccggag	cggctctttg	actcgcaccg	gcttcggggt	60
gactgcttcc	tactgctcgt	gctgctgctc	tacgcgccag	tggggttctg	cctcctcgtc	120
ctgcgcctct	ttctcgggat	ccacgtcttc	ctggtcagct	gcgcgctgcc	agacagcgtc	180
cttcgcagat	tcgtagtgcg	gaccatgtgt	gcggtgctag	ggctcgtggc	ccggcaggag	240
gactcgggac	tccgggatca	cagtgtcagg	gtcctcattt	ccaaccatgt	gacacctttc	300
gaccacaaca	tagtcaattt	gcttaccacc	tgtagcacco	ctctactcaa	tagtcccccc	360

WO 00/29448

PCT/JP99/06412

71/233

agctttgtgt gctggtctcg gggcttcatg gagatgaatg ggogggggga gttggtggag	420
tcactcaaga gattctgtgc ttccacgagg ctcccccca ctctctgct gctattccct	480
gaggaagagg ccaccaatgg cggggagggg ctctgcgct tcagttcctg gccattttct	540
atccaagatg tggtaacaac tcttaccctg caagttcaga gacccctggt ctctgtgacg	600
gtgtcagatg cctcctgggt ctcagaactg ctgtggtcac ttttcgtccc ttacacggtg	660
tatcaagtaa ggtggtctcg tctgttcat cgccaactag gggaagcgaa tgaggagttt	720
gcactccgtg tacaacagct ggtggccaag gaattgggcc agacagggac acggtcact	780
ccagctgaca aagcagagca catgaagcga caaagacacc ccagattgcg cccccagtca	840
gccagttctt ctttccctcc ctcccctggt ctttctctg atgtgcaact ggcaactctg	900
gtcagagag tcaaggaagt tttgccccat gtgccattgg gtgtcatcca gagagacctg	960
gccaaagactg gctgtgtaga cttgactatc actaatctgc ttgagggggc cgtagctttc	1020
atgcctgaag acatcaccaa gggaactcag tccctaccca cagcctctgc ctccaagttt	1080
cccagctctg gcccggtgac cctcagcca acagccctaa catttgccaa gtcttcctgg	1140
gcccggcagg agagcctgca ggagcgcaag caagcactat atgaatacgc aagaaggaga	1200
ttcacagaga gacgagccca ggaggctgac	1230

<210> 44

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 44

atggaggaag gaggcggcgg cgtacggagt ctggtcccg gggggccggt gttactggtc	60
ctctgcggcc tcttgaggc gtccggcggc ggccgagccc ttctcaact cagcgatgac	120
atccctttcc gagtcaactg gcccggcacc gagttctctc tgcccacaac tggagtttta	180
tataaagaag ataattatgt catcatgaca actgcacata aagaaaaata taaatgcata	240
cttcccttg tgacaagtgg ggatgaggaa gaagaaaagg attataaagg ccctaattcca	300
agagagcttt tggagccact atttaaaca agcagttggt cctacagaat tgagtcttat	360
tggacttacg aagtatgtca tggaaaacac attcggcagt accatgaaga gaaagaaact	420
ggtcagaaaa taaatattca cgagtactac cttgggaata tgttgcccaa gaaccttcta	480
tttgaaaaag aacgagaagc agaagaaaag gaaaaatcaa atgagattcc cactaaaaat	540
atcgaaggtc agatgacacc atactatcct gtgggaatgg gaaatggtac acctgtagt	600
ttgaaacaga accggcccag atcaagtact gtgatgtaca tatgtcatcc tgaatctaag	660
catgaaatcc tttcagtagc tgaagttaca acttgtgaat atgaagttgt cattttgaca	720
ccactcttgt gcagtcaccc taaatatagg ttcagagcat ctctgtgaa tgacatattt	780
tgtcaatcac tgccaggatc tccatttaag cccctcacc tgaggcagct ggagcagcag	840

atcgggctttg	aggagctgct	ggagcaggtg	ggcggctttg	ggcccttcca	actgcggaat	60
gtggcaactgc	tggccctgcc	ccgagtgtctg	ctaccactgc	acttctctct	gcccattctt	120
ctggctgccg	tgcctgccc	ccgatgtgcc	ctgccgggtg	cccctgccaa	cttcagccat	180
caggatgtgt	ggctggaggc	ccattctccc	cgggagcctg	atggcacgct	cagctcctgc	240
ctccgctttg	cctatcccca	ggctctcccc	aacaccacgt	tgggggaaga	aaggcagagc	300
cgtggggagc	tggaggatga	acctgccaca	gtgccctgct	ctcagggtctg	ggagtacgac	360
cactcagaat	tctctctac	cattgcaact	gagtcccagg	tcggtattta	cataatccat	420
ctggaggttg	aatgtcgtg	gaggcagttc	ccctgggagg	cagcaggctg	aggccttctt	480
tgggaagaag	ctgaggctgc	aggactgggg	agggacaaa	tttctattt	cccaagctgg	540
cgtgaatcgt	tgggaggttt	attatctggc	atggagtggg	atctggtgtg	tgagcagaaa	600
ggtctgaaca	gagctgcgtc	cactttcttc	ttcgccggtg	tgtgtgtggg	ggctgtggcc	660
tttggaatc	tgtccgacag	gtttggggcg	cggcgtctgc	tgtgtgtagc	ctacgtgagt	720
accctggtgc	tgggcctggc	atctgcagcc	tccgtcagct	atgtaatgtt	tgccatcacc	780
cgcaccctta	ctggctcagc	cctggtcgtt	tttaccatca	togtgatgcc	actggagctg	840
gagtggcttg	atgtggagca	ccgcaccgtg	gctggagtc	tgagcagcac	cttctggaca	900
gggggcgtga	tgtctgtggc	actggttggg	tacctgatac	gggactggcg	atggcttctg	960
ctagctgtca	ccctgccttg	tgccccaggc	atcctcagcc	tctggtgggt	gcctgagtct	1020
gcacgctggc	ttctgaccca	aggccatgtg	aaagaggccc	acaggtactt	gctccactgt	1080

WO 00/29448

PCT/JP99/06412

73/233

gccaggctca atgggcggcc agtgtgtgag gacagcttca gccaggaggc tgtgagcaaa	1140
gtggccgccc gggaacgggt ggtccgaaga ccttcatacc tagacctgtt ccgcacacca	1200
cggtccgac acatctcact gtgctgcgtg gtggtgtggt tcggagtga cttctcctat	1260
tacggcctga gtctggatgt gtcggggctg gggtgaacg tgtaccagac acagctgttg	1320
ttcggggctg tggaactgcc ctccaagctg ctggtctact tgtcgggtgcg ctacgcagga	1380
cgcgcctca cgcaagccgg gacactgctg ggcacggccc tggcgctcgg cactagactg	1440
ctagtgtcct ctgatatgaa gtccctggagc actgtcctgg cagtgatggg gaaagctttt	1500
tctgaagctg ccttcaccac tgcctacctg ttcacttcag agttgtaccc tacgggtgctc	1560
agacagacag ggatggggct gactgcaactg gtgggcgggc tggggggctc tttggcccca	1620
ctggcggcct tgcctggatgg agtgtggctg tcaactgccc agcttactta tggggggatc	1680
gccctgctgg ctgccggcac cgcctcctg ctgccagaga cgaggcaggc acagctgccca	1740
gagaccatcc aggacgtgga gagaaagagt gcccacaacca gtcttcagga ggaagagatg	1800
cccatgaagc aggtccagaa c	1821

<210> 46

<211> 942

<212> DNA

<213> Homo sapiens

<400> 46

atgggcgccc gcggggcgct gctgctggcg ctgctgctgg ctgggctgg actcaggaag	60
ccggagtgcg aggaggcggc gccgttatca ggaccatgcg gccgacgggt catcacgtcg	120
cgcacgtgg gtggagagga cgcgaactc gggcggttggc cgtggcaggg gagcctgcgc	180
ctgtgggatt ccacgtatg cggagtgage ctgctcagcc accgctgggc actcacggcg	240
gcgactgct ttgaaacctc tagtgacctt agtgatccct ccgggtggat ggtccagttt	300
ggccagctga cttccatgcc atcctttctg agcctgcagg cctactacac ccgttacttc	360
gtatcgaaata tctatctgag cctcgcctac ctggggaatt caccctatga cattgccttg	420
gtgaagctgt ctgcacctgt cactacaact aaacacatcc agcccatctg tctccaggcc	480
tccacatttg agtttgagaa ccggacagac tgctgggtga ctggctgggg gtacatcaaa	540
gaggatgagg cactgccatc tccccacacc ctccaggaag ttcaggctgc catcataaac	600
aactctatgt gcaaccacct cttcctcaag tacagtttcc gcaaggacat ctttgagac	660
atggtttgtg ctggcaatgc ccaaggcggg aaggatgcct gcttcgggtga ctcagggtga	720
cccttgccct gtaacaagaa tggactgtgg tatcagattg gactcgtgag ctggggagtg	780
ggctgtggtc ggcccaatcg gcccggtgct tacaccaata tcagccacca ctttgagtgg	840
atccagaagc tgatggccca gactggcatg tccagccag acccctcctg gccgctactc	900
ttttccctc ttctctgggc tctccactc ctggggcgcg tc	942

WO 00/29448

PCT/JP99/06412

74/233

<210> 47

<211> 282

<212> DNA

<213> Homo sapiens

<400> 47

atggagctct ctgatgtcac cctcattgag ggtgtgggta atgaggtgat ggtggtggca	60
ggtgtggtgg tgetgattct agcettggte ctagcttgge totctaccta cgtagcagac	120
agcggtagca accagctcct gggcgctatt gtgtcagcag gcgacacatc cgtcctccac	180
ctggggcatg tggaccacct ggtggcagge caaggcaacc ccgagccaac tgaactcccc	240
catccatcag aggcaaatac ttccctggac aagaaagcca ga	282

<210> 48

<211> 654

<212> DNA

<213> Homo sapiens

<400> 48

atggcgctga agatagggtc gagacggtgg atgttgacgc tgatcatgca gttgggttcg	60
gtgctgetca cacgctgccc cttttggggc tgettcagcc agctcatget gtacgetgag	120
agggctgagg cacgccggaa gcccgacatc ccagtgcctt acctgtattt cgacatgggg	180
gcagccgtgc tgtgcgctag ttcatgtcc tttggcgtga agcggcgctg gttcgcgctg	240
ggggccgcac tccaattggc cattagcacc tacgcgcctt acatcggggg ctacgtccac	300
tacggggact ggctgaaggt ccgtatgtac tcgcgcacag ttgccatcat cggcgggactt	360
tcttgtgttg gccagcggtg ctggggagct gtaccgcggg aaacctcgca gccgctccct	420
gcagtcacac ggccaggtgt tcctgggtat ctacctatc tgtgtggcct actcactgca	480
gcacagcaag gaggaccggc tggcgtatct gaaccatctc ccaggagggg agotgatgat	540
ccagctgttc ttctgtctgt atggcaccct ggccctggcc tttctgtcag gctactacgt	600
gacctcget gccagatcc tggtgtact gctgccccct gtcatgetgc tcat	654

<210> 49

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 49

atgttcacaa ttaagctcct tctttttatt gttcctctag ttatttctc cagaattgat	60
--	----

atggtgccaa	tgcacttact	ggggagactg	gagaagccgc	ttctcctcct	gtgctgcgcc	60
tccttcctac	tggggctggc	tttgetgggc	ataaagacgg	acatcacccc	cgttgcttat	120
ttctttctca	cattgggttg	cttctctcttg	tttgcctatc	tcctggtcgg	gtttctggaa	180
tgggggcttc	ggccccagct	ccaatcaatg	cagactgaga	gcccagggcc	ctcaggcaat	240
gcacgggaca	atgaagcctt	tgaagtgcc	gtctatgaag	aggccgtggg	gggactagaa	300
tcccagtgcc	gcccccaaga	gttggaacca	ccacccccct	acagcactgt	tgtgatacce	360
ccagcacctg	aggaggaaca	acctagccat	ccaagagggg	ccaagagagc	caaactggaa	420

WO 00/29448

PCT/JP99/06412

76/233

cagagggcgaa tggcctcaga ggggtccatg gccaggaag gaagccctgg aagagctcca 480
atcaaccttc ggcttcgggg accacgggct gtgtccactg ctctgatct gcagagcttg 540
gcggcagtc ccacattaga gcctctgact ccacccctg cctatgatgt ctgctttggt 600
caccctgatg atgatagtgt tttttatgag gacaactggg caccct 648

<210> 51

<211> 4473

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)...(4382)

<400> 51

aacttccccg gcagcggact gtagcccagg cagacgccgt cgag atg cag ggc cca 56
Met Gln Gly Pro

1

cag ctg ctg acc gcc gcc cac ctg ctg tgc gtg tgc acc gcc ggc ctg 104
Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys Thr Ala Ala Leu
5 10 15 20

gcc gtg gct ccc ggg cct cgg ttt ctg gtg aca gcc cca ggg atc atc 152
Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala Pro Gly Ile Ile
25 30 35

agg ccc gga gga aat gtg act att ggg gtg gag ctt ctg gaa cac tgc 200
Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu Leu Glu His Cys
40 45 50

cct tca cag gtg act gtg aag ggc gag ctg ctg aag aca gca tca aac 248
Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys Thr Ala Ser Asn
55 60 65

ctc act gtc tct gtc ctg gaa gca gaa gga gtc ttt gaa aaa ggc tct 296
Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe Glu Lys Gly Ser
70 75 80

ttt aag aca ctt act ctt cca tca cta cct ctg aac agt gca gat gag 344
Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn Ser Ala Asp Glu
85 90 95 100

att tat gag cta cgt gta acc gga cgt acc cag gat gag att tta ttc 392

WO 00/29448

PCT/JP99/06412

77/233

Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp Glu Ile Leu Phe	
105 110 115	
tct aat agt acc cgc tta tca ttt gag acc aag aga ata tct gtc ttc	440
Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg Ile Ser Val Phe	
120 125 130	
att caa aca gac aag gcc tta tac aag cca aag caa gaa gtg aag ttt	488
Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln Glu Val Lys Phe	
135 140 145	
cgc att gtt aca ctc ttc tca gat ttt aag cct tac aaa acc tct tta	536
Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr Lys Thr Ser Leu	
150 155 160	
aac att ctc att aag gac ccc aaa tca aat ttg atc caa cag tgg ttg	584
Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile Gln Gln Trp Leu	
165 170 175 180	
tca caa caa agt gat ctt gga gtc att tcc aaa act ttt cag cta tct	632
Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr Phe Gln Leu Ser	
185 190 195	
tcc cat cca ata ctt ggt gac tgg tct att caa gtt caa gtg aat gac	680
Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val Gln Val Asn Asp	
200 205 210	
cag aca tat tat caa tca ttt cag gtt tca gaa tat gta tta cca aaa	728
Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr Val Leu Pro Lys	
215 220 225	
ttt gaa gtg act ttg cag aca cca tta tat tgt tct atg aat tct aag	776
Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser Met Asn Ser Lys	
230 235 240	
cat tta aat ggt acc atc acg gca aag tat aca tat ggg aag cca gtg	824
His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr Gly Lys Pro Val	
245 250 255 260	
aaa gga gac gta acg ctt aca ttt tta cct tta tcc ttt tgg gga aag	872
Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser Phe Trp Gly Lys	
265 270 275	
aag aaa aat att aca aaa aca ttt aag ata aat gga tct gca aac ttc	920
Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly Ser Ala Asn Phe	
280 285 290	

WO 00/29448

PCT/JP99/06412

78/233

tct ttt aat gat gaa gag atg aaa aat gta atg gat tct tca aat gga	968
Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp Ser Ser Asn Gly	
295 300 305	
ctt tct gaa tac ctg gat cta tct ttc cct gga cca gta gaa att tta	1016
Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro Val Glu Ile Leu	
310 315 320	
acc aca gtg aca gaa tca gtt aca ggt att tca aga aat gta agc act	1064
Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg Asn Val Ser Thr	
325 330 335 340	
aat gtg ttc ttc aag caa cat gat tac atc att gag ttt ttt gat tat	1112
Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu Phe Phe Asp Tyr	
345 350 355	
act act gtc ttg aag cca tct ctc aac ttc aca gcc act gtg aag gta	1160
Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala Thr Val Lys Val	
360 365 370	
act cgt gct gat ggc aac caa ctg act ctt gaa gaa aga aga aat aat	1208
Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu Arg Arg Asn Asn	
375 380 385	
gta gtc ata aca gtg aca cag aga aac tat act gag tac tgg agc gga	1256
Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu Tyr Trp Ser Gly	
390 395 400	
tct aac agt gga aat cag aaa atg gaa gct gtt cag aaa ata aat tat	1304
Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln Lys Ile Asn Tyr	
405 410 415 420	
act gtc ccc caa agt gga act ttt aag att gaa ttc cca atc ctg gag	1352
Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe Pro Ile Leu Glu	
425 430 435	
gat tcc agt gag cta cag ttg aag gcc tat ttc ctt ggt agt aaa agt	1400
Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu Gly Ser Lys Ser	
440 445 450	
agc atg gca gtt cat agt ctg ttt aag tct cct agt aag aca tac atc	1448
Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser Lys Thr Tyr Ile	
455 460 465	
caa cta aaa aca aga gat gaa aat ata aag gtg gga tcg cct ttt gag	1496
Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly Ser Pro Phe Glu	

WO 00/29448

PCT/JP99/06412

79/233

470	475	480	
ttg gtg gtt agt ggc aac aaa cga ttg aag gag tta agc tat atg gta			1544
Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu Ser Tyr Met Val			
485	490	495	500
gta tcc agg gga cag ttg gtg gct gta gga aaa caa aat tca aca atg			1592
Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln Asn Ser Thr Met			
505	510	515	
ttc tct tta aca cca gaa aat tct tgg act cca aaa gcc tgt gta att			1640
Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys Ala Cys Val Ile			
520	525	530	
gtg tat tat att gaa gat gat ggg gaa att ata agt gat gtt cta aaa			1688
Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser Asp Val Leu Lys			
535	540	545	
att cct gtt cag ctt gtt ttt aaa aat aag ata aag cta tat tgg agt			1736
Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys Leu Tyr Trp Ser			
550	555	560	
aaa gtg aaa gct gaa cca tct gag aaa gtc tct ctt agg atc tct gtg			1784
Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu Arg Ile Ser Val			
565	570	575	580
aca cag cct gac tcc ata gtt ggg att gta gct gtt gac aaa agt gtg			1832
Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val Asp Lys Ser Val			
585	590	595	
aat ctg atg aat gcc tct aat gat att aca atg gaa aat gtg gtc cat			1880
Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu Asn Val Val His			
600	605	610	
gag ttg gaa ctt tat aac aca gga tat tat tta ggc atg ttc atg aat			1928
Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly Met Phe Met Asn			
615	620	625	
tct ttt gca gtc ttt cag gaa tgt gga ctc tgg gta ttg aca gat gca			1976
Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val Leu Thr Asp Ala			
630	635	640	
aac ctc acg aag gat tat att gat ggt gtt tat gac aat gca gaa tat			2024
Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp Asn Ala Glu Tyr			
645	650	655	660
gct gag agg ttt atg gag gaa aat gaa gga cat att gta gat att cat			2072

Ala	Glu	Arg	Phe	Met	Glu	Glu	Asn	Glu	Gly	His	Ile	Val	Asp	Ile	His		
665				670				675									
gac	ttt	tct	ttg	ggt	agc	agt	cca	cat	gtc	cga	aag	cat	ttt	cca	gag	2120	
Asp	Phe	Ser	Leu	Gly	Ser	Ser	Pro	His	Val	Arg	Lys	His	Phe	Pro	Glu		
680				685				690									
act	tgg	att	tgg	cta	gac	acc	aac	atg	ggt	tcc	agg	att	tac	caa	gaa	2168	
Thr	Trp	Ile	Trp	Leu	Asp	Thr	Asn	Met	Gly	Ser	Arg	Ile	Tyr	Gln	Glu		
695				700				705									
ttt	gaa	gta	act	gta	cct	gat	tct	atc	act	tct	tgg	gtg	gct	act	ggt	2216	
Phe	Glu	Val	Thr	Val	Pro	Asp	Ser	Ile	Thr	Ser	Trp	Val	Ala	Thr	Gly		
710				715				720									
ttt	gtg	atc	tct	gag	gac	ctg	ggt	ctt	gga	cta	aca	act	act	cca	gtg	2264	
Phe	Val	Ile	Ser	Glu	Asp	Leu	Gly	Leu	Gly	Leu	Thr	Thr	Thr	Pro	Val		
725				730				735				740					
gag	ctc	caa	gcc	ttc	caa	cca	ttt	ttc	att	ttt	ttg	aat	ctt	ccc	tac	2312	
Glu	Leu	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Ile	Phe	Leu	Asn	Leu	Pro	Tyr		
745				750				755									
tct	gtt	atc	aga	ggt	gaa	gaa	ttt	gct	ttg	gaa	ata	act	ata	ttc	aat	2360	
Ser	Val	Ile	Arg	Gly	Glu	Glu	Phe	Ala	Leu	Glu	Ile	Thr	Ile	Phe	Asn		
760				765				770									
tat	ttg	aaa	gat	gcc	act	gag	gtt	aag	gta	atc	att	gag	aaa	agt	gac	2408	
Tyr	Leu	Lys	Asp	Ala	Thr	Glu	Val	Lys	Val	Ile	Ile	Glu	Lys	Ser	Asp		
775				780				785									
aaa	ttt	gat	att	cta	atg	act	tca	agt	gaa	ata	aat	gcc	aca	ggc	cac	2456	
Lys	Phe	Asp	Ile	Leu	Met	Thr	Ser	Ser	Glu	Ile	Asn	Ala	Thr	Gly	His		
790				795				800									
cag	cag	acc	ctt	ctg	gtt	ccc	agt	gag	gat	ggg	gca	act	gtt	ctt	ttt	2504	
Gln	Gln	Thr	Leu	Leu	Val	Pro	Ser	Glu	Asp	Gly	Ala	Thr	Val	Leu	Phe		
805				810				815				820					
ccc	atc	agg	cca	aca	cat	ctg	gga	gaa	att	cct	atc	aca	gtc	aca	gct	2552	
Pro	Ile	Arg	Pro	Thr	His	Leu	Gly	Glu	Ile	Pro	Ile	Thr	Val	Thr	Ala		
825				830				835									
ctt	tca	ccc	act	gct	tct	gat	gct	atc	acc	cag	atg	att	tta	gta	aag	2600	
Leu	Ser	Pro	Thr	Ala	Ser	Asp	Ala	Ile	Thr	Gln	Met	Ile	Leu	Val	Lys		
840				845				850									

WO 00/29448

PCT/JP99/06412

81/233

gct gaa gga ata gaa aaa tca tat tca caa tcc atc tta tta gac ttg	2648
Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile Leu Leu Asp Leu	
855 860 865	
act gac aat agg cta cag agt acc ctg aaa act ttg agt ttc tca ttt	2696
Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu Ser Phe Ser Phe	
870 875 880	
cct cct aat aca gtg act ggc agt gaa aga gtt cag atc act gca att	2744
Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln Ile Thr Ala Ile	
885 890 895 900	
gga gat gtt ctt ggt cct tcc atc aat ggc tta gcc tca ttg att cgg	2792
Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala Ser Leu Ile Arg	
905 910 915	
atg cct tat ggc tgt ggt gaa cag aac atg ata aat ttt gct cca aat	2840
Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn Phe Ala Pro Asn	
920 925 930	
att tac att ttg gat tat ctg act aaa aag aaa caa ctg aca gat aat	2888
Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln Leu Thr Asp Asn	
935 940 945	
ttg aaa gaa aaa gct ctt tca ttt atg agg caa ggt tac cag aga gaa	2936
Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly Tyr Gln Arg Glu	
950 955 960	
ctt ctc tat cag agg gaa gat ggc tct ttc agt gct ttt ggg aat tat	2984
Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala Phe Gly Asn Tyr	
965 970 975 980	
gac cct tct ggg agc act tgg ttg tca gct ttt gtt tta aga tgt ttc	3032
Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val Leu Arg Cys Phe	
985 990 995	
ctt gaa gcc gat cct tac ata gat att gat cag aat gtg tta cac aga	3080
Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn Val Leu His Arg	
1000 1005 1010	
aca tac act tgg ctt aaa gga cat cag aaa tcc aac ggt gaa ttt tgg	3128
Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn Gly Glu Phe Trp	
1015 1020 1025	
gat cca gga aga gtg att cat agt gag ctt caa ggt ggc aat aaa agt	3176
Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly Gly Asn Lys Ser	

WO 00/29448

PCT/JP99/06412

82/233

1030	1035	1040	
cca gta aca ctt aca gcc tat att gta act tct ctc ctg gga tat aga			3224
Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu Leu Gly Tyr Arg			
1045	1050	1055	1060
aag tat cag cct aac att gat gtg caa gag tct atc cat ttt ttg gag			3272
Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile His Phe Leu Glu			
1065	1070	1075	
tct gaa ttc agt aga gga att tca gac aat tat act cta gcc ott ata			3320
Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr Leu Ala Leu Ile			
1080	1085	1090	
act tat gca ttg tca tca gtg ggg agt cct aaa gcg aag gaa gct ttg			3368
Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala Lys Glu Ala Leu			
1095	1100	1105	
aat atg ctg act tgg aga gca gaa caa gaa ggt ggc atg caa ttc tgg			3416
Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly Met Gln Phe Trp			
1110	1115	1120	
gtg tca tca gag tcc aaa ctt tct gac tcc tgg cag cca cgc tcc ctg			3464
Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln Pro Arg Ser Leu			
1125	1130	1135	1140
gat att gaa gtt gca gcc tat gca ctg ctc tca cac ttc tta caa ttt			3512
Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His Phe Leu Gln Phe			
1145	1150	1155	
cag act tct gag gga atc cca att atg agg tgg cta agc agg caa aga			3560
Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu Ser Arg Gln Arg			
1160	1165	1170	
aat agc ttg ggt ggt ttt gca tct act cag gat acc act gtg gct tta			3608
Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr Thr Val Ala Leu			
1175	1180	1185	
aag gct ctg tct gaa ttt gca gcc cta atg aat aca gaa agg aca aat			3656
Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr Glu Arg Thr Asn			
1190	1195	1200	
atc caa gtg acc gtg acg ggg cct agc tca cca agt cct gta aag ttt			3704
Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser Pro Val Lys Phe			
1205	1210	1215	1220
ctg att gac aca cac aac cgc tta ctc ctt cag aca gca gag ctt gct			3752

WO 00/29448

PCT/JP99/06412

83/233

Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr Ala Glu Leu Ala	
1225 1230 1235	
gtg gta cag cca acg gca gtt aat att tcc gca aat ggt ttt gga ttt	3800
Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn Gly Phe Gly Phe	
1240 1245 1250	
gct att tgt cag ctc aat gtt gta tat aat gtg aag gct tct ggg tct	3848
Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys Ala Ser Gly Ser	
1255 1260 1265	
tct aga aga cga aga tct atc caa aat caa gaa gcc ttt gat tta gat	3896
Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala Phe Asp Leu Asp	
1270 1275 1280	
gtt gct gta aaa gaa aat aaa gat gat ctc aat cat gtg gat ttg aat	3944
Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His Val Asp Leu Asn	
1285 1290 1295 1300	
gtg tgt aca agc ttt tcg ggc ccg ggt agg agt ggc atg gct ctt atg	3992
Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly Met Ala Leu Met	
1305 1310 1315	
gaa gtt aac cta tta agt ggc ttt atg gtg cct tca gaa gca att tct	4040
Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser Glu Ala Ile Ser	
1320 1325 1330	
ctg agc gag aca gtg aag aaa gtg gaa tat gat cat gga aaa ctc aac	4088
Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His Gly Lys Leu Asn	
1335 1340 1345	
ctc tat tta gat tct gta aat gaa acc cag ttt tgt gtt aat att cct	4136
Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys Val Asn Ile Pro	
1350 1355 1360	
gct gtg aga aac ttt aaa gtt tca aat acc caa gat gct tca gtg tcc	4184
Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp Ala Ser Val Ser	
1365 1370 1375 1380	
ata gtg gat tac tat gag cca agg aga cag gcg gtg aga agt tac aac	4232
Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val Arg Ser Tyr Asn	
1385 1390 1395	
tct gaa gtg aag ctg tcc tcc tgt gac ctt tgc agt gat gtc cag ggc	4280
Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser Asp Val Gln Gly	
1400 1405 1410	

WO 00/29448

PCT/JP99/06412

84/233

tgc cgt cct tgt gag gat gga gct tca ggc tcc cat cat cac tct tca 4328
 Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His His His Ser Ser
 1415 1420 1425
 gtc att ttt att ttc tgt ttc aag ctt ctg tac ttt atg gaa ctt tgg 4376
 Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe Met Glu Leu Trp
 1430 1435 1440
 ctg tgatttattt ttaaaggact ctgtgtaaca ctaacatttc cagtagtcac a 4430
 Leu
 1445
 tgtgattgtt ttgttttcgt agaagaatac tgcttctatt ttg 4473

<210> 52
 <211> 2630
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (82)...(1830)
 <400> 52
 agttctgaggga ggcggggggga aggaggttgg tggcgactcc ctcgctcgcc ctcaactgcc 60
 gcggtcccaa ctccaggcac c atg ttc ccc gcg ggc ccc ccc agc cac agc 111
 Met Phe Pro Ala Gly Pro Pro Ser His Ser
 1 5 10
 ctc ctc cgg ctc ccc ctg ctg cag ttg ctg cta ctg gtg gtg cag gcc 159
 Leu Leu Arg Leu Pro Leu Leu Gln Leu Leu Leu Leu Val Val Gln Ala
 15 20 25
 gtg ggg agg ggg ctg ggc cgc gcc agc ccg gcc ggg ggc ccc ctg gaa 207
 Val Gly Arg Gly Leu Gly Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu
 30 35 40
 gat gtg gtc atc gag agg tac cac atc ccc agg gcc tgt ccc cgg gaa 255
 Asp Val Val Ile Glu Arg Tyr His Ile Pro Arg Ala Cys Pro Arg Glu
 45 50 55
 gtg cag atg ggg gat ttt gtg cgc tac cac tac aac ggc act ttt gaa 303
 Val Gln Met Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Phe Glu
 60 65 70

WO 00/29448

PCT/JP99/06412

85/233

gat ggc aag aag ttt gat tca agc tat gat cgc aac acc ttg gtg gcc	351
Asp Gly Lys Lys Phe Asp Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala	
75 80 85 90	
atc gtg gtg ggt gtg ggg cgc ctc atc act ggc atg gac cga ggc ctc	399
Ile Val Val Gly Val Gly Arg Leu Ile Thr Gly Met Asp Arg Gly Leu	
95 100 105	
atg ggc atg tgt gtc aac gag cgg cga cgc ctc att gtg cct ccc cac	447
Met Gly Met Cys Val Asn Glu Arg Arg Arg Leu Ile Val Pro Pro His	
110 115 120	
ctg ggc tat ggg agc atc ggc ctg gcg ggg ctc att cca ccg gat gcc	495
Leu Gly Tyr Gly Ser Ile Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala	
125 130 135	
acc ctc tac ttc gat gtg gtt ctg ctg gat gtg tgg aac aag gaa gac	543
Thr Leu Tyr Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp	
140 145 150	
acc gtg cag gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg	591
Thr Val Gln Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met	
155 160 165 170	
gtc cag gac ggc gac ttt gtc cgc tac cac tac aat ggc acc ctg ctg	639
Val Gln Asp Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu	
175 180 185	
gac ggc acc tcc ttc gac acc agc tac agt aag ggc ggc act tat gac	687
Asp Gly Thr Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp	
190 195 200	
acc tac gtc ggc tct ggt tgg ctg atc aag ggc atg gac cag ggg ctg	735
Thr Tyr Val Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu	
205 210 215	
ctg ggc atg tgt cct gga gag aga agg aag att atc atc cct cca ttc	783
Leu Gly Met Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe	
220 225 230	
ctg gcc tat ggc gag aaa ggc tat ggg acg gtg atc ccc cca cag gcc	831
Leu Ala Tyr Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala	
235 240 245 250	
tcg ctg gtc ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac	879
Ser Leu Val Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp	

WO 00/29448

PCT/JP99/06412

86/233

255	260	265	
gct gtc cag cta gag acg ctg gag ctc ccc ccc ggc tgt gtc cgc aga			927
Ala Val Gln Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg			
270	275	280	
gcc ggg gcc ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg			975
Ala Gly Ala Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met			
285	290	295	
gac ggc acc ctc ttc gat tcc agc tac tcc cgc aac cac acc tac aat			1023
Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn			
300	305	310	
acc tat atc ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg			1071
Thr Tyr Ile Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu			
315	320	325	330
cag ggt gcc tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac			1119
Gln Gly Ala Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His			
335	340	345	
ctc gcc tat ggg gag aat gga act gga gac aag atc cct ggc tct gcc			1167
Leu Ala Tyr Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala			
350	355	360	
gtg cta atc ttc aac gtc cat gtc att gac ttc cac aac cct gcg gat			1215
Val Leu Ile Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp			
365	370	375	
gtg gtg gaa atc agg aca ctg tcc cgg cca tct gag acc tgc aat gag			1263
Val Val Glu Ile Arg Thr Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu			
380	385	390	
acc acc aag ctt ggg gac ttt gtt cga tac cat tac aac tgt tct ttg			1311
Thr Thr Lys Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu			
395	400	405	410
ctg gac ggc acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag			1359
Leu Asp Gly Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln			
415	420	425	
gag gcg act ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc			1407
Glu Ala Thr Leu Gly Ala Asn Lys Val Ile Glu Gly Leu Asp Thr Gly			
430	435	440	
ctg cag ggc atg tgt gtg gga gag agg cgg cag ctc atc gtg ccc ccg			1455

Leu	Gln	Gly	Met	Cys	Val	Gly	Glu	Arg	Arg	Gln	Leu	Ile	Val	Pro	Pro		
445						450						455					
cac	ctg	gcc	cac	ggg	gag	agt	gga	gcc	cgg	gga	gtc	cca	ggc	agt	gct	1503	
His	Leu	Ala	His	Gly	Glu	Ser	Gly	Ala	Arg	Gly	Val	Pro	Gly	Ser	Ala		
460						465						470					
gtg	ctg	ctg	ttt	gag	gtg	gag	ctg	gtg	tcc	cgg	gag	gat	ggg	ctg	ccc	1551	
Val	Leu	Leu	Phe	Glu	Val	Glu	Leu	Val	Ser	Arg	Glu	Asp	Gly	Leu	Pro		
475						480						485			490		
aca	ggc	tac	ctg	ttt	gtg	tgg	cac	aag	gac	cct	cct	gcc	aac	ctg	ttt	1599	
Thr	Gly	Tyr	Leu	Phe	Val	Trp	His	Lys	Asp	Pro	Pro	Ala	Asn	Leu	Phe		
			495						500						505		
gaa	gac	atg	gac	ctc	aac	aag	gat	ggc	gag	gtc	cct	ccg	gag	gag	ttc	1647	
Glu	Asp	Met	Asp	Leu	Asn	Lys	Asp	Gly	Glu	Val	Pro	Pro	Glu	Glu	Phe		
			510						515						520		
tcc	acc	ttc	atc	aag	gct	caa	gtg	agt	gag	ggc	aaa	gga	cgc	ctc	atg	1695	
Ser	Thr	Phe	Ile	Lys	Ala	Gln	Val	Ser	Glu	Gly	Lys	Gly	Arg	Leu	Met		
525						530						535					
cct	ggg	cag	gac	cct	gag	aaa	acc	ata	gga	gac	atg	ttc	cag	aac	cag	1743	
Pro	Gly	Gln	Asp	Pro	Glu	Lys	Thr	Ile	Gly	Asp	Met	Phe	Gln	Asn	Gln		
540						545						550					
gac	cgc	aac	cag	gac	ggc	aag	atc	aca	gtc	gac	gag	ctc	aag	ctg	aag	1791	
Asp	Arg	Asn	Gln	Asp	Gly	Lys	Ile	Thr	Val	Asp	Glu	Leu	Lys	Leu	Lys		
555						560						565			570		
tca	gat	gag	gac	gag	gag	cgg	gtc	cac	gag	gag	ctc	tga	ggggc	caggga		1840	
Ser	Asp	Glu	Asp	Glu	Glu	Arg	Val	His	Glu	Glu	Leu						
			575						580								
gcctggccag	gcctgagaca	cagaggccca	ctgcgagggg	gacagtggcg	gtgggactga											1900	
cctgctgaca	gtcaccctcc	ctctgctggg	atgaggtcca	ggagccaact	aaaacaatgg											1960	
cagaggagac	atctctgggtg	ttcccaccac	cctagatgaa	aatccacagc	acagacctct											2020	
accgtgtttc	tcttccatcc	ctaaaccact	tccttaaaat	gtttggattt	gcaaagccaa											2080	
tttggggcct	gtggagcctg	gggttgata	gggccatggc	tgggtcccca	ccatacctcc											2140	
cctccacatc	actgacacag	ctgagcttgt	tatccatctc	cccaaacttt	ctctttcttt											2200	
gtactttcttg	tcacccccac	tcccagcccc	tattccteta	tgtgacaget	ggctaggacc											2260	
cctctgcctt	cctccccaat	cctgactggc	tcctagggaa	ggggaaggct	cctggaggggc											2320	
agccctacct	ctcccatgcc	ctttgccttc	ctccctcgcc	tccagtggag	gctgagctga											2380	

WO 00/29448

PCT/JP99/06412

88/233

ccctgggctg ctggaggcca gactgggctg tagttagctt ttcaccccta aagaaggctt 2440
 tccctaagga accatagaag agaggaagaa aacaaagggc atgtgtgagg gaagctgctt 2500
 ggggtgggtgt tagggctatg aaatottgga tttggggctg aggggtggga gggagggcag 2560
 agctctgcac actcaaaggc taaactggtg tcagtccttt tttcctttgt tccaaataaa 2620
 agattaaacc 2630

<210> 53

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)...(1321)

<400> 53

aaaaagactc cgccttccca agagcccttg cggccggggc cgaaaatggc ggcggggcg 60
 acggccgggc gtcctgaag cagcagtt atg gag ctt ccc tca ggg ccg ggg 112
 Met Glu Leu Pro Ser Gly Pro Gly
 1 5
 ccg gag cgg ctc ttt gac tcg cac cgg ctt ccg ggt gac tgc ttc cta 160
 Pro Glu Arg Leu Phe Asp Ser His Arg Leu Pro Gly Asp Cys Phe Leu
 10 15 20
 ctg ctc gtg ctg ctg ctc tac gcg cca gtc ggg ttc tgc ctc ctc gtc 208
 Leu Leu Val Leu Leu Leu Tyr Ala Pro Val Gly Phe Cys Leu Leu Val
 25 30 35 40
 ctg cgc ctc ttt ctc ggg atc cac gtc ttc ctg gtc agc tgc gcg ctg 256
 Leu Arg Leu Phe Leu Gly Ile His Val Phe Leu Val Ser Cys Ala Leu
 45 50 55
 cca gac agc gtc ctt cgc aga ttc gta gtg cgg acc atg tgt gcg gtg 304
 Pro Asp Ser Val Leu Arg Arg Phe Val Val Arg Thr Met Cys Ala Val
 60 65 70
 cta ggg ctc gtg gcc cgg cag gag gac tcc gga ctc cgg gat cac agt 352
 Leu Gly Leu Val Ala Arg Gln Glu Asp Ser Gly Leu Arg Asp His Ser
 75 80 85
 gtc agg gtc ctc att tcc aac cat gtg aca cct ttc gac cac aac ata 400
 Val Arg Val Leu Ile Ser Asn His Val Thr Pro Phe Asp His Asn Ile

WO 00/29448

PCT/JP99/06412

89/233

90	95	100	
gtc aat ttg ctt acc acc tgt agc acc cct cta ctc aat agt ccc ccc			448
Val Asn Leu Leu Thr Thr Cys Ser Thr Pro Leu Leu Asn Ser Pro Pro			
105	110	115	120
agc ttt gtg tgc tgg tct cgg ggc ttc atg gag atg aat ggg cgg ggg			496
Ser Phe Val Cys Trp Ser Arg Gly Phe Met Glu Met Asn Gly Arg Gly			
125	130	135	
gag ttg gtg gag tca ctc aag aga ttc tgt gct tcc acg agg ctt ccc			544
Glu Leu Val Glu Ser Leu Lys Arg Phe Cys Ala Ser Thr Arg Leu Pro			
140	145	150	
ccc act cct ctg ctg cta ttc cct gag gaa gag gcc acc aat ggc cgg			592
Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu Glu Ala Thr Asn Gly Arg			
155	160	165	
gag ggg ctc ctg cgc ttc agt tcc tgg cca ttt tct atc caa gat gtg			640
Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro Phe Ser Ile Gln Asp Val			
170	175	180	
gta caa cct ctt acc ctg caa gtt cag aga ccc ctg gtc tct gtg acg			688
Val Gln Pro Leu Thr Leu Gln Val Gln Arg Pro Leu Val Ser Val Thr			
185	190	195	200
gtg tca gat gcc tcc tgg gtc tca gaa ctg ctg tgg tca ctt ttc gtc			736
Val Ser Asp Ala Ser Trp Val Ser Glu Leu Leu Trp Ser Leu Phe Val			
205	210	215	
cct ttc acg gtg tat caa gta agg tgg ctt cgt cct gtt cat cgc caa			784
Pro Phe Thr Val Tyr Gln Val Arg Trp Leu Arg Pro Val His Arg Gln			
220	225	230	
cta ggg gaa gcg aat gag gag ttt gca ctc cgt gta caa cag ctg gtg			832
Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val			
235	240	245	
gcc aag gaa ttg ggc cag aca ggg aca cgg ctc act cca gct gac aaa			880
Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys			
250	255	260	
gca gag cac atg aag cga caa aga cac ccc aga ttg cgc ccc cag tca			928
Ala Glu His Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser			
265	270	275	280
gcc cag tct tct ttc cct ccc tcc cct ggt cct tct cct gat gtg caa			976

WO 00/29448

PCT/JP99/06412

90/233

Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln	
285 290 295	
ctg gca act ctg gct cag aga gtc aag gaa gtt ttg ccc cat gtg cca	1024
Leu Ala Thr Leu Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro	
300 305 310	
ttg ggt gtc atc cag aga gac ctg gcc aag act ggc tgt gta gac ttg	1072
Leu Gly Val Ile Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu	
315 320 325	
act atc act aat ctg ctt gag ggg gcc gta gct ttc atg cct gaa gac	1120
Thr Ile Thr Asn Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp	
330 335 340	
atc acc aag gga act cag tcc cta ccc aca gcc tct gcc tcc aag ttt	1168
Ile Thr Lys Gly Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe	
345 350 355 360	
ccc agc tct ggc ccg gtg acc cct cag cca aca gcc cta aca ttt gcc	1216
Pro Ser Ser Gly Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala	
365 370 375	
aag tct tcc tgg gcc cgg cag gag agc ctg cag gag cgc aag caa gca	1264
Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala	
380 385 390	
cta tat gaa tac gca aga agg aga ttc aca gag aga cga gcc cag gag	1312
Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu	
395 400 405	
gct gac tgagctcaaa ggaacaggat ggcacccaga gccgcaggac ggagactggg gg	1370
Ala Asp	
410	
cagccctcac ccaactcaca acaggctgga tgggtgggtg gtaaaaaggg aaggatgagg	1430
ctcccccaat gtcacattaa attcatgggtt ttcattcaag gc	1472

<210> 54

<211> 1652

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

WO 00/29448

PCT/JP99/06412

91/233

<222> (17)...(1468)

<400> 54

aaagcggcgg	cggagg	atg	gag	gaa	gga	ggc	ggc	ggc	gta	cgg	agt	ctg	gtc	52		
Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val																
1			5			10										
ccg	ggc	ggg	ccg	gtg	tta	ctg	gtc	ctc	tgc	ggc	ctc	ctg	gag	gcg	tcc	100
Pro Gly Gly Pro Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser																
15			20			25										
ggc	ggc	ggc	cga	gcc	ctt	cct	caa	ctc	agc	gat	gac	atc	cct	ttc	cga	148
Gly Gly Gly Arg Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg																
30			35			40										
gtc	aac	tgg	ccc	ggc	acc	gag	ttc	tct	ctg	ccc	aca	act	gga	gtt	tta	196
Val Asn Trp Pro Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu																
45			50			55			60							
tat	aaa	gaa	gat	aat	tat	gtc	atc	atg	aca	act	gca	cat	aaa	gaa	aaa	244
Tyr Lys Glu Asp Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys																
65			70			75										
tat	aaa	tgc	ata	ctt	ccc	ctt	gtg	aca	agt	ggg	gat	gag	gaa	gaa	gaa	292
Tyr Lys Cys Ile Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu																
80			85			90										
aag	gat	tat	aaa	ggc	cct	aat	cca	aga	gag	ctt	ttg	gag	cca	cta	ttt	340
Lys Asp Tyr Lys Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe																
95			100			105										
aaa	caa	agc	agt	tgt	tcc	tac	aga	att	gag	tct	tat	tgg	act	tac	gaa	388
Lys Gln Ser Ser Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu																
110			115			120										
gta	tgt	cat	gga	aaa	cac	att	cgg	cag	tac	cat	gaa	gag	aaa	gaa	act	436
Val Cys His Gly Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr																
125			130			135			140							
ggt	cag	aaa	ata	aat	att	cac	gag	tac	tac	ctt	ggg	aat	atg	ttg	gcc	484
Gly Gln Lys Ile Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala																
145			150			155										
aag	aac	ctt	cta	ttt	gaa	aaa	gaa	cga	gaa	gca	gaa	gaa	aag	gaa	aaa	532
Lys Asn Leu Leu Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys																
160			165			170										

WO 00/29448

PCT/JP99/06412

92/233

tca aat gag att ccc act aaa aat atc gaa ggt cag atg aca cca tac	580
Ser Asn Glu Ile Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr	
175 180 185	
tat cct gtg gga atg gga aat ggt aca cct tgt agt ttg aaa cag aac	628
Tyr Pro Val Gly Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn	
190 195 200	
egg ccc aga tca agt act gtg atg tac ata tgt cat cct gaa tct aag	676
Arg Pro Arg Ser Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys	
205 210 215 220	
cat gaa att ctt tca gta gct gaa gtt aca act tgt gaa tat gaa gtt	724
His Glu Ile Leu Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val	
225 230 235	
gtc att ttg aca cca ctc ttg tgc agt cat cct aaa tat agg ttc aga	772
Val Ile Leu Thr Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg	
240 245 250	
gca tct cct gtg aat gac ata ttt tgt caa tca ctg cca gga tct cca	820
Ala Ser Pro Val Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro	
255 260 265	
ttt aag ccc ctc acc ctg agg cag ctg gag cag cag gaa gaa ata cta	868
Phe Lys Pro Leu Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu	
270 275 280	
agg gtg cct ttt agg aga aat aaa gag gaa gat ttg caa tca act aaa	916
Arg Val Pro Phe Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys	
285 290 295 300	
gaa gag aga ttt cca gcg atc cac aag tcg att gct att ggc tct cag	964
Glu Glu Arg Phe Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln	
305 310 315	
cca gtg ctc act gtt ggg aca acc cac ata tcc aaa ttg aca gat gac	1012
Pro Val Leu Thr Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp	
320 325 330	
caa ctc ata aaa gag ttt ctt agt ggt tct tac tgc ttt cgt ggg ggt	1060
Gln Leu Ile Lys Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly	
335 340 345	
gtc ggt tgg tgg aaa tat gaa ttc tgc tat ggc aaa cat gta cat caa	1108
Val Gly Trp Trp Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln	

<221> CDS

attttggtgg gtgagcagc atg ggc ttt gag gag ctg ctg gag cag gtg ggc																52
Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly																
1					5					10						
ggc ttt ggg ccc ttc caa ctg cgg aat gtg gca ctg ctg gcc ctg ccc																100
Gly Phe Gly Pro Phe Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro																
15					20					25						
cga gtg ctg cta cca ctg cac ttc ctc ctg ccc atc ttc ctg gct gcc																148
Arg Val Leu Leu Pro Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala																
30					35					40						
gtg cct gcc cac cga tgt gcc ctg ccg ggt gcc cct gcc aac ttc agc																196
Val Pro Ala His Arg Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser																
45					50					55						
cat cag gat gtg tgg ctg gag gcc cat ctt ccc cgg gag cct gat ggc																244
His Gln Asp Val Trp Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly																
60					65					70					75	
acg ctc agc tcc tgc ctc cgc ttt gcc tat ccc cag gct ctc ccc aac																292
Thr Leu Ser Ser Cys Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn																
80					85					90						
acc acg ttg ggg gaa gaa agg cag agc cgt ggg gag ctg gag gat gaa																340
Thr Thr Leu Gly Glu Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu																
95					100					105						
cct gcc aca gtg ccc tgc tct cag ggc tgg gag tac gac cac tca gaa																388
Pro Ala Thr Val Pro Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu																
110					115					120						
ttc tcc tct acc att gca act gag tcc cag gtc ggt att tac ata atc																436
Phe Ser Ser Thr Ile Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile																
125					130					135						
cat ctg gag gtg gaa tgt cgg tgg agg cag tct ccc tgg gag gca gca																484
His Leu Glu Val Glu Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala																
140					145					150					155	
ggg cga ggc ctt cct tgg gaa gaa gct gag gct gca gga ctg ggg agg																532
Gly Arg Gly Leu Pro Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg																
160					165					170						

WO 00/29448

PCT/JP99/06412

95/233

gac aaa gtt tcc tat tcc cca agc tgg cgt gaa tcg ttg gga ggt tta	580
Asp Lys Val Ser Tyr Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu	
175 180 185	
tta tct ggc atg gag tgg gat ctg gtg tgt gag cag aaa ggt ctg aac	628
Leu Ser Gly Met Glu Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn	
190 195 200	
aga gct gcg tcc act ttc ttc ttc gcc ggt gtg ctg gtg ggg gct gtg	676
Arg Ala Ala Ser Thr Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val	
205 210 215	
gcc ttt gga tat ctg tcc gac agg ttt ggg cgg cgg cgt ctg ctg ctg	724
Ala Phe Gly Tyr Leu Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu	
220 225 230 235	
gta gcc tac gtg agt acc ctg gtg ctg ggc ctg gca tct gca gcc tcc	772
Val Ala Tyr Val Ser Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser	
240 245 250	
gtc agc tat gta atg ttt gcc atc acc cgc acc ctt act ggc tca gcc	820
Val Ser Tyr Val Met Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala	
255 260 265	
ctg gct ggt ttt acc atc atc gtg atg cca ctg gag ctg gag tgg ctg	868
Leu Ala Gly Phe Thr Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu	
270 275 280	
gat gtg gag cac cgc acc gtg gct gga gtc ctg agc agc acc ttc tgg	916
Asp Val Glu His Arg Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp	
285 290 295	
aca ggg ggc gtg atg ctg ctg gca ctg gtt ggg tac ctg ata cgg gac	964
Thr Gly Gly Val Met Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp	
300 305 310 315	
tgg cga tgg ctt ctg cta gct gtc acc ctg cct tgt gcc cca ggc atc	1012
Trp Arg Trp Leu Leu Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile	
320 325 330	
ctc agc ctc tgg tgg gtg cct gag tct gca cgc tgg ctt ctg acc caa	1060
Leu Ser Leu Trp Trp Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln	
335 340 345	
ggc cat gtg aaa gag gcc cac agg tac ttg ctc cac tgt gcc agg ctc	1108
Gly His Val Lys Glu Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu	

WO 00/29448

PCT/JP99/06412

96/233

350	355	360	
aat ggg cgg cca gtg tgt gag gac agc ttc agc cag gag gct gtg agc			1156
Asn Gly Arg Pro Val Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser			
365	370	375	
aaa gtg gcc gcc ggg gaa cgg gtg gtc cga aga cct tca tac cta gac			1204
Lys Val Ala Ala Gly Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp			
380	385	390	395
ctg ttc cgc aca cca cgg ctc cga cac atc tca ctg tgc tgc gtg gtg			1252
Leu Phe Arg Thr Pro Arg Leu Arg His Ile Ser Leu Cys Cys Val Val			
400	405	410	
gtg tgg ttc gga gtg aac ttc tcc tat tac ggc ctg agt ctg gat gtg			1300
Val Trp Phe Gly Val Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val			
415	420	425	
tcg ggg ctg ggg ctg aac gtg tac cag aca cag ctg ttg ttc ggg gct			1348
Ser Gly Leu Gly Leu Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala			
430	435	440	
gtg gaa ctg ccc tcc aag ctg ctg gtc tac ttg tcg gtg cgc tac gca			1396
Val Glu Leu Pro Ser Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala			
445	450	455	
gga cgc cgc ctc acg caa gcc ggg aca ctg ctg ggc acg gcc ctg gcg			1444
Gly Arg Arg Leu Thr Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala			
460	465	470	475
ttc ggc act aga ctg cta gtg tcc tct gat atg aag tcc tgg agc act			1492
Phe Gly Thr Arg Leu Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr			
480	485	490	
gtc ctg gca gtg atg ggg aaa gct ttt tct gaa gct gcc ttc acc act			1540
Val Leu Ala Val Met Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr			
495	500	505	
gcc tac ctg ttc act tca gag ttg tac cct acg gtg ctc aga cag aca			1588
Ala Tyr Leu Phe Thr Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr			
510	515	520	
ggg atg ggg ctg act gca ctg gtg ggc cgg ctg ggg ggc tct ttg gcc			1636
Gly Met Gly Leu Thr Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala			
525	530	535	
cca ctg gcg gcc ttg ctg gat gga gtg tgg ctg tca ctg ccc aag ctt			1684

WO 00/29448

PCT/JP99/06412

97/233

Pro Leu Ala Ala Leu Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu
 540 545 550 555
 act tat ggg ggg atc gcc ctg ctg gct gcc ggc acc gcc ctc ctg ctg 1732
 Thr Tyr Gly Gly Ile Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu
 560 565 570
 cca gag acg agg cag gca cag ctg cca gag acc atc cag gac gtg gag 1780
 Pro Glu Thr Arg Gln Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu
 575 580 585
 aga aag agt gcc cca acc agt ctt cag gag gaa gag atg ccc atg aag 1828
 Arg Lys Ser Ala Pro Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys
 590 595 600
 cag gtc cag aac taagtgggag tggaggcagg coctccacag aagctctgca 1880
 Gln Val Gln Asn
 605
 gcaggggctg ggagagcaga agggcaggcc ctgcaactca ggctgggagt atcgaaccct 1940
 ctgcctaggg ccggagttgc tgccagtacc cgctccctct gctcatccat ccttgattat 2000
 ttggcttcta ggaacagttg acttcccaga atgcagtggg ctgctgggca cccctctcac 2060
 gggtggggag gattctgtaa ataaaggtgc cccttgggtt ggggcagtgg tg 2112

<210> 56
 <211> 1087
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (33)...(977)
 <400> 56

agagggggcg tcaggccgcg ggagaggagg cc atg ggc gcg cgc ggg gcg ctg 53
 Met Gly Ala Arg Gly Ala Leu
 1 5
 ctg ctg gcg ctg ctg ctg gct cgg gct gga ctc agg aag ccg gag tcg 101
 Leu Leu Ala Leu Leu Leu Ala Arg Ala Gly Leu Arg Lys Pro Glu Ser
 10 15 20
 cag gag gcg gcg ccg tta tca gga cca tgc ggc cga cgg gtc atc acg 149
 Gln Glu Ala Ala Pro Leu Ser Gly Pro Cys Gly Arg Arg Val Ile Thr

WO 00/29448

PCT/JP99/06412

98/233

25	30	35	
tcg cgc atc gtg ggt gga gag gac gcc gaa ctc ggg cgt tgg ccg tgg			197
Ser Arg Ile Val Gly Gly Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp			
40	45	50	55
cag ggg agc ctg cgc ctg tgg gat tcc cac gta tgc gga gtg agc ctg			245
Gln Gly Ser Leu Arg Leu Trp Asp Ser His Val Cys Gly Val Ser Leu			
60	65	70	
ctc agc cac cgc tgg gca ctc acg gcg gcg cac tgc ttt gaa acc tat			293
Leu Ser His Arg Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr			
75	80	85	
agt gac ctt agt gat ccc tcc ggg tgg atg gtc cag ttt ggc cag ctg			341
Ser Asp Leu Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu			
90	95	100	
act tcc atg cca tcc ttc tgg agc ctg cag gcc tac tac acc cgt tac			389
Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr			
105	110	115	
ttc gta tcg aat atc tat ctg agc cct cgc tac ctg ggg aat tca ccc			437
Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro			
120	125	130	135
tat gac att gcc ttg gtg aag ctg tct gca cct gtc acc tac act aaa			485
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr Lys			
140	145	150	
cac atc cag ccc atc tgt ctc cag gcc tcc aca ttt gag ttt gag aac			533
His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe Glu Asn			
155	160	165	
cgg aca gac tgc tgg gtg act ggc tgg ggg tac atc aaa gag gat gag			581
Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys Glu Asp Glu			
170	175	180	
gca ctg cca tct ccc cac acc ctc cag gaa gtt cag gtc gcc atc ata			629
Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln Val Ala Ile Ile			
185	190	195	
aac aac tct atg tgc aac cac ctc ttc ctc aag tac agt ttc cgc aag			677
Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys Tyr Ser Phe Arg Lys			
200	205	210	215
gac atc ttt gga gac atg gtt tgt gct ggc aat gcc caa ggc ggg aag			725

WO 00/29448

PCT/JP99/06412

99/233

Asp Ile Phe Gly Asp Met Val Cys Ala Gly Asn Ala Gln Gly Gly Lys
 220 225 230
 gat gcc tgc ttc ggt gac tca ggt gga ccc ttg gcc tgt aac aag aat 773
 Asp Ala Cys Phe Gly Asp Ser Gly Gly Pro Leu Ala Cys Asn Lys Asn
 235 240 245
 gga ctg tgg tat cag att gga gtc gtg agc tgg gga gtg ggc tgt ggt 821
 Gly Leu Trp Tyr Gln Ile Gly Val Val Ser Trp Gly Val Gly Cys Gly
 250 255 260
 cgg ccc aat cgg ccc ggt gtc tac acc aat atc agc cac cac ttt gag 869
 Arg Pro Asn Arg Pro Gly Val Tyr Thr Asn Ile Ser His His Phe Glu
 265 270 275
 tgg atc cag aag ctg atg gcc cag agt ggc atg tcc cag cca gac ccc 917
 Trp Ile Gln Lys Leu Met Ala Gln Ser Gly Met Ser Gln Pro Asp Pro
 280 285 290 295
 tcc tgg ccg cta ctc ttt ttc cct ctt ctc tgg gct ctc cca ctc ctg 965
 Ser Trp Pro Leu Leu Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu
 300 305 310
 ggg ccg gtc tgagcctacc tgagcccatg cagcctgggg ccaactgccaa gtcagg 1020
 Gly Pro Val
 ccctggttet cttctgtctt gtttggtaat aaacacattc cagttgatgc cttgcagggc 1080
 attcttc 1087

<210> 57

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (216)...(500)

<400> 57

cccgaagttt gaggggtgtg gacggtttgt gacccctta gccgacccta ctctcactg 60
 gccgggacaa ctggttatt caccggaggct ggggccaggc agcccttcgg ttccgggtggg 120
 cccatggacc ccagtccaac gccgagggaa taggaccatc caaaagcggg accttcgct 180
 cagaaaaagg cgtggaccct gccagcagcc aggcc atg gag ctc tct gat gtc 233

tttttctct accccttagc aggaataggg tctcctcct tctttcgaag gaattttgctt 1420

WO 00/29448

PCT/JP99/06412

101/233

gcatttttatt ttattttttt aagagtcctt catagagctc agtcaggaag gggatggggc 1480
 accaagccaa gccccagca ttgggagcgg ccagccaca gctgctgctc ccgtagtcct 1540
 caggctgtaa gcaagagaca gcactggccc ttggccagcg tcctaccctg cccaactcca 1600
 aggactgggt atggattgct gggccctagg ctcttgcttc tggggctatt ggagggtcag 1660
 tgtctgtgac tgaataaagt tccattttgt ggtc 1694

<210> 58
 <211> 1522
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (12)...(668)
 <400> 58

cctttcccaa g atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag 50
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln
 1 5 10
 ctg atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg 98
 Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp
 15 20 25
 ggc tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc 146
 Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg
 30 35 40 45
 cgg aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca 194
 Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
 50 55 60
 gcc gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg 242
 Ala Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp
 65 70 75
 ttc gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc 290
 Phe Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala
 80 85 90
 tac atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg 338
 Tyr Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met
 95 100 105

WO 00/29448

PCT/JP99/06412

102/233

tac tcg cgc aca gtt gcc atc atc ggc gga ctt tct tgt gtt ggc cag	386
Tyr Ser Arg Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln	
110 115 120 125	
cgg tgc tgg gga gct gta ccg ccg gaa acc tcg cag ccg ctc cct gca	434
Arg Cys Trp Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala	
130 135 140	
gtc cac cgg cca ggt gtt cct ggg tat cta cct cat ctg tgt ggc cta	482
Val His Arg Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu	
145 150 155	
ctc act gca gca cag caa gga gga ccg gct ggc gta tct gaa cca tct	530
Leu Thr Ala Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser	
160 165 170	
ccc agg agg gga gct gat gat cca gct gtt ctt cgt gct gta tgg cat	578
Pro Arg Arg Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His	
175 180 185	
cct ggc cct ggc ctt tct gtc agg cta cta cgt gac cct cgc tgc cca	626
Pro Gly Pro Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro	
190 195 200 205	
gat cct ggc tgt act gct gcc ccc tgt cat gct gct cat tgatg	670
Asp Pro Gly Cys Thr Ala Ala Pro Cys His Ala Ala His	
210 215	
gcaatgttgc ttactggcac aacacgcggc gtgttgagtt ctggaaccag atgaagctcc	730
ttggagagag tgtgggcac ttccggaactg ctgtcatctg gccactgatg gctgagtttt	790
atggcaagag gctgagatgg gcacagggag ccactgaggg tcaccctgcc ttctctcttg	850
ctggcccagc tgcgtgtttat ttatgctttt tggctctgttt gtttgatctt ttgctttttt	910
aaaattgttt tttgcagtta agaggcagct catttgtcca aatttctggg ctccagcgtt	970
gggagggcag gagccctggc actaatgctg tacaggtttt tttcctgtta ggagagctga	1030
ggccagctgc ccactgagtc tcctgtccct gagaagggag tatggcaggg ctgggatgag	1090
gctactgaga gtgggagagt gggagacaga ggaaggaaga tggagattgg aagtgagcaa	1150
atgtgaaaaa ttctcttttg aacctggcag atgcagctag gctctgcagt gctgttttga	1210
gactgtgaga gggagtgcgt gtgttgacac atgtggatca ggcccaggaa gggcacaggg	1270
gctgagcact acagaagtca catgggttct cagggtatgc caggggcaga aacagtaccg	1330
gctctctgtc actcaccttg agagtagagc agaccctgtt ctgctctggg ctgtgaaggg	1390
gtggagcagg cagtggccag ctttgccctt cctgctgtct ctgtttctag ctccatggtt	1450
ggcctggtgg ggggtggagt cctcccaaa caccagacca cacagtcctc caaaaataaa	1510

WO 00/29448

PCT/JP99/06412

103/233

cattttatat ag 1522

<210> 59
 <211> 1591
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (44)...(1426)
 <400> 59

gaaaacagtt ccacgttgct tgaaattgaa aatcaagata aaa atg ttc aca att 55
 Met Phe Thr Ile
 1

aag ctc ctt ctt ttt att gtt cct cta gtt att tcc tcc aga att gat 103
 Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser Ser Arg Ile Asp
 5 10 15 20

caa gac aat tca tca ttt gat tct cta tct cca gag cca aaa tca aga 151
 Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu Pro Lys Ser Arg
 25 30 35

ttt gct atg tta gac gat gta aaa att tta gcc aat ggc ctc ctt cag 199
 Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn Gly Leu Leu Gln
 40 45 50

ttg gga cat ggt ctt aaa gac ttt gtc cat aag acg aag ggc caa att 247
 Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr Lys Gly Gln Ile
 55 60 65

aat gac ata ttt caa aaa ctc aac ata ttt gat cag tct ttt tat gat 295
 Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln Ser Phe Tyr Asp
 70 75 80

cta tcg ctg caa acc agt gaa atc aaa gaa gaa gaa aag gaa ctg aga 343
 Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg
 85 90 95 100

aga act aca tat aaa cta caa gtc aaa aat gaa gag gta aag aat atg 391
 Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met
 105 110 115

tca ctt gaa ctc aac tca aaa ctt gaa agc ctc cta gaa gaa aaa att 439

WO 00/29448

PCT/JP99/06412

104/233

Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile	
120	125
cta ctt caa caa aaa gtg aaa tat tta gaa gag caa cta act aac tta	487
Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu	
135	140
att caa aat caa cct gaa act cca gaa cac cca gaa gta act tca ctt	535
Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu	
150	155
aaa act ttt gta gaa aaa caa gat aat agc atc aaa gac ctt ctc cag	583
Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln	
165	170
acc gtg gaa gac caa tat aaa caa tta aac caa cag cat agt caa ata	631
Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln Ile	
185	190
aaa gaa ata gaa aat cag ctc aga agg act agt att caa gaa ccc aca	679
Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu Pro Thr	
200	205
gaa att tct cta tct tcc aag cca aga gca cca aga act act ccc ttt	727
Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr Thr Pro Phe	
215	220
cta cag ttg aat gaa ata aga aat gta aaa cat gat ggc att cct gct	775
Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp Gly Ile Pro Ala	
230	235
gaa tgt acc acc att tat aac aga ggt gaa cat aca agt ggc atg tat	823
Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr Ser Gly Met Tyr	
245	250
gcc atc aga ccc agc aac tct caa gtt ttt cat gtc tac tgt gat gtt	871
Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val Tyr Cys Asp Val	
265	270
ata tca ggt agt cca tgg aca tta att caa cat cga ata gat gga tca	919
Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg Ile Asp Gly Ser	
280	285
caa aac ttc aat gaa acg tgg gag aac tac aaa tat ggt ttt ggg agg	967
Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr Gly Phe Gly Arg	
295	300
	305

WO 00/29448

PCT/JP99/06412

105/233

ctt gat gga gaa ttt tgg ttg ggc cta gag aag ata tac tcc ata gtg	1015
Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile Tyr Ser Ile Val	
310 315 320	
aag caa tct aat tat gtt tta cga att gag ctg gaa gac tgg aaa gac	1063
Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp	
325 330 335 340	
aac aaa cat tat att gaa tat tct ttt tac ttg gga aat cac gaa acc	1111
Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr	
345 350 355	
aac tat acg cta cat cta gtt gcg att act ggc aat gtc ccc aat gca	1159
Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala	
360 365 370	
atc ccg gaa aac aaa gat ttg gtg ttt tct act tgg gat cac aaa gca	1207
Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala	
375 380 385	
aaa gga cac ttc aac tgt cca gag ggt tat tca gga ggc tgg tgg tgg	1255
Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp	
390 395 400	
cat gat gag tgt gga gaa aac aac cta aat ggt aaa tat aac aaa cca	1303
His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro	
405 410 415 420	
aga gca aaa tct aag cca gag agg aga aga gga tta tct tgg aag tct	1351
Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys Ser	
425 430 435	
caa aat gga agg tta tac tct ata aaa tca acc aaa atg ttg atc cat	1399
Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu Ile His	
440 445 450	
cca aca gat tca gaa agc ttt gaa tgaactgagg caaatttaaa aggcaat	1450
Pro Thr Asp Ser Glu Ser Phe Glu	
455 460	
aattttaaca ttaacotcat tccaagttaa tgtggtctaa taatctggta ttaaatoctt	1510
aagagaaagc ttgagaaata gatttttttt tatcttaaag tcaactgteta ttaaagatta	1570
aacatacaat cacataacct t	1591

WO 00/29448

PCT/JP99/06412

106/233

<211> 1249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134)...(784)

<400> 60

aacagtctgt ggagacagtt gtgtccctgt ggctttggtg cgcctgtgtg cactttctcc	60
ctccacctgg agcatgggct aacaccggag gaaaggaaaa gacagagtca gacagggagc	120
ctggggaggg gcc atg gtg cca atg cac tta ctg ggg aga ctg gag aag	169
Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys	
1 5 10	
ccg ctt ctc ctc ctg tgc tgc gcc tcc ttc cta ctg ggg ctg gct ttg	217
Pro Leu Leu Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu	
15 20 25	
ctg ggc ata aag acg gac atc acc ccc gtt gct tat ttc ttt ctc aca	265
Leu Gly Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr	
30 35 40	
ttg ggt ggc ttc ttc ttg ttt gcc tat ctc ctg gtc cgg ttt ctg gaa	313
Leu Gly Gly Phe Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu	
45 50 55 60	
tgg ggg ctt cgg tcc cag ctc caa tca atg cag act gag agc cca ggg	361
Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly	
65 70 75	
ccc tca ggc aat gca cgg gac aat gaa gcc ttt gaa gtg cca gtc tat	409
Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr	
80 85 90	
gaa gag gcc gtg gtg gga cta gaa tcc cag tgc cgc ccc caa gag ttg	457
Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu	
95 100 105	
gac caa cca ccc ccc tac agc act gtt gtg ata ccc cca gca cct gag	505
Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu	
110 115 120	
gag gaa caa cct agc cat cca gag ggg tcc agg aga gcc aaa ctg gaa	553
Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu	

WO 00/29448

PCT/JP99/06412

107/233

125	130	135	140	
cag agg cga atg gcc tca gag ggg tcc atg gcc cag gaa gga agc cct				601
Gln Arg Arg Met Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro				
	145	150	155	
gga aga gct cca atc aac ctt cgg ctt cgg gga cca cgg gct gtg tcc				649
Gly Arg Ala Pro Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser				
	160	165	170	
act gct cct gat ctg cag agc ttg gcg gca gtc ccc aca tta gag cct				697
Thr Ala Pro Asp Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro				
	175	180	185	
ctg act cca ccc cct gcc tat gat gtc tgc ttt ggt cac cct gat gat				745
Leu Thr Pro Pro Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp				
	190	195	200	
gat agt gtt ttt tat gag gac aac tgg gca ccc cct taaatgact				790
Asp Ser Val Phe Tyr Glu Asp Asn Trp Ala Pro Pro				
205	210	215		
ctcccaagat ttctcttctc tccacaccag acctcggtca tttgactaac attttccagc				850
gcctactatg tgtcagaaac aagtgtttct gcctggacat cataaatggg gacttggacc				910
ctgaggagag tcaggccacg gtaagccctt cccagctgag atatgggtgg cataatttga				970
gtcttctggc aacatttggt gacctacccc atatccaata tttccagcgt tagattgagg				1030
atgaggtagg gaggtgatcc agagaaggcg gagaaggaag aagtaacctc tgagtggcgg				1090
ctattgcttc tgttccaggt gctgttcgag ctgttagaac ccttaggcct gacagctttg				1150
tgagttatta ttgaaaaatg aggattccaa gagtcagagg agtttgataa tgtgcacgag				1210
ggcacactgc tagtaaataa cattaaaata actggaatg				1249

<210> 61

<211> 392

<212> PRT

<213> Homo sapiens

<400> 61

Met	Glu	Gly	Val	Ser	Ala	Leu	Leu	Ala	Arg	Cys	Pro	Thr	Ala	Gly	Leu
1					5				10					15	
Ala	Gly	Gly	Leu	Gly	Val	Thr	Ala	Cys	Ala	Ala	Ala	Gly	Val	Leu	Leu
			20					25					30		
Tyr	Arg	Ile	Ala	Arg	Arg	Met	Lys	Pro	Thr	His	Thr	Met	Val	Asn	Cys

[illegible]

Met	Ala	Leu	Trp	Arg	Gly	Ser	Ala	Tyr	Ala	Gly	Phe	Leu	Ala	Leu	Ala
1					5				10					15	
Val	Gly	Cys	Val	Phe	Leu	Leu	Glu	Pro	Glu	Leu	Pro	Gly	Ser	Ala	Leu
			20					25					30		
Arg	Ser	Leu	Trp	Ser	Ser	Leu	Cys	Leu	Gly	Pro	Ala	Pro	Ala	Pro	Pro
		35					40					45			
Gly	Pro	Val	Ser	Pro	Glu	Gly	Arg	Leu	Ala	Ala	Ala	Trp	Asp	Ala	Leu
	50					55					60				
Ile	Val	Arg	Pro	Val	Arg	Arg	Trp	Arg	Arg	Val	Ala	Val	Gly	Val	Asn
65					70					75				80	
Ala	Cys	Val	Asp	Val	Val	Leu	Ser	Gly	Val	Lys	Leu	Leu	Gln	Ala	Leu
				85					90					95	
Gly	Leu	Ser	Pro	Gly	Asn	Gly	Lys	Asp	His	Ser	Ile	Leu	His	Ser	Arg
		100						105					110		
Asn	Asp	Leu	Glu	Glu	Ala	Phe	Ile	His	Phe	Met	Trp	Lys	Gly	Ala	Ala
		115					120					125			
Ala	Glu	Arg	Phe	Phe	Ser	Asp	Lys	Glu	Thr	Phe	His	Asp	Ile	Ala	Gln
	130					135				140					
Val	Ala	Ser	Glu	Phe	Pro	Gly	Ala	Gln	His	Tyr	Val	Gly	Gly	Asn	Ala

145					150						155				160
Ala	Leu	Ile	Gly	Gln	Lys	Phe	Ala	Ala	Asn	Ser	Asp	Leu	Lys	Val	Leu
				165					170					175	
Leu	Cys	Gly	Pro	Val	Gly	Pro	Arg	Leu	His	Glu	Leu	Leu	Asp	Asp	Asn
			180					185					190		
Val	Phe	Val	Pro	Pro	Glu	Ser	Leu	Gln	Glu	Val	Asp	Glu	Phe	His	Leu
	195						200				205				
Ile	Leu	Glu	Tyr	Gln	Ala	Gly	Glu	Glu	Trp	Gly	Gln	Leu	Lys	Ala	Pro
	210					215				220					
His	Ala	Asn	Arg	Phe	Ile	Phe	Ser	His	Asp	Leu	Ser	Asn	Gly	Ala	Met
225					230					235					240
Asn	Met	Leu	Glu	Val	Phe	Val	Ser	Ser	Leu	Glu	Glu	Phe	Gln	Pro	Asp
			245						250				255		
Leu	Val	Val	Leu	Ser	Gly	Leu	His	Met	Met	Glu	Gly	Gln	Ser	Lys	Glu
	260							265					270		
Leu	Gln	Arg	Lys	Arg	Leu	Leu	Glu	Val	Val	Thr	Ser	Ile	Ser	Asp	Ile
	275						280					285			
Pro	Thr	Gly	Ile	Pro	Val	His	Leu	Glu	Leu	Ala	Ser	Met	Thr	Asn	Arg
	290					295					300				
Glu	Leu	Met	Ser	Ser	Ile	Val	His	Gln	Gln	Val	Phe	Pro	Ala	Val	Thr
305					310					315				320	
Ser	Leu	Gly	Leu	Asn	Glu	Gln	Glu	Leu	Leu	Phe	Leu	Thr	Gln	Ser	Ala
			325						330					335	
Ser	Gly	Pro	His	Ser	Ser	Leu	Ser	Ser	Trp	Asn	Gly	Val	Pro	Asp	Val
	340						345				350				
Gly	Met	Val	Ser	Asp	Ile	Leu	Phe	Trp	Ile	Leu	Lys	Glu	His	Gly	Arg
	355					360					365				
Ser	Lys	Ser	Arg	Ala	Ser	Asp	Leu	Thr	Arg	Ile	His	Phe	His	Thr	Leu
	370				375				380						
Val	Tyr	His	Ile	Leu	Ala	Thr	Val	Asp	Gly	His	Trp	Ala	Asn	Gln	Leu
385				390					395					400	
Ala	Ala	Val	Ala	Ala	Gly	Ala	Arg	Val	Ala	Gly	Thr	Gln	Ala	Cys	Ala
			405						410				415		
Thr	Glu	Thr	Ile	Asp	Thr	Ser	Arg	Val	Ser	Leu	Arg	Ala	Pro	Gln	Glu
	420						425					430			

WO 00/29448

PCT/JP99/06412

111/233

Phe Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro
 435 440 445
 Asn Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe
 450 455 460
 Thr Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly
 465 470 475 480
 Asp Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His
 485 490 495
 Tyr

<210> 63
 <211> 417
 <212> PRT
 <213> Homo sapiens
 <400> 63

Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro Phe Pro
 1 5 10 15
 Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala Val Arg
 20 25 30
 Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val Ala His
 35 40 45
 Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu Ala Pro
 50 55 60
 Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu Leu Gly
 65 70 75 80
 Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala Leu Cys
 85 90 95
 Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val Val Gly
 100 105 110
 Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro His Leu
 115 120 125
 Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala Leu Val
 130 135 140
 Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val Val Ala
 145 150 155 160

WO 00/29448

PCT/JP99/06412

112/233

Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser Gln Asn
165 170 175
Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu Leu Thr
180 185 190
Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met Ala Val
195 200 205
Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys Gln Pro
210 215 220
Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys
225 230 235 240
Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu Phe Lys
245 250 255
Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln
260 265 270
Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg Leu Thr
275 280 285
Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu
290 295 300
Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu Gln Ile
305 310 315 320
Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr
325 330 335
Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala
340 345 350
Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile
355 360 365
Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met Val Leu
370 375 380
Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr
385 390 395 400
Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val Gln Arg
405 410 415
Leu

WO 00/29448

PCT/JP99/06412

115/233

Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr Gly Asn Leu Ala Gln
530 535 540
Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu Ile Pro Asn Asp His
545 550 555 560
Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly Lys Ser Gln Lys Tyr
565 570 575
Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile Lys Ala Asn Pro Asn
580 585 590
Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu Tyr His Arg Trp Gly
595 600 605
His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile Ser Leu Gln Leu Asp
610 615 620
Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly Leu Leu Arg Arg Lys
625 630 635 640
Leu Glu Leu Met Gln Lys Lys Ala Val
645

<210> 65

<211> 93

<212> PRT

<213> Homo sapiens

<400> 65

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
1 5 10 15
Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
20 25 30
Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
35 40 45
Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
50 55 60
Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
65 70 75 80
Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
85 90

WO 00/29448

PCT/JP99/06412

116/233

<210> 66

<211> 425

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
1 5 10 15
Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
20 25 30
Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
35 40 45
Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
50 55 60
Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
65 70 75 80
His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
85 90 95
Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
100 105 110
Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
115 120 125
Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
130 135 140
Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
145 150 155 160
Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
165 170 175
Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
180 185 190
Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu
195 200 205
Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
210 215 220
Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
225 230 235 240

WO 00/29448

PCT/JP99/06412

117/233

```

Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
      245                      250                      255
Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
      260                      265                      270
Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
      275                      280                      285
Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
      290                      295                      300
Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
      305                      310                      315                      320
Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
      325                      330                      335
Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
      340                      345                      350
Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
      355                      360                      365
Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
      370                      375                      380
Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
      385                      390                      395                      400
Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
      405                      410                      415
Lys Asp Cys Ala Asp Pro Cys Asp Ser
      420                      425

```

<210> 67

<211> 149

<212> PRT

<213> Homo sapiens

<400> 67

```

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
  1                      5                      10                      15
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
      20                      25                      30
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile

```

WO 00/29448

PCT/JP99/06412

118/233

35 40 45
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 50 55 60
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 65 70 75 80
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 85 90 95
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 100 105 110
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
 115 120 125
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
 130 135 140
 Gly Tyr Leu Met Gly
 145

<210> 68

<211> 396

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu
 1 5 10 15
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala
 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln
 35 40 45
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr
 50 55 60
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu
 65 70 75 80
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp
 85 90 95
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu
 100 105 110

WO 00/29448

PCT/JP99/06412

119/233

Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr
115 120 125
Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg
130 135 140
His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile
145 150 155 160
Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys
165 170 175
Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val
180 185 190
Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser
195 200 205
Glu Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser
210 215 220
Arg Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro
225 230 235 240
Thr Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser
245 250 255
Asp Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp
260 265 270
Ile Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln
275 280 285
Lys Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr
290 295 300
His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser
305 310 315 320
Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met
325 330 335
Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro
340 345 350
Arg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu
355 360 365
Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu
370 375 380
Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

WO 00/29448

PCT/JP99/06412

120/233

385 390 395

<210> 69

<211> 350

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu Ser Glu Glu
1 5 10 15

Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu Gln Asp Lys
20 25 30

Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly Leu Asp Ser
35 40 45

Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys Leu Lys Asn
50 55 60

Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu Met Ala Val
65 70 75 80

Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg Glu Lys Leu
85 90 95

Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp Arg Tyr Asp
100 105 110

Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu Leu Ser Cys
115 120 125

Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro Gly Gln Pro
130 135 140

Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr Asp Pro Phe
145 150 155 160

Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly Pro Arg Glu
165 170 175

Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu Asn Lys Ser
180 185 190

Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser Ser Phe Gln
195 200 205

Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln Ala Cys Glu
210 215 220

WO 00/29448

PCT/JP99/06412

121/233

Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg Thr Trp Val
 225 230 235 240
 Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg Glu Ala Val
 245 250 255
 Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp Gln Arg Pro
 260 265 270
 Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe Glu Trp Lys
 275 280 285
 Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala Asn Pro Trp
 290 295 300
 Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu Phe Lys Ala
 305 310 315 320
 Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys Ile Arg Lys
 325 330 335
 Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile Ser
 340 345 350

<210> 70

<211> 153

<212> PRT

<213> Homo sapiens

<400> 70

Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe Ser Ala
 1 5 10 15
 Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln Val Pro
 20 25 30
 Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr His Arg
 35 40 45
 Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly Ala Leu
 50 55 60
 Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp Ala Pro
 65 70 75 80
 Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe Arg Pro
 85 90 95
 Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr Ser Gly

<210> 72

WO 00/29448

PCT/JP99/06412

123/233

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 72

atggcgctgt ggcgcggctc cgcgtacgcg ggcttcctgg cgcctggccgt ggctgcgctc	60
ttcctgctgg agccagagct gccaggctcg gcgctgcgct ctctctggag ctgcctgtgt	120
ctggggcccg cgcctgcgcc cccgggaccc gtctcccccg agggccggtt ggccgcagcc	180
tgggacgcgc ttatcgtgcg gccagtcggc cgcctggcgc gcctggcagt gggagtcaat	240
gcctgtgttg atgtggtgct ctcaggggtg aagctcttgc aggcacttgg ccttagtcct	300
gggaatggga aagatcacag cattctgcct tcaaggaatg atctggaaga agccttcatt	360
cacttcctgt ggaagggagc agctgctgag cgcctcttca gtgataagga aacttttcac	420
gacattgccc aggttgcgct agagttccca ggagcccagc actatgtagg aggaaatgca	480
gctttaattg gacagaaatt tgcagccaac tcagatttaa aggttcttct ttgcggtcca	540
gttgcccaaa ggctacatga gcttcttgat gacaatgtct ttgttccacc agagtcattg	600
caggaagtgg atgagttcca cctcatttta gagtatcaag caggggagga gtggggccag	660
ttaaaagctc cccatgcca cccattccac ttctctcacg accctcccaa cggggccatg	720
aatatgctgg aggtgtttgt gtctagcctg gaggagtctt agccagacct ggtggtcctc	780
tctggattgc acatgatgga gggacaaaagc aaggagctcc agaggaagag actcttggag	840
gttgtaacct ccatttctga catccccact ggtattccag ttcacctaga gctggccagt	900
atgactaaca gggagctcat gacgagcatt gtccatcagc aggtctttcc cgcggtgact	960
tcccttgggc tgaatgaaca ggagctgtta ttctcacc agtcagcctc tggacctcac	1020
tcttctctct ctctctggaa cgggtgttct gatgtgggca tggctcagtga catcctcttc	1080
tggatcttga aagaacatgg gaggagtaaa agcagagcct cggatctcac caggatccat	1140
ttccacacgc tggcttacca catcctggca actgtggatg gacactgggc caaccagctg	1200
gcagccgtgg ctgcaggagc tcgtgtggct gggacacagg cctgcgccac agaaaccata	1260
gacaccagcc gagtgtctct gagggcacc ccaagagttca tgaattccca ttcggaggca	1320
ggctocagga ttgtattaaa cccaaacaag ccagtagtag aatggcacag agaggggaata	1380
tccttccact tcacaccagt attggtgtgt aaagaccca ttcgaactgt aggccttggga	1440
gatgccattt cagccgaagg actcttctat tcggaagta caccctcacta t	1491

<210> 73

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 73

WO 00/29448

PCT/JP99/06412

124/233

atgctggtgc atttatttcg ggtcgggatt cgggggtggcc cattcccagg caggetgcta	60
ccgccccctcc gcttccagac attctcagct gtcagggtact ctgatggcta ccgcagctcc	120
tccctccctcc gggccgtggc ccacctgogg tcccagctct gggccccacct cctctgagcc	180
cccctagctc ccagatggag cccctctgcc tgggtgctggg ttggggggagc cctgctaggc	240
cccctaggtac tgagtaagca tccccacctc tgccttgtgg ccctgtgtga ggcagaagag	300
gccccctctg ccagctccac accccatgtc gtgggggtctc gctttaactg gaagctcttc	360
tggcagtttc tgcacccccca cctgctgggc ctgggggttag ccgtcgtgct ggccttgggt	420
gcggcactcg tgaatgtaca gatccccctg ctctggggcc agctggtaga ggtcgtggcc	480
aagtacacaa gggaccacgt agggagtctt atgactgagt ccagaaatct cagcaccac	540
ctgcttatcc tctatggtgt ccagggactg ctgaccttcg ggtacctggt gctgctgtcc	600
cacgttggcg agcgcctggc tgtggacatg cggagggccc tcttcagctc cctgctccgg	660
tactgccagc cgcagggtgc agagtggga caagacatca ccttctttga cgcgaataag	720
acagggcagc tggtagcccg cttgacaact gacgtgcagg agtttaagtc atccttcaag	780
cttgtcatct cccaggggct gcgaagctgc acccagggtg caggctgcct ggtgtccctg	840
tccatgctgt cgacacgcct cacgctgctg ctgatggtgg ccacaccagc cctgatggga	900
gtgggcaccc tgatgggctc aggcctccga aaattgtctt gccagtgtca ggagcagatc	960
gccagggcaa tgggcgtagc agacgaggcc ctggggcaatg tgcggactgt gcgtgccttc	1020
gccatggagc aacgggaaga ggagcgctat ggggcagagc tggaaacctg ccgctgccgg	1080
gcagaggagc tgggcccgcg catcgctctg ttccaagggc tttccaacat cgccttcaac	1140
tgcattggtct tgggtaccct atttattggg ggctcccttg tggccggaca gcagctgaca	1200
gggggagacc tcatgtcctt cctggtggcc tcccagacag tgcaaaggct g	1251

<210> 74

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 74

atgattccta accagcataa tgctggagcc gggagccacc aacctgcagt tttcagaatg	60
gccgtgttgg acaactgattt ggatcacatt ctccatctt ctgttcttcc tccattctgg	120
gotaagttag tagtgggacg ggttgccatt gtgtgttttg cacgcagcta tgatggagac	180
tttgtctttg atgactcaga agctattgtt aacaataagg ttgctggtgt tgcggccgt	240
gcagacctcc tgtgtgccct gttcttcttg ttatctttcc ttggctactg taaagcattt	300
agagaaagta acaaggaggg agcgcattct tccacctctt ggggtgctgt gagtatcttt	360
ctgggagcag tggccatgct gtgcaaagag caagggatca ctgtgctggg tttaaatgcg	420
gtatttgaca tcttggtgat aggcaaattc aatgttcttg aaattgtcca gaaggacta	480

WO 00/29448

PCT/JP99/06412

126/233

gaagatggca aagtctacat caacatgccca ggcaggggc

279

<210> 76

<211> 1275

<212> DNA

<213> Homo sapiens

<400> 76

atgggctcct gggctgcggt caatgggato tgggtggagc tacctgtggt ggtcaaagag	60
cttccagagg gttggagcct cccctcttac gtctctgtgc ttgtggctct ggggaacctg	120
gggtctgctgg tggtagccct ctggaggagg ctggccccag gaaaggacga gcaggtcccc	180
atccgggtgg tgcaggtgct gggcatggtg ggcacagccc tgetggcctc tctgtggcac	240
catgtggccc cagtggcagg acagttgcat tctgtggcct tottagcact ggcctttgtg	300
ctggcactgg catgctgtgc ctgcaatgtc actttctctgc ccttcttgag ccacctgcca	360
cctcgtctct tacggtcatt cttcctgggt caaggcctga gtgccctgct gccctgcgtg	420
ctggccctag tgcaggggtg gggccgcctc gagtggccgc cagcccccat caacggcacc	480
cctggccccc cgtctgactt ccttgagcgt tttcccgcca gcaccttctt ctgggcactg	540
actgcccttc tggctgcttc agctgtgcc ttccagggtc ttctgctgct gttgccgcca	600
ccaccatctg taccacaggg ggagttagga tcaggcctcc aggtgggagc cccaggagca	660
gaggaagagg tgaagagtc ctcaccactg caagagccac caagccaggc agcaggcacc	720
accctggtc cagaccctaa ggctatcag cttctatcag cccgcagtgc ctgcctgctg	780
ggcctgttg ccccaacca cgcgtgacc aatggcgtgc tgcctgccgt gcagagcttt	840
tcctgcttac cctacgggcg tctggcctac cacctggctg tgggtgctggg cagtgtgcc	900
aateccctgg cctgcttct ggccatgggt gtgtgtgca ggtecttggc agggctgggc	960
ggcctctctc tgetgggct gttctgtggg ggctacctga tggcgtggc agtcctgagc	1020
ccctgcccgc ccctggtggg cactcgggcg ggggtggtcc tctgtgtgct gtcgtgggtg	1080
ctgtgtcttg gctgttctc ctacgtgaag gtggcagcca gctccctgct gcatggcggg	1140
ggccggccgg cattgctggc agccggcgtg gccatccagg tgggctctct gctcggcgt	1200
gttgctatgt tcccccgac cagcatctat cactgtttcc acagcagaaa ggactgtgca	1260
gaccctgtg actcc	1275

<210> 77

<211> 447

<212> DNA

<213> Homo sapiens

<400> 77

WO 00/29448

PCT/JP99/06412

127/233

atggagactt	tgtaccgtgt	cccgttctta	gtgctcgaat	gtcccaacct	gaagctgaag	60
aagccgccct	ggttgcaaat	gcgctggccc	atgactgtgt	atgetctggt	ggtggtgtct	120
tacttcctca	tcaccggagg	aataatttat	gatgttattg	ttgaacctcc	aagtgtcggt	180
tctatgactg	atgaacatgg	gcacagagg	ccagtagctt	tcttggccta	cagagtaaag	240
ggacaatata	ttatggaagg	acttgcaccc	agcttcctat	ttacaatggg	aggttttaggt	300
ttcataatcc	tggaccgatc	gaatgcacca	aatatcccaa	aactcaatag	attccttctt	360
ctgttcattg	gattcgtctg	tgtcctattg	agttttttca	tggctagagt	attcatgaga	420
atgaaactgc	cgggctatct	gatgggt				447

<210> 78

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 78

atggcgatga	togaattggg	gtttggaaga	cagaattttc	atcattaaa	gaggaagagt	60
tcattgctgt	tgaaaactcat	agctgtgtgc	tttgcgtgtc	ttctattttg	tgaattttta	120
atctattact	tagcgatctt	tcagtgtaat	tggcctgaag	tgaaaaccac	agcctctgat	180
ggtgaacaga	ccacacgtga	gcctgtgctc	aaagccatgt	ttttggctga	cacctatttg	240
cttgggggaat	tcctaggcca	ctggctggac	aaattacgaa	gggaatggca	gatggagaga	300
gcgttccaga	cagctctgtg	gttgcgtcag	ccggaagtcg	tcttcacctc	gggggatata	360
tttgatgaag	ggaagtggag	cacctctgag	gcctgggcgg	atgatgtgga	gcggtttcag	420
aaaatgttca	gacacccaag	tcattgtacag	ctgaaggtag	ttgctggaaa	ccatgacatt	480
ggcttccatt	atgagatgaa	cacatacaaa	gtagaacgct	ttgagaaagt	gttcagctct	540
gaaagactgt	tttcttggaa	aggcattaac	tttgtgatgg	tcaacagcgt	ggcgtgaac	600
ggggatggct	gtggcatctg	ctctgaaaca	gaagcagagc	tcattgaagt	ttctcacaga	660
ctgaactgct	cccagagagg	acgtggctcc	agccggtgtg	gacctgggcc	tctgctgccc	720
acgtctgccc	ctgtcctcct	gcagcattat	cctctgtatc	ggagaagtga	tgctaactgt	780
tctggggaag	acgtgctctc	tgcagaggaa	agggacatcc	catttaagga	gaactatgac	840
gtgctttcac	gggaggcatc	acaaaagctg	ctgtgggtgg	tccagccgcg	cctggttctc	900
agtggccaca	cgcacagcgc	ctgcgaggtg	caccacgggg	gccgagtcgc	cgagctcagc	960
gtcccatctt	tcagttggag	gaacagaaac	aacccaggtt	tcattcatgg	tagcatcacg	1020
cccacagact	acacctctc	caagtgtctc	ctccacgctg	aggatgtggt	tttgatcatc	1080
tactgtggag	tgggtgggctt	ccttgtggct	ctcacactca	ctcactttgg	gcttctagcc	1140
tcaccttttc	tttctgggtt	gaactgtctc	ggaaagcgta	agacaaga		1188

WO 00/29448

PCT/JP99/06412

128/233

<210> 79

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 79

atgatccggc	aggagcgctc	cacatcctac	caggagctga	gtgaggagt	gggccagggtg	60
gttgagaact	cagagctggc	agacgagcag	gacaaggaga	cggtcagagt	ccaagggtccg	120
ggatatctac	caggcctgga	cagcgagtcc	gcctccagca	gcacccgctt	cagcaaggccc	180
tgcctgaaga	acgtcttctc	ggcctactc	atcttcatct	acctgctgct	catggctgtg	240
gccgtcttcc	tgggtctaccg	gaccatcaca	gactttcgtg	agaaactcaa	gcaccctgtc	300
atgtctgtgt	cttacaagga	agtggatcgc	tatgatgccc	caggatttgc	cttgtacccc	360
ggtcaggccc	agttgctcag	ctgtaagcac	cattacgagg	tcattcctcc	tctgacaagc	420
cctggccagc	cgggtgacat	gaattgcacc	accagagga	tcaactacac	ggaccccttc	480
tccaatcaga	ctgtgaaatc	tgcctgatt	gtccaggggc	ccggggaagt	gaaaaagcgg	540
gagctggtct	tcctccagtt	ccgcctgaac	aagagtagtg	aggacttcag	cgccattgat	600
tacctctct	tctcttcttt	ccaggagttc	ctgcaaagcc	caaacagggt	aggcttcatg	660
caggcctgtg	agagtgccta	ttccagctgg	aagttctctg	ggggcttccg	cacctgggtc	720
aagatgtcac	tggtaaagac	caaggaggag	gatgggagg	aagcagtggg	gttccggcag	780
gagacaagtg	tggtaacta	cattgaccag	aggccagctg	ccaaaaaag	tgtcaattg	840
ttttttgtgg	tctttgaatg	gaaagatcct	ttcatccaga	aagtccaaga	tatagtcaact	900
gccaatcctt	ggaacacaat	tgtcttctc	tgtggcgctc	tcttggcatt	atttaaagca	960
gcagagtttg	ccaaactgag	tataaaatgg	atgatcaaaa	ttagaaagag	ataccttaaa	1020
agaagaggtc	aggcaacgag	ccacataagc				1050

<210> 80

<211> 459

<212> DNA

<213> Homo sapiens

<400> 80

atgactatcc	acatcctcat	cctgctgttg	ctcctcgctc	tctccgccc	aggggacctg	60
gacactgcag	ccaggcgagg	ccagcaccag	gtccccagc	accgaggga	cgtctgctac	120
ctgggcgtat	gccggaccca	ccgcctggcg	gagatcatat	actggattcg	ctgtctccac	180
caaggagccc	tgggggaagg	ccagccacga	gccccaggac	ccctacagct	atggggcgccg	240
ccggtggcgc	gaggcggaag	cccggctcgg	ttcccaggat	tccggcctgc	agcgagggggg	300
ctagcgcagt	gccagctcgc	ctgggtgacc	tggggcacgg	ctcgtccctc	cctcggttcc	360

WO 00/29448

PCT/JP99/06412

129/233

agtttgcta tctgtatgtt ggagcttcta ctccacattt cttctccct aactccagcc 420
cctgaaaccg tcttccccag tccctccccg ggctgcgac 459

<210> 81

<211> 4027

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)...(1370)

<400> 81

gcccgtaca aagcggcgaa ggtcacggcg cgaggaggcg cgcgtcgccg ccccgcgccc 60
cgcctgcggc ccgcgcccc ggcgtcaccg cctcctgccc gcctgcccgc ctgcccgcct 120
gcccgcctac ccgcctaccc gcctaccgc ctacccccct gccggcctgc cgtccttcca 180
cgcgagagagc c atg gag gga gtg agc gcg ctg ctg gcc cgc tgc ccc acg 230
Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr
1 5 10
gcc ggc ctg gcc ggc ggc ctg ggg gtc acg gcg tgc gcc gcg gcc ggc 278
Ala Gly Leu Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly
15 20 25
gtg ttg ctc tac cgg atc gcg cgg agg atg aag cca acg cac acg atg 326
Val Leu Leu Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met
30 35 40 45
gtc aac tgc tgg ttc tgc aac cag gat acg ctg gtg ccc tat ggg aac 374
Val Asn Cys Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn
50 55 60
cgc aac tgc tgg gac tgt ccc cac tgc gag cag tac aac ggc ttc cag 422
Arg Asn Cys Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln
65 70 75
gag aac ggc gac tac aac aag ccg atc ccc gcc cag tac ttg gag cac 470
Glu Asn Gly Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His
80 85 90
ctg aac cac gtg gtg agc agc gcg ccc agc ctg cgc gac cct tcg cag 518
Leu Asn His Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln
95 100 105

WO 00/29448

PCT/JP99/06412

130/233

cgc cag cag tgg gtg agc agc caa gtc ctg ctg tgc aag agg tgc aac	566
Pro Gln Gln Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn	
110 115 120 125	
cac cac cag acc acc aag atc aag cag ctg gcc gcc ttc gct ccc cgc	614
His His Gln Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg	
130 135 140	
gag gag ggc agg tat gac gag gag gtc gag gtg tac cgg cat cac ctg	662
Glu Glu Gly Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu	
145 150 155	
gag cag atg tac aag ctg tgc cgg ccg tgc caa gcg gct gtg gag tac	710
Glu Gln Met Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr	
160 165 170	
tac atc aag cac cag aac cgc cag ctg cgc gcc ctg ttg ctc agc cac	758
Tyr Ile Lys His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His	
175 180 185	
cag ttc aag cgc cgg gag gcc gac cag acc cac gca cag aac ttc tcc	806
Gln Phe Lys Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser	
190 195 200 205	
tcc gcc gtg aag tcc ccg gtc cag gtc atc ctg ctc cgt gcc ctc gcc	854
Ser Ala Val Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala	
210 215 220	
ttc ctg gcc tgc gcc ttc cta ctg acc acc gcg ctg tat ggg gcc agc	902
Phe Leu Ala Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser	
225 230 235	
gga cac ttc gcc cca ggc acc act gtg ccc ctg gcc ctg cca cct ggt	950
Gly His Phe Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly	
240 245 250	
ggc aat ggc tca gcc aca cct gac aat ggc acc acc cct ggg gcc gag	998
Gly Asn Gly Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu	
255 260 265	
ggc tgg cgg cag ttg ctg ggc cta ctc ccc gag cac atg gcg gag aag	1046
Gly Trp Arg Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys	
270 275 280 285	
ctg tgt gag gcc tgg gcc ttt ggg cag agc cac cag acg ggc gtc gtg	1094
Leu Cys Glu Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val	

WO 00/29448

PCT/JP99/06412

131/233

290	295	300	
gca ctg ggc cta ctc acc tgc ctg ctg gca atg ctg ctg gct ggc cgc			1142
Ala Leu Gly Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg			
305	310	315	
atc agg ctc cgg agg atc gat gcc ttc tgc acc tgc ctg tgg gcc ctg			1190
Ile Arg Leu Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu			
320	325	330	
ctg ctg ggg ctg cac ctg gct gag cag cac ctg cag gcc gcc tcg cct			1238
Leu Leu Gly Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro			
335	340	345	
agc tgg cta gac acg ctc aag ttc agc acc aca tct ttg tgc tgc ctg			1286
Ser Trp Leu Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu			
350	355	360	365
gtt ggc ttc acg gcg gct gtg gcc aca agg aag gca acg ggc cca cgg			1334
Val Gly Phe Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg			
370	375	380	
agg ttc cgg ccc cga agg tca gag aag cag cca tgactgcggg ggg			1380
Arg Phe Arg Pro Arg Arg Ser Glu Lys Gln Pro			
385	390		
aggacacacg gatgctcagg cccaggcttt gccagggtccg aagcggggccc ctctctgtcc			1440
tgctcttttt cacctgctca cgccctccca cccccaccct acagccccag gtccctggccc			1500
agtcctccca ctgcctcgaa gagtcagtct gccctgcctt ttcttttcgg gcaccaccag			1560
ccatccccga gtgccctgta gccactcacc actgctgcca cctctctggc caatggccct			1620
ttcactggcc tggtgactgg aatgtgggca gcgcccacac aggetctggc ccattggttc			1680
ctactggcag ctccaggcac cccctctca ccacgccgtt tgettggtct gacactgttg			1740
ggtgagggtc ctggctctgc tgtcttccct tctggcctct gcacaggggt ggtgacagtg			1800
gctacaggct gggccctgg cgtgccctga ccgtgcagea gagtgaggct ggggcagcag			1860
agagccccag cctcaccct gaggagcacc tgtggtctgt ccccttggtc ctgcttatgg			1920
ctggaccggc cctgcaggag gtggtggagc cgtgaaggag gccagactgc agctctggct			1980
gctgcttggc ctctgctcc aagaccctcc cgagtccccg gaaatggaga gtgcagttct			2040
tgggcccagc ctggccttcg ccatgagttt ggggagcgag accccacctg agacaggcag			2100
taggagcctg tgctgacctt ggggaatctg agcttttcca agggtaaggg gcccagggtta			2160
tgaggcctt cagtgcacac aggtcgttgt cctctttcc ctccctgacc tgtcacgagc			2220
ctctgcagggt gctgctcac catggcccag cgccactctg tctccgact caggtagagg			2280
ggcagcccac agacctgctc ctcatgagca gggcctggcc agggccctgc tgttctcagc			2340

WO 00/29448

PCT/JP99/06412

132/233

```

ctcagtttgc catctatgaa atgaggtgga cccctctcca tagcccttgg gtgccagctc 2400
agtgggtgtg gggatcacat gaggtggctc atgaggacac actctggaag tcgaggggct 2460
gccacgtgca gaggaagttc ccggcctggg ggctttatcc aggggtccca gtcgagagtg 2520
gcccagagcc gtccctcacc gggcatgttc cctctggctg cccactccct cagggccac 2580
atgtcctgcc actcgccact ctgagcacga gttcaccttc cagatgtggc caggggtgtgc 2640
cagctcctct ctctgtgctg ttggaacccc gggggaggca agagcagatc acaggtgcat 2700
gaggggttaca ccgctcacct gggctctgccg ggatgggttg ggggggcagg tgccaggcct 2760
cactgctgtg aatctgccac gcctgggggt cctagaggct gccccacccc agtgattggg 2820
tagcagctca catccacccc agcttcacaa gtgaggaacc caggtgcacg gggagaccct 2880
cggggggcttc tgtggcctct gtgcccgatg acctgcgtgg cttcagacaa ggccccagcg 2940
ttactgggct cagcttggtt ttctgtgtgg agcgtgaggt gagaaaaccc ctctgaaaag 3000
atgtggtcgg ggccacgctt cccactgggt ctgcagttag gaggtagggc ggggtgagcca 3060
aagcggcccc ccatggtgtc tacctgaggg gcagggaacc gcctgcctgt gcactcacgc 3120
cacccccag cccacaaaga gcccatctga gagaaggacg tggtaggagc aggacgggaa 3180
agcgtcctgt cggctggcca tgctgttget tgcgtctcga atcttcggtt ctcgaggaag 3240
tgttgacagt gtgatgctaa tgtctgcttt tcttggcgtt gggtagaagc aggacatctg 3300
tgtgtatgtg cgtattttaa ttagattatt tataataacc agagccagcc ctgcgctgg 3360
ccaggatcct cctgccgagc tgatgtgctt cctgccctct gccgggggtc ggaagcgaca 3420
tctcaggagg tagctctcag cagagttagg attcctgcct ttcgtagagt tttgtgtgac 3480
tttttaaatt attcatgtgt cccttaaaag tttcactacg tggagaaaat tccagcacca 3540
agtgttgtgg caacagctga gagagtgcag gcaccactgt gttgtggctt gttgaccggg 3600
aatgtgtcac ccctgccagg gaactcttct cctgcggggg gacttgggat ggccatcaga 3660
ccttotaggg tctggctggg gtaatcctag gtatgggtga ccgtccctga gacataagcg 3720
aggtagattc agccatcctc accctcagac ttgaggtccc caccagggc aagccggccc 3780
cccgtagccc ttgctggga gcaaaccgcc aggacgcagc ctccacgccg cacctgccac 3840
acccagccct gccaggaag gaacacatga cccttctgtc tgtgactgtt gctgagtctc 3900
tgtctcatgt cgtagaattg tggataattg tctagtacc ctctcatcac tgtaaccatc 3960
gcgcctggcc tagatgtcgt gttttggatg ctgtgttttc aataaatgcc tctggggccc 4020
tgetttt 4027

```

<210> 82

<211> 2495

<212> DNA

<213> Homo sapiens

<220>

gttcgcgcag	gtggggcgcc	tgggtcccc	atg	gcg	ctg	tgg	cgc	ggc	tcc	gcg							53
			Met	Ala	Leu	Trp	Arg	Gly	Ser	Ala							
			1				5										
tac	gcg	ggc	ttc	ctg	gcg	ctg	gcc	gtg	ggc	tgc	gtc	ttc	ctg	ctg	gag		101
Tyr	Ala	Gly	Phe	Leu	Ala	Leu	Ala	Val	Gly	Cys	Val	Phe	Leu	Leu	Glu		
	10				15				20								
cca	gag	ctg	cca	ggc	tcg	gcg	ctg	cgc	tct	ctc	tgg	agc	tcg	ctg	tgt		149
Pro	Glu	Leu	Pro	Gly	Ser	Ala	Leu	Arg	Ser	Leu	Trp	Ser	Ser	Leu	Cys		
	25				30				35						40		
ctg	ggg	ccc	gcg	cct	gcg	ccc	ccg	gga	ccc	gtc	tcc	ccc	gag	ggc	cgg		197
Leu	Gly	Pro	Ala	Pro	Ala	Pro	Pro	Gly	Pro	Val	Ser	Pro	Glu	Gly	Arg		
			45					50						55			
ttg	gcg	gca	gcc	tgg	gac	gcg	ctt	atc	gtg	cgg	cca	gtc	cgg	cgc	tgg		245
Leu	Ala	Ala	Ala	Trp	Asp	Ala	Leu	Ile	Val	Arg	Pro	Val	Arg	Arg	Trp		
			60					65				70					
cgc	cgc	gtg	gca	gtg	gga	gtc	aat	gca	tgt	gtt	gat	gtg	gtg	ctc	tca		293
Arg	Arg	Val	Ala	Val	Gly	Val	Asn	Ala	Cys	Val	Asp	Val	Val	Leu	Ser		
	75							80				85					
ggg	gtg	aag	ctc	ttg	cag	gca	ctt	ggc	ctt	agt	cct	ggg	aat	ggg	aaa		341
Gly	Val	Lys	Leu	Leu	Gln	Ala	Leu	Gly	Leu	Ser	Pro	Gly	Asn	Gly	Lys		
	90						95				100						
gat	cac	agc	att	ctg	cat	tca	agg	aat	gat	ctg	gaa	gaa	gcc	ttc	att		389
Asp	His	Ser	Ile	Leu	His	Ser	Arg	Asn	Asp	Leu	Glu	Glu	Ala	Phe	Ile		
105					110				115					120			
cac	ttc	atg	tgg	aag	gga	gca	gct	gct	gag	cgc	ttc	ttc	agt	gat	aag		437
His	Phe	Met	Trp	Lys	Gly	Ala	Ala	Ala	Glu	Arg	Phe	Phe	Ser	Asp	Lys		
			125					130					135				
gaa	act	ttt	cac	gac	att	gcc	cag	gtt	gcg	tca	gag	ttc	cca	gga	gcc		485
Glu	Thr	Phe	His	Asp	Ile	Ala	Gln	Val	Ala	Ser	Glu	Phe	Pro	Gly	Ala		
			140					145					150				
cag	cac	tat	gta	gga	gga	aat	gca	gct	tta	att	gga	cag	aaa	ttt	gca		533
Gln	His	Tyr	Val	Gly	Gly	Asn	Ala	Ala	Leu	Ile	Gly	Gln	Lys	Phe	Ala		

WO 00/29448

PCT/JP99/06412

134/233

155	160	165	
gcc aac tca gat tta aag gtt ctt ctt tgc ggt cca gtt ggc cca agg			581
Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly Pro Val Gly Pro Arg			
170	175	180	
cta cat gag ctt ctt gat gac aat gtc ttt gtt cca cca gag tca ttg			629
Leu His Glu Leu Leu Asp Asp Asn Val Phe Val Pro Pro Glu Ser Leu			
185	190	195	200
cag gaa gtg gat gag ttc cac ctc att tta gag tat caa gca ggg gag			677
Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu Tyr Gln Ala Gly Glu			
205	210	215	
gag tgg ggc cag tta aaa got ccc cat gcc aac cga ttc atc ttc tot			725
Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn Arg Phe Ile Phe Ser			
220	225	230	
cac gac ctc tcc aac ggg gcc atg aat atg ctg gag gtg ttt gtg tot			773
His Asp Leu Ser Asn Gly Ala Met Asn Met Leu Glu Val Phe Val Ser			
235	240	245	
agc ctg gag gag ttt cag cca gac ctg gtg gtc ctc tot gga ttg cac			821
Ser Leu Glu Glu Phe Gln Pro Asp Leu Val Val Leu Ser Gly Leu His			
250	255	260	
atg atg gag gga caa agc aag gag ctc cag agg aag aga ctc ttg gag			869
Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg Lys Arg Leu Leu Glu			
265	270	275	280
gtt gta acc tcc att tct gac atc ccc act ggt att cca gtt cac cta			917
Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly Ile Pro Val His Leu			
285	290	295	
gag ctg gcc agt atg act aac agg gag ctc atg agc agc att gtc cat			965
Glu Leu Ala Ser Met Thr Asn Arg Glu Leu Met Ser Ser Ile Val His			
300	305	310	
cag cag gtc ttt ccc gcg gtg act tcc ctt ggg ctg aat gaa cag gag			1013
Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly Leu Asn Glu Gln Glu			
315	320	325	
ctg tta ttt ctc acc cag tca gcc tct gga cct cac tct tct ctc tct			1061
Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro His Ser Ser Leu Ser			
330	335	340	
tcc tgg aac ggt gtt cct gat gtg ggc atg gtc agt gac atc ctc ttc			1109

Ser Trp Asn Gly Val Pro Asp Val Gly Met Val Ser Asp Ile Leu Phe			
345	350	355	360
tgg atc ttg aaa gaa cat ggg agg agt aaa agc aga gcc tcg gat ctc			1157
Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser Arg Ala Ser Asp Leu			
365	370	375	
acc agg atc cat ttc cac acg ctg gtc tac cac atc ctg gca act gtg			1205
Thr Arg Ile His Phe His Thr Leu Val Tyr His Ile Leu Ala Thr Val			
380	385	390	
gat gga cac tgg gcc aac cag ctg gca gcc gtg gct gca gga gct cgt			1253
Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val Ala Ala Gly Ala Arg			
395	400	405	
gtg gct ggg aca cag gcc tgc gcc aca gaa acc ata gac acc agc cga			1301
Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr Ile Asp Thr Ser Arg			
410	415	420	
gtg tct ctg agg gca ccc caa gag ttc atg act tcc cat tcg gag gca			1349
Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr Ser His Ser Glu Ala			
425	430	435	440
ggc tcc agg att gta tta aac cca aac aag cca gta gta gaa tgg cac			1397
Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro Val Val Glu Trp His			
445	450	455	
aga gag gga ata tcc ttc cac ttc aca cca gta ttg gtg tgt aaa gac			1445
Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val Leu Val Cys Lys Asp			
460	465	470	
ccc att cga act gta ggc ctt gga gat gcc att tca gcc gaa gga etc			1493
Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile Ser Ala Glu Gly Leu			
475	480	485	
ttc tat tcg gaa gta cac cct cac tat taggaagatt cttaggggta			1540
Phe Tyr Ser Glu Val His Pro His Tyr			
490	495		
atTTTTTctga ggaaggagaa ctagccaact taagaattac aggaagaaaag tggTTTtgGaa			1600
gacagccaaa gaaataaaaag cagattaaac tgtatcaggt acattccagc ctgTTtgGcaa			1660
ctccataaaaa acatttcaga ttttaatccg aatttagcta atgagactgg atTTTTgttt			1720
tttatgttgt gtgtcacaga gctaaaaaact cagtTccccaa atCCCCagtt tatgcagcgc			1780
cacCaggtat tttAagctaa acttcttcac ccctgagagc atgtcagctg gagaaaagca			1840
gttcttcctt qcccaottqa qaagtqcacq cccactcacc caacatcctg gtctctagga			1900

WO 00/29448

PCT/JP99/06412

136/233

aagcctcatg tgaggttcct ctttctttca gctcagtgcc catgggcaag gatcatgatt 1960
 tccattccgt gttacaatga caatatttaa tgagcataac cttctcagtc tcctgctctc 2020
 aaatttagga cagagccgct aaggacaaaa caatccctcc cgtgctttat gatggcagca 2080
 ggggctgggg agcctctgag ggactctttc attctgcagt tgtctggaag cctgggtggc 2140
 gtcatgagct gaaggatcat gctttcctgt cctggctcca taggttatag gctggctggt 2200
 gaaaggttca cgtggcccag gctgaacttc attgcctagc tttggatgtg ctttctgcca 2260
 taaagactga tttttgttcg ttctgagcct tcaaggaatt tgttttttac aactggaata 2320
 tgctcctgtg tgtgttaaca gatcatggat gttttatgtt ttcactgac atttaaagag 2380
 tttgacctca gagctccagg atcatcagta aatttgtcat gttatatatt tattttttta 2440
 taaatcaaga cttctgtgtg ctcttaaata tattaaaaac aatttacatt tcagg 2495

<210> 83

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1320)

<400> 83

atagagccct cagtgggatg aggggtgaaac tgctattgcc ggcggctcct gttttaccgc 60
 gtcage atg ctg gtg cat tta ttt cgg gtc ggg att cgg ggt ggc cca 108
 Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro
 1 5 10
 ttc cca ggc agg ctg cta ccg ccc ctc cgc ttc cag aca ttc tca gct 156
 Phe Pro Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala
 15 20 25 30
 gtc agg tac tct gat ggc tac cgc agc tcc tcc ctc ctc cgg gcc gtg 204
 Val Arg Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val
 35 40 45
 gcc cac ctg cgg tcc cag ctc tgg gcc cac ctc cct cga gcc ccc cta 252
 Ala His Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu
 50 55 60
 gct ccc aga tgg agc ccc tct gcc tgg tgc tgg gtt ggg gga gcc ctg 300
 Ala Pro Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu
 65 70 75

WO 00/29448

PCT/JP99/06412

137/233

cta ggc ccc atg gta ctg agt aag cat ccc cac ctc tgc ctt gtg gcc	348
Leu Gly Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala	
80 85 90	
ctg tgt gag gca gaa gag gcc cct cct gcc agc tcc aca ccc cat gtc	396
Leu Cys Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val	
95 100 105 110	
gtg ggg tct cgc ttt aac tgg aag ctc ttc tgg cag ttt ctg cac ccc	444
Val Gly Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro	
115 120 125	
cac ctg ctg gtc ctg ggg gta gcc gtc gtg ctg gcc ttg ggt gcg gca	492
His Leu Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala	
130 135 140	
ctc gtg aat gta cag atc ccc ctg ctc ctg ggc cag ctg gta gag gtc	540
Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val	
145 150 155	
gtg gcc aag tac aca agg gac cac gta ggg agt ttc atg act gag tcc	588
Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser	
160 165 170	
cag aat ctc agc acc cac ctg ctt atc ctc tat ggt gtc cag gga ctg	636
Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu	
175 180 185 190	
ctg acc ttc ggg tac ctg gtg ctg ctg tcc cac gtt ggc gag cgc atg	684
Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met	
195 200 205	
gct gtg gac atg cgg agg gcc ctc ttc agc tcc ctg ctc cgg tac tgc	732
Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys	
210 215 220	
cag ccg cag ggt gca gag ttg gga caa gac atc acc ttc ttt gac gcc	780
Gln Pro Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala	
225 230 235	
aat aag aca ggg cag ctg gtg agc cgc ttg aca act gac gtg cag gag	828
Asn Lys Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu	
240 245 250	
ttt aag tca tcc ttc aag ctt gtc atc tcc cag ggg ctg cga agc tgc	876
Phe Lys Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys	

WO 00/29448

PCT/JP99/06412

138/233

255	260	265	270	
acc cag gtg gca ggc tgc ctg gtg tcc ctg tcc atg ctg tcg aca cgc				924
Thr Gln Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg				
275	280	285		
ctc acg ctg ctg ctg atg gtg gcc aca cca gcc ctg atg gga gtg ggc				972
Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly				
290	295	300		
acc ctg atg ggc tca ggc ctc cga aaa ttg tct tgc cag tgt cag gag				1020
Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu				
305	310	315		
cag atc gcc agg gca atg ggc gta gca gac gag gcc ctg ggc aat gtg				1068
Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val				
320	325	330		
cgg act gtg cgt gcc ttc gcc atg gag caa cgg gaa gag gag cgc tat				1116
Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr				
335	340	345	350	
ggg gca gag ctg gaa gcc tgc cgc tgc cgg gca gag gag ctg ggc cgc				1164
Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg				
355	360	365		
ggc atc gcc ttg ttc caa ggg ctt tcc aac atc gcc ttc aac tgc atg				1212
Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met				
370	375	380		
gtc ttg ggt acc cta ttt att ggg ggc tcc ctt gtg gcc gga cag cag				1260
Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln				
385	390	395		
ctg aca ggg gga gac ctc atg tcc ttc ctg gtg gcc tcc cag aca gtg				1308
Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val				
400	405	410		
caa agg ctg tgacattcca tgcattggaag gaccatcctt gacaggctgt gtg				1360
Gln Arg Leu				
415				
agctgccctt ccccatgcct gccacttcca gggatgacaa gctgaccctt gtccccacac				1420
acccccacct tatagcttat tgctttgcgt tgggtccaaaa ccaccgcgc agctgagcct				1480
ctgggatgac cagagctgat caccagacag ctcaaggcgg gcctcccccc tcctatctct				1540
ttccaagcta aacacaagca gttctacata aatatgttat ggtaaataat gagatagtaa				1600

WO 00/29448

PCT/JP99/06412

139/233

atatgctgta acagatc

1617

<210> 84

<211> 3269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (260)...(2209)

<400> 84

agagtttccg caccgggag ggagatgagg cgggggctca ggctccttgc agttgtaatt	60
tagattcgag aagtggttta tcctttgact ggaaaagaaa agtagctgca gtattccccc	120
agcaattgct gagagcatgc cgtatgccag gctgtgaggc tcgagagaca agcagtggaa	180
gagttggggc ctgtttcatc tctggattgt aaatctgagc ctccctctgg cccctggaag	240
gggacagcat cacgatgga atg att cct aac cag cat aat gct gga gcc ggg	292
Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly	
1 5 10	
agc cac caa cct gca gtt ttc aga atg gcc gtg ttg gac act gat ttg	340
Ser His Gln Pro Ala Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu	
15 20 25	
gat cac att ctt cca tct tct gtt ctt cct cca ttc tgg gct aag tta	388
Asp His Ile Leu Pro Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu	
30 35 40	
gta gtg gga tcg gtt gcc att gtg tgt ttt gca cgc agc tat gat gga	436
Val Val Gly Ser Val Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly	
45 50 55	
gac ttt gtc ttt gat gac tca gaa gct att gtt aac aat aag gtt gct	484
Asp Phe Val Phe Asp Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala	
60 65 70 75	
ggg gtt gtc ggc cgt gca gac ctc ctg tgt gcc ctg ttc ttc ttg tta	532
Gly Val Val Gly Arg Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu	
80 85 90	
tct ttc ctt ggc tac tgt aaa gca ttt aga gaa agt aac aag gag gga	580
Ser Phe Leu Gly Tyr Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly	
95 100 105	

WO 00/29448

PCT/JP99/06412

140/233

gcg cat tct tcc acc ttc tgg gtg ctg ctg agt atc ttt ctg gga gca	628
Ala His Ser Ser Thr Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala	
110 115 120	
gtg gcc atg ctg tgc aaa gag caa ggg atc act gtg ctg ggt tta aat	676
Val Ala Met Leu Cys Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn	
125 130 135	
gcg gta ttt gac atc ttg gtg ata ggc aaa ttc aat gtt ctg gaa att	724
Ala Val Phe Asp Ile Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile	
140 145 150 155	
gtc cag aag gta cta cat aag gac aag tca tta gag aat ctc ggc atg	772
Val Gln Lys Val Leu His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met	
160 165 170	
ctc agg aac ggg ggc ctc ctc ttc aga atg acc ctg ctc acc tct gga	820
Leu Arg Asn Gly Gly Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly	
175 180 185	
ggg gct ggg atg ctc tac gtg cgc tgg agg atc atg ggc acg ggc ccg	868
Gly Ala Gly Met Leu Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro	
190 195 200	
ccg gcc ttc acc gag gtg gac aac ccg gcc tcc ttt gct gac agc atg	916
Pro Ala Phe Thr Glu Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met	
205 210 215	
ctg gtg agg gcc gta aac tac aat tac tac tat tca ttg aat gcc tgg	964
Leu Val Arg Ala Val Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp	
220 225 230 235	
ctg ctg ctg tgt ccc tgg tgg ctg tgt ttt gat tgg tca atg ggc tgc	1012
Leu Leu Leu Cys Pro Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys	
240 245 250	
atc ccc ctc att aag tcc atc agc gac tgg agg gta att gca ctt gca	1060
Ile Pro Leu Ile Lys Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala	
255 260 265	
gca ctc tgg ttc tgc cta att ggc ctg ata tgc caa gcc ctg tgc tct	1108
Ala Leu Trp Phe Cys Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser	
270 275 280	
gaa gac ggc cac aag aga agg atc ctt act ctg ggc ctg gga ttt ctc	1156
Glu Asp Gly His Lys Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu	

142/233

Ala Ala Glu Gln Ser Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr	
480 485 490	
cca gac tgt tac tac aac ctc ggg cgt ctg tat gca gat ctc aat cgc	1780
Pro Asp Cys Tyr Tyr Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg	
495 500 505	
cac gtg gat gcc ttg aat gcg tgg aga aat gcc acc gtg ctg aaa cca	1828
His Val Asp Ala Leu Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro	
510 515 520	
gag cac agc ctg gcc tgg aac aac atg att ata ctc ctc gac aat aca	1876
Glu His Ser Leu Ala Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr	
525 530 535	
ggt aat tta gcc caa gct gaa gca gtt gga aga gag gca ctg gaa tta	1924
Gly Asn Leu Ala Gln Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu	
540 545 550 555	
ata cct aat gat cac tct ctc atg ttc tcg ttg gca aac gtg ctg ggg	1972
Ile Pro Asn Asp His Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly	
560 565 570	
aaa tcc cag aaa tac aag gaa tct gaa gct tta ttc ctc aag gca att	2020
Lys Ser Gln Lys Tyr Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile	
575 580 585	
aaa gca aat cca aat gct gca agt tac cat ggt aat ttg gct gtg ctt	2068
Lys Ala Asn Pro Asn Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu	
590 595 600	
tat cat cgt tgg gga cat cta gac ttg gcc aag aaa cac tat gaa atc	2116
Tyr His Arg Trp Gly His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile	
605 610 615	
tcc ttg cag ctt gac ccc acg gca tca gga act aag gag aat tac ggt	2164
Ser Leu Gln Leu Asp Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly	
620 625 630 635	
ctg ctg aga aga aag cta gaa cta atg caa aag aaa gct gtc tgat	2210
Leu Leu Arg Arg Lys Leu Glu Leu Met Gln Lys Lys Ala Val	
640 645	
cctgtttcct tcatgttttg agtttgagtg tgtgtgtgca tgaggcatat cattaatagt	2270
atgtgggttac atttaacat ttaaaagtct tagacatgtt attttactga tttttttcta	2330
tgaaaacaaa gacatgcaaa aagattatag caccagcaat ataactottga atgcgtgata	2390

WO 00/29448

PCT/JP99/06412

143/233

tgatttttca ttgaaattgt attttttcag acaactcaaa tgtaattcta aaattccaaa	2450
aatgtctttt ttaattaaac agaaaaagag aaaaaattat cttgagcaac ttttagtaga	2510
attgagctta catttgggat ctgagccttg tegtgtatgg actagcacta ttaaacttca	2570
attatgacca agaaaggata cactggcccc tacaatttgt ataaatattg aacatgtcta	2630
tatattagca tttttattta atgacaaagc aaattaagtt tttttatctc ttttttttaa	2690
aacaacatac tgtgaacttt gtaaggaaat atttatttgt atttttatgt tttgaatagg	2750
gcaaataatc gaatgaggaa tggaagtttt aacatagtat atctatatgc ttttccccat	2810
aggaagaaat tgactcttgc agtttttgga tgetctgact tgtgcaattt caatacacag	2870
gagattatgt aatgtaatat ttttcataag cggttactat caattgaaag ttcaagccat	2930
gcttttaggca agagcaggca gcctcacatc tttatttttg ttacatccaa ggtgaagagg	2990
gcaacacatc tgtgtaagct gctttttagt gtgtttatct gaaggccgtt ttccattttg	3050
cttaatgtaa ctacagacat tatccagaaa atgcaaaaatt ttctatcaaa tggagccaca	3110
ttcggggaat tegtgttatt tttaagaatt gagttgttcc tgetgttttt tatttgatcc	3170
aaacaatgtt ttgttttggt cttctctgta tgetgttgac ctaatgattt atgcaatctc	3230
tgtaatttct tatgcagtaa aattactaca caaactagc	3269

<210> 85

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66)...(347)

<400> 85

acagttcctc tggacttctc tggaccacag tcctctgcc aacccctgcc agaccocagt	60
ccacc atg atc cat ctg ggt cac atc ctc ttc ctg ctt ttg ctc cca gtg	110
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val	
1 5 10 15	
gct gca gct cag acg act cca gga gag aga tca tca ctc cct gcc ttt	158
Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe	
20 25 30	
tac cct ggc act tca ggc tct tgt tcc gga tgt ggg tcc ctc tct ctg	206
Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu	
35 40 45	
ccg ctc ctg gca ggc ctc gtg gct gct gat gcg gtg gca tcc ctg ctc	254

WO 00/29448

PCT/JP99/06412

144/233

```

Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu
      50              55              60
atc gtg ggg gcg gtg ttc ctg tgc gca cgc cca cgc cgc agc ccc gcc      302
Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala
      65              70              75
caa gaa gat ggc aaa gtc tac atc aac atg cca ggc agg ggc tgaccc      350
Gln Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
      80              85              90
tcctgcagct tggacctttg acttctgacc ctctcatcct ggatgggtgtg tgggtggcaca      410
ggaacccccg ccccaacttt tggattgtaa taaaacaatt gaaacacc      458

```

<210> 86

<211> 1712

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (180)...(1457)

<400> 86

```

tcccgcgtggc tagaagaagt cttcaacttcc caggagagcc aaagcgtgtc tggccctagg      60
tgggaaaaga actggctgtg acctttgccc tgacctgaa gggcccagcc ttgggctgaa      120
tggcagcacc cacgcccgcc cgtccggtgc tgaccacact gctggtggct ctcttcggc
atg ggc tcc tgg gct gcg gtc aat ggg atc tgg gtg gag cta cct gtg      227
Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
      1              5              10              15
gtg gtc aaa gag ctt cca gag ggt tgg agc ctc ccc tct tac gtc tct      275
Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
      20              25              30
gtg ctt gtg gct ctg ggg aac ctg ggt ctg ctg gtg gtg acc ctc tgg      323
Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
      35              40              45
agg agg ctg gcc cca gga aag gac gag cag gtc ccc atc cgg gtg gtg      371
Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
      50              55              60
cag gtg ctg ggc atg gtg ggc aca gcc ctg ctg gcc tct ctg tgg cac      419

```

Gln	Val	Leu	Gly	Met	Val	Gly	Thr	Ala	Leu	Leu	Ala	Ser	Leu	Trp	His	
65					70					75					80	
cat	gtg	gcc	cca	gtg	gca	gga	cag	ttg	cat	tct	gtg	gcc	ttc	tta	gca	467
His	Val	Ala	Pro	Val	Ala	Gly	Gln	Leu	His	Ser	Val	Ala	Phe	Leu	Ala	
				85					90					95		
ctg	gcc	ttt	gtg	ctg	gca	ctg	gca	tgc	tgt	gcc	tcg	aat	gtc	act	ttc	515
Leu	Ala	Phe	Val	Leu	Ala	Leu	Ala	Cys	Cys	Ala	Ser	Asn	Val	Thr	Phe	
				100				105					110			
ctg	ccc	ttc	ttg	agc	cac	ctg	cca	cct	cgc	ttc	tta	cgg	tca	ttc	ttc	563
Leu	Pro	Phe	Leu	Ser	His	Leu	Pro	Pro	Arg	Phe	Leu	Arg	Ser	Phe	Phe	
				115				120					125			
ctg	ggt	caa	ggc	ctg	agt	gcc	ctg	ctg	ccc	tgc	gtg	ctg	gcc	cta	gtg	611
Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Leu	Pro	Cys	Val	Leu	Ala	Leu	Val	
				130				135					140			
cag	ggt	gtg	ggc	cgc	ctc	gag	tgc	ccg	cca	gcc	ccc	atc	aac	ggc	acc	659
Gln	Gly	Val	Gly	Arg	Leu	Glu	Cys	Pro	Pro	Ala	Pro	Ile	Asn	Gly	Thr	
145				150					155					160		
cct	ggc	ccc	ccg	ctc	gac	ttc	ctt	gag	cgt	ttt	ccc	gcc	agc	acc	ttc	707
Pro	Gly	Pro	Pro	Leu	Asp	Phe	Leu	Glu	Arg	Phe	Pro	Ala	Ser	Thr	Phe	
				165					170					175		
ttc	tgg	gca	ctg	act	gcc	ctt	ctg	gtc	gct	tca	gct	gct	gcc	ttc	cag	755
Phe	Trp	Ala	Leu	Thr	Ala	Leu	Leu	Val	Ala	Ser	Ala	Ala	Ala	Phe	Gln	
				180					185					190		
ggt	ctt	ctg	ctg	ctg	ttg	ccg	cca	cca	cca	tct	gta	ccc	aca	ggg	gag	803
Gly	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Ser	Val	Pro	Thr	Gly	Glu	
				195				200					205			
tta	gga	tca	ggc	ctc	cag	gtg	gga	gcc	cca	gga	gca	gag	gaa	gag	gtg	851
Leu	Gly	Ser	Gly	Leu	Gln	Val	Gly	Ala	Pro	Gly	Ala	Glu	Glu	Glu	Val	
				210				215					220			
gaa	gag	tcc	tca	cca	ctg	caa	gag	cca	cca	agc	cag	gca	gca	ggc	acc	899
Glu	Glu	Ser	Ser	Pro	Leu	Gln	Glu	Pro	Pro	Ser	Gln	Ala	Ala	Gly	Thr	
225				230					235					240		
acc	cct	ggt	cca	gac	cct	aag	gcc	tat	cag	ctt	cta	tca	gcc	cgc	agt	947
Thr	Pro	Gly	Pro	Asp	Pro	Lys	Ala	Tyr	Gln	Leu	Leu	Ser	Ala	Arg	Ser	
				245					250					255		

WO 00/29448

PCT/JP99/06412

146/233

gcc tgc ctg ctg ggc ctg ttg gcc gcc acc aac gcg ctg acc aat ggc	995
Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly	
260 265 270	
gtg ctg cct gcc gtg cag agc ttt tcc tgc tta ccc tac ggg cgt ctg	1043
Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu	
275 280 285	
gcc tac cac ctg gct gtg gtg ctg ggc agt gct gcc aat ccc ctg gcc	1091
Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala	
290 295 300	
tgc ttc ctg gcc atg ggt gtg ctg tgc agg tcc ttg gca ggg ctg ggc	1139
Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly	
305 310 315 320	
ggc ctc tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg gcg ctg	1187
Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu	
325 330 335	
gca gtc ctg agc ccc tgc ccg ccc ctg gtg ggc acc tcg gcg ggg gtg	1235
Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val	
340 345 350	
gtc ctc gtg gtg ctg tcg tgg gtg ctg tgt ctt ggc gtg ttc tcc tac	1283
Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr	
355 360 365	
gtg aag gtg gca gcc agc tcc ctg ctg cat ggc ggg ggc cgg ccg gca	1331
Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala	
370 375 380	
ttg ctg gca gcc ggc gtg gcc atc cag gtg ggc tct ctg ctc ggc gct	1379
Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala	
385 390 395 400	
gtt gct atg ttc ccc ccg acc agc atc tat cac gtg ttc cac agc aga	1427
Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg	
405 410 415	
aag gac tgt gca gac ccc tgt gac tcc tgagcctggg caggtgggga ccccg	1480
Lys Asp Cys Ala Asp Pro Cys Asp Ser	
420 425	
tccccaacac ctgtctttcc ctcaatgctg ccaccatgcc tgagtgcctg cagcccagga	1540
ggccccgaca ccggtacact cgtggacacc tacacactcc ataggagatc ctggctttcc	1600

WO 00/29448

PCT/JP99/06412

147/233

agggtgggca agggcaagga gcaggcttgg agccagggac cagtgggggc ttaggggtaa 1660
gcccctgagc ctggggaccta catgtgggtt gcgtaataaa acatttgtat tt 1712

<210> 87

<211> 1055

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)...(502)

<400> 87

accgggagggc gcgtggggct tgaggccgag aacggccctt gctgccacca ac atg 55
Met
1
gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg 103
Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu
5 10 15
aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg 151
Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val
20 25 30
tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att 199
Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile
35 40 45
tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa 247
Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu
50 55 60 65
cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga 295
His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly
70 75 80
caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga 343
Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly
85 90 95
ggg tta ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca 391
Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro
100 105 110

WO 00/29448

PCT/JP99/06412

148/233

aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta 439
 Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu
 115 120 125
 ttg agt ttt ttc atg gct aga gta ttc atg aga atg aaa ctg ccg ggc 487
 Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly
 130 135 140 145
 tat ctg atg ggt tagagtgcct ttgagaagaa atcagtggat actggatttg c 540
 Tyr Leu Met Gly

tcctgtcaat gaagttttaa aggctgtacc aatcctctaa tatgaaatgt ggaaaagaat 600
 gaagagcagc agtaaaagaa atatctagtg aaaaaacagg aagcgtattg aagcttggac 660
 tagaatttct tcttggtatt aaagagacaa gtttatcaca gaattttttt tcctgctggc 720
 ctattgctat accaatgatg ttgagtggca ttttcttttt agtttttcat taaaatatat 780
 tccatatcta caactataat atcaaataaa gtgattatatt tttacaaccc tcttaacatt 840
 ttttggagat gacatttctg attttcagaa attaacataa aatccagaag caagattccg 900
 taagctgaga actctggaca gttgatcagc tttacctatg gtgctttgcc ttttaactaga 960
 gtgtgtgatg gtagattatt tcagatatgt atgtaaaact gtttcttgaa caataagatg 1020
 tatgaacgga gcagaaataa atactttttc taatt 1055

<210> 88

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)...(1412)

<400> 88

gagctctcac ggtttcctct ttctgacaa aaagaatatt aatgaaactt tatcatcttg 60
 gtgagaaaag cattctaata gctttattct gacatacggg ggtatggaga gcttgaagga 120
 gtcagagagg tgcccagcta agacctgaat gccatcacc tccccagggc tctgcagttt 180
 tctcgtggtg aacccttgat ggatttggtg ttgcttgaga a atg gcg atg atc 233
 Met Ala Met Ile

1

gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag agt 281
 Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys Ser

WO 00/29448

PCT/JP99/06412

149/233

5	10	15	20	
tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta ttt				329
Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu Phe				
25	30	35		
tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg cct				377
Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp Pro				
40	45	50		
gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag cct				425
Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu Pro				
55	60	65		
gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa ttc				473
Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu Phe				
70	75	80		
cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag aga				521
Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu Arg				
85	90	95	100	
gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc atc				569
Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe Ile				
105	110	115		
ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc tgg				617
Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala Trp				
120	125	130		
gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt cat				665
Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser His				
135	140	145		
gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat tat				713
Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His Tyr				
150	155	160		
gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc tct				761
Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser Ser				
165	170	175	180	
gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac agc				809
Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn Ser				
185	190	195		
gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa gca				857

WO 00/29448

PCT/JP99/06412

150/233

Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu Ala	
200 205 210	
gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag gca cgt	905
Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala Arg	
215 220 225	
ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg tct gcc cct	953
Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala Pro	
230 235 240	
gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat gct aac tgt	1001
Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn Cys	
245 250 255 260	
tct ggg gaa gac gct gct cct gca gag gaa agg gac atc cca ttt aag	1049
Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe Lys	
265 270 275	
gag aac tat gac gtg ctt tca cgg gag gca tca caa aag ctg ctg tgg	1097
Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu Trp	
280 285 290	
tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc gcc tgc	1145
Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser Ala Cys	
295 300 305	
gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca tct ttc	1193
Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser Phe	
310 315 320	
agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc atc acg	1241
Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser Ile Thr	
325 330 335 340	
ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag gat gtg	1289
Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu Asp Val	
345 350 355	
gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc ctc aca	1337
Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val Leu Thr	
360 365 370	
ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt ttg aac	1385
Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly Leu Asn	
375 380 385	

WO 00/29448

PCT/JP99/06412

151/233

ttg ctc gga aag cgt aag aca aga tgaagagcag ggcgcattat a 1430
 Leu Leu Gly Lys Arg Lys Thr Arg
 390 395
 aatatcaaag cccaagaaat ggaactttgg gcagagatca tgtagaatc aagtggatga 1490
 tgagaccaat tacaggccgt ctctctgcac agcacagaaa ttctcaatca ctgaaatgag 1550
 taactgcaaa ataaatagtt gattgtactg ttctcatgct ataaaagtgg acagggtactc 1610
 tacaac 1616

<210> 89
 <211> 1860
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (69)...(1121)
 <400> 89

gagaagtgtc ggcgtccgtgc gccgcgggct ggggcgggtct caggtgtgcc gaagctctgg 60
 tcagtgcc atg atc cgg cag gag cgc tcc aca tcc tac cag gag ctg 107
 Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu
 1 5 10
 agt gag gag ttg gtc cag gtg gtt gag aac tca gag ctg gca gac gag 155
 Ser Glu Glu Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu
 15 20 25
 cag gac aag gag acg gtc aga gtc caa ggt ccg ggt atc tta cca ggc 203
 Gln Asp Lys Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly
 30 35 40 45
 ctg gac agc gag tcc gcc tcc agc agc atc cgc ttc agc aag gcc tgc 251
 Leu Asp Ser Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys
 50 55 60
 ctg aag aac gtc ttc tcg gtc cta ctc atc ttc atc tac ctg ctg ctc 299
 Leu Lys Asn Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu
 65 70 75
 atg gct gtg gcc gtc ttc ctg gtc tac cgg acc atc aca gac ttt cgt 347
 Met Ala Val Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg
 80 85 90

WO 00/29448

PCT/JP99/06412

153/233

270	275	280	285	
gaa tgg aaa gat cct ttc atc cag aaa gtc caa gat ata gtc act gcc				971
Glu Trp Lys Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala				
	290	295	300	
aat cct tgg aac aca att gct ctt ctc tgt ggc gcc ttc ttg gca tta				1019
Asn Pro Trp Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu				
	305	310	315	
ttt aaa gca gca gag ttt gcc aaa ctg agt ata aaa tgg atg atc aaa				1067
Phe Lys Ala Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys				
	320	325	330	
att aga aag aga tac ctt aaa aga aga ggt cag gca acg agc cac ata				1115
Ile Arg Lys Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile				
	335	340	345	
agc tgaagtcacc tcgcgttggt tagagaactg tccacatcaa tgggagctgt ca				1170
Ser				
350				
tcacttccac tttgtaaacg gagctatcaa caatcctgta ctcaactgaa gaaatggggc				1230
cttgctggga ggaacagcat gtaaaactgg aacttctaac cccgtcccaa aagaggcggc				1290
gtagagccta atagaagaga ctaatggata aacctacaag ttattttaaatt atttaaatta				1350
ttaataaaact ttttaaagag ctggccaatg acttttgaat agggtttgta gaagatgcct				1410
ttcttcctgt ttggttcatt gtattgtatt aggttaagct ctactagggc aatgaaggct				1470
ctacttttca ctttttaaaa gtggacaaaa gagggtgatt ttctttttcc aaaaattcct				1530
gagtatcaag acgtgcaggc catgctttgg agcctatgca ctgtacacaa aggcaaaacc				1590
ctatgacttt ggcacatctt gccattgatg tccagcctct gacatgctct ttgatttggt				1650
aaatgttaaa tgagacttta aggctactag aaactagtaa ttaagtttct taatggactg				1710
agtagccacc tacttgtccg gctagaatgt ttgttgatgt atgagtttag attaacactc				1770
aaaagcacta ggacagatgt acatagaagg tgcctactca ttgtattttg atgatttcat				1830
taacaggtaa ataaaagtta atacaaaagg				1860

<210> 90

<211> 783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

WO 00/29448

PCT/JP99/06412

154/233

<222> (245)...(706)

<400> 90

```

acacacccag tgaggtctct ggagccgcgg tgcgggaagc ggggacccgg gtttgaatcc      60
tgcccctctg gtgtggtgcg gcctcttccc acagactttt ggcctcagtg ttccccgcct      120
gggaagtggg gactggccct ggtacctggc tccagagctg caccagagg cgatcagccc      180
ggtgcgggaa cggggcgggg tggccgcaac tacgggccac ggatcctgac ccgccctgcc      240
cacg atg act atc cac atc ctc atc ctg ctg ttg ctc ctc gcc ttc      286
      Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe
              1              5              10
tcc gcc caa ggg gac ctg gac act gca gcc agg cga ggc cag cac cag      334
Ser Ala Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln
      15              20              25              30
gtc ccc cag cac cgc ggg cac gtc tgc tac ctg ggc gta tgc cgg acc      382
Val Pro Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr
              35              40              45
cac cgc ctg gcg gag atc ata tac tgg att cgc tgt ctc cac caa gga      430
His Arg Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly
              50              55              60
gcc ctc ggg gaa ggc cag cca cga gcc cca gga ccc cta cag cta tgg      478
Ala Leu Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp
              65              70              75
gcg ccg ccg gtg gcg cga ggc gga agc ccg gct cgg ttc cca gga ttc      526
Ala Pro Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe
              80              85              90
cgg cct gca gcg agg ggg cta gcg cag tgc cca gct cgc tgg gtg acc      574
Arg Pro Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr
              95              100              105              110
tcg ggc acg gct cgt ccc ctc ctc ggc ttc agt ttg cct atc tgt atg      622
Ser Gly Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met
              115              120              125
ttg gag ctt cta ctc cac att tct tct ccc cta act cca gcc cct gaa      670
Leu Glu Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu
              130              135              140
acc gtc ttc ccc agt ccc tcc ccg ggc tgc gac taggttgac ctagaag      720
Thr Val Phe Pro Ser Pro Ser Pro Gly Cys Asp

```

WO 00/29448

PCT/JP99/06412

155/233

145 150

cacacggggac caggtgtgggc gaagaacact gacgcccaga gccgaataaa caagagttcc 780

gtg 783

<210> 91

<211> 303

<212> PRT

<213> Homo sapiens

<400> 91

Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr

1 5 10 15

Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala

20 25 30

Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His

35 40 45

Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val

50 55 60

Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser

65 70 75 80

Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp

85 90 95

Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro

100 105 110

Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val

115 120 125

Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn

130 135 140

Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala

145 150 155 160

Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp

165 170 175

Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu

180 185 190

Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg

195 200 205

WO 00/29448

PCT/JP99/06412

157/233

130	135	140
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser		
145	150	155
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser		
165	170	175
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val		
180	185	190
Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met		
195	200	205
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys		
210	215	220
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile		
225	230	235
Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn		
245	250	255
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met		
260	265	270
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg		
275	280	

<210> 93

<211> 488

<212> PRT

<213> Homo sapiens

<400> 93

Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu
1 5 10 15
Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys
20 25 30
Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
35 40 45
Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val
50 55 60
Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
65 70 75 80

WO 00/29448

PCT/JP99/06412

158/233

Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln			
	85	90	95
Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp			
	100	105	110
Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr			
	115	120	125
Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys			
	130	135	140
Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala			
	145	150	155
Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser			
	165	170	175
Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly			
	180	185	190
Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg			
	195	200	205
Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr			
	210	215	220
Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly			
	225	230	235
Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly			
	245	250	255
Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu			
	260	265	270
Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr			
	275	280	285
His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu			
	290	295	300
Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu			
	305	310	315
Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys			
	325	330	335
Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu			
	340	345	350
Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe			

Met	Trp	Pro	Pro	Asp	Pro	Asp	Pro	Asp	Pro	Asp	Pro	Glu	Pro	Ala	Gly
1				5						10					15
Gly	Ser	Arg	Pro	Gly	Pro	Ala	Val	Pro	Gly	Leu	Arg	Ala	Leu	Leu	Pro
			20						25					30	
Ala	Arg	Ala	Phe	Leu	Cys	Ser	Leu	Lys	Gly	Arg	Leu	Leu	Leu	Ala	Glu
		35					40					45			
Ser	Gly	Leu	Ser	Phe	Ile	Thr	Phe	Ile	Cys	Tyr	Val	Ala	Ser	Ser	Ala
	50					55					60				
Ser	Ala	Phe	Leu	Thr	Ala	Pro	Leu	Leu	Glu	Phe	Leu	Leu	Ala	Leu	Tyr
65					70					75					80
Phe	Leu	Phe	Ala	Asp	Ala	Met	Gln	Leu	Asn	Asp	Lys	Trp	Gln	Gly	Leu
				85						90				95	

WO 00/29448

PCT/JP99/06412

160/233

Cys Trp Pro Met Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile
100 105 110
Tyr Phe Ala Ile Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala
115 120 125
Ser Lys Ala Ala Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala
130 135 140
Thr Asp Phe Tyr Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln
145 150 155 160
Gly Asp Ser Ala Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn
165 170 175
Ser Asp Ser Asp Ser Asp
180

<210> 95

<211> 184

<212> PRT

<213> Homo sapiens

<400> 95

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn
1 5 10 15
Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu
20 25 30
Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu
35 40 45
Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val
50 55 60
Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp
65 70 75 80
Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly
85 90 95
Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr
100 105 110
Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro
115 120 125
Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe

<212> PRT

WO 00/29448

PCT/JP99/06412

162/233

<213> Homo sapiens

<400> 97

```

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
  1             5             10            15
Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
      20             25             30
Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
      35             40             45
Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
      50             55             60
His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
      65             70             75            80
Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
      85             90             95
Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
      100            105            110
Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
      115            120            125
Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
      130            135            140
Val Arg Ile Phe Gly Ile Asn Lys Tyr
145             150

```

<210> 98

<211> 173

<212> PRT

<213> Homo sapiens

<400> 98

```

Met Ala Ala Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val
  1             5             10            15
Gly Val Leu Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu
      20             25             30
Ile Ser Thr Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu
      35             40             45
Pro Met Arg Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr

```

WO 00/29448

PCT/JP99/06412

163/233

50	55	60
Ile Arg Ile Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys		
65	70	75
Phe Met Leu Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser		80
85	90	95
Pro Glu Ser Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro		
100	105	110
Ser Val Ala Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val		
115	120	125
Ser Gly Ser Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys		
130	135	140
Thr Met Gly Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln		
145	150	155
Lys Phe Glu Lys Lys Ser Val His Asn Lys Ala Tyr Phe		160
165	170	

<210> 99

<211> 75

<212> PRT

<213> Homo sapiens

<400> 99

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly		
1	5	10
Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln Gly Phe Gly		15
20	25	30
Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu		
35	40	45
Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Ile Phe		
50	55	60
Met Met Phe Cys Met Ile Val Leu Phe Gly Ser		
65	70	75

<210> 100

<211> 159

<212> PRT

WO 00/29448

PCT/JP99/06412

164/233

<213> Homo sapiens

<400> 100

```

Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly His Trp
  1             5             10             15
Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp
             20             25             30
Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg
             35             40             45
Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr
             50             55             60
Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser
             65             70             75             80
Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu
             85             90             95
Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu
             100            105            110
Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln
             115            120            125
Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp
             130            135            140
Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr
             145            150            155

```

<210> 101

<211> 909

<212> DNA

<213> Homo sapiens

<400> 101

```

atggagggcag agcagcggcc ggcggcgggg gccagcgaag gggcgacccc tggactggag      60
ggggtgcctc ccgttgctcc ccgcctgog accgcggcct caggctcgat ccccaaactc      120
gggcctgagc ctaagaggag gcacctggg acgtgctcc agcctacggt caacaagttc      180
tcccttcggg tggtcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca      240
gggggggcct ggatcatcca cccctacagc gacttcgggt tttactggga cctgatcatg      300
ctgctgctga tggtggggaa cctcatcgtc ctgcctgtgg gcacacctt cttcaaggag      360
gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat      420

```



```
atgtggcccc cagaccccga ccccgacccg gaccccgagc ctgccggcgg ctcccgctcc 60
ggcccccggg tccccggggt ccgcgcacct ctgccggcgc gggttttct ctgtctcttc 120
aaaggccgcc tctgtctggc cgagtcgggt ctctcattea tcaactttat ctgtatgtg 180
```

WO 00/29448

PCT/JP99/06412

167/233

gcgtcctcag catctgcctt cctcacagcg cctctgettg agttcctgct ggccttgtag	240
ttcctctttg ctgatgccat gcagctgaat gacaagtggc agggcttggtg ctggcccatg	300
atggacttcc tgcgtgtgt caccgcggcc ctcatctact ttgtatctc catcacggcc	360
atcgccaagt actcggtatg ggttccaaa gccgtgggg tgtttggett ctttgetacc	420
atcgtgtttg caactgattt ctacctgac tttaacgac tggccaaatt cctcaaacaa	480
ggggactctg cagatgagac cacagccac aagacagaag aagagaattc cgactcggac	540
tctgac	546

<210> 105

<211> 552

<212> DNA

<213> Homo sapiens

<400> 105

atggacggcc tgaggcagcg cgtggagcac ttctggagc aaaggaacct ggtcaccgaa	60
gtgtggggg cgctggaggc caagaccggg gtggagaagc ggtatctggc tgcaggagcc	120
gtcactctgc taagcctgta totgtgttc ggctacggag cgtctctgct gtgcaatctc	180
atcggtattg tgtacccgc atatgcctca atcaaagcta tcgagagccc aagcaaggac	240
gacgacactg tgtggctcac ctactgggtg gtgtacgcc tgtttgggct ggccgagttc	300
ttcagcgatc tactcctgtc ctggttccct ttctactacg tgggcaagtg cgccttctg	360
ttgtttctgca tggctcccag gccctggaac ggggctctca tgcgttatca gcgcgtcgtg	420
cgtccgctgt tctaaggca ccacggggcc gtagacagaa tcatgaacga cctcagcggg	480
cgagccctgg acgcggcgcc cggaataacc aggaacgtca agccaagcca gaccccgag	540
ccgaaggaca ag	552

<210> 106

<211> 420

<212> DNA

<213> Homo sapiens

<400> 106

atgagccgtt tctgaatgt gttaagaagt tggctgggta tgggtgccat catagccatg	60
gggaacacgc tgcagagctt ccgagaccac acttttctct atgaaaaget ctacactggc	120
aagccaaacc ttgtgaatgg cctccaagct cggacctttg ggatctggac gctgctctca	180
tcagtgatc gctgcctctg tgcattgac attcacaaca agacgtctc tcacatcaca	240
ctctggacct tctccttgc cctggggcat ttctctctg agttgtttgt ctatggaaet	300
gcagctccca cgattggcgt cctggcaccc ctgatgggtg caagtttctc catcctgggt	360

WO 00/29448

PCT/JP99/06412

168/233

atgctggtcg ggctccgga tctagaagta gaaccagtat ccagacagaa gaagagaaac 420

<210> 107

<211> 459

<212> DNA

<213> Homo sapiens

<400> 107

atgaacgttg gagttgcca cagtgaagtg aatccaaata cccgtgtcat gaacagccgg 60
 ggtatgtggc tgacatatgc attgggagtt ggcttgcttc atattgtctt actcagcatt 120
 cccttcttca gtgttcctgt tgcctggact ttaacaaata ttatacataa tctggggatg 180
 tacgtatttt tgcattgcagt gaaaggaaca cctttcgaaa ctctgacca gggtaaagca 240
 aggtctctaa ctcatggga acaactggac tatggagtac agtttacatc ttcacggaag 300
 tttttcacia tttctccaat aattctatat tttctggcaa gtttctatac gaagtatgat 360
 ccaactcact tcactctaaa cacagcttct ctctgagtg tactaattcc caaaatgcc 420
 caactacatg gtgttcggat ctttgaatt aataagtat 459

<210> 108

<211> 519

<212> DNA

<213> Homo sapiens

<400> 108

atggctgcct tcctgataca gaccaaggac aaccccatga aggcctggg tgtgctggcc 60
 ggcaccatgg ccaccgtcgt ggccatcact gtctctatct ccaccgccac cttctggcgc 120
 aacaagaagt ctaacaaggt cctgccaatg cggcggtgc tccgaagcg gccagccct 180
 gcgccccgca ccatccgcat tgagtggctc aagtccaaga gcaccaaagc cgctaccaag 240
 ttcatgctca aagagaaacc tccaatgag aactgtaaca acaacagccc agaaaactct 300
 ctgtctccga gagctccgc tctcctcca ccaccagcg tggcgccag cactggcgca 360
 gccagtgga cgtgcctac tgtctctggc tetctcactc cgcagccgac ccaacccccg 420
 ccaaaaccca aaactatggg aagccccgtc cagtcaactc tgatctctga gctcaagcaa 480
 aagtttgaga agaagagtgt gcacaacaag gcttacttc 519

<210> 109

<211> 225

<212> DNA

<213> Homo sapiens

WO 00/29448

PCT/JP99/06412

169/233

<400> 109

atgatcggag acatcctget gttcgggaacg ttgetgatga atgccggggc ggtgetgaac	60
tttaagctga aaaagaagga cacgcagggc tttggggagg agtccaggga gccagcaca	120
ggtgacaaca tccgggaatt cttgetgagc ctcagatact ttcgaatctt catcgccctg	180
tggaaacatct tcatgatgtt ctgcattgatt gtgetgttcg gctct	225

<210> 110

<211> 477

<212> DNA

<213> Homo sapiens

<400> 110

atggagctgc ctgctgtgaa cctgaagggtg attctcctag gtcactggct gctgacaacc	60
tggggctgca ttgtattctc aggtcctat gcctgggcca acttcaccat cctggccttg	120
ggcgtgtggg ctgtggetca ggggactcc atcgacgcca taagcatgtt tctgggtggc	180
ttgctggcca ccatcttctt ggacatcgtg cacatcagca tcttctaccc gggggtcagc	240
ctcaccggaca cgggcccgtt tggcgtgggc atggccatcc tcagcttget gctcaagccg	300
ctctcctget gcttcgtcta ccacatgtac cgggagcgcg ggggtgagct cctgggccac	360
actggtttcc ttgggtcttc tcaggaccgt agtgcctacc agacgattga ctcagcagag	420
gcccgcgag atccctttgc agtccagag ggcaggagtc aagatgcccg agggtag	477

<210> 111

<211> 3438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1032)

<400> 111

gectacgacg cctccgetag agcccgcggg gctgcgccga ctcctgetct ggaggggttg	60
cgggtacctg atggccacag agggctctag gaggccgagc gtgtaagcgg ggtgggcgcc	120
atg gag gca gag cag cgg ccg gcg gcg ggg gcc agc gaa ggg gcg acc	168
Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr	
1 5 10 15	
cct gga ctg gag gcg gtg cct ccc gtt gct ccc ccg cct gcg acc gcg	216
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala	

WO 00/29448

PCT/JP99/06412

170/233

20	25	30	
gcc tca ggt ccg atc ccc aaa tct ggg cct gag cct aag agg agg cac			264
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His			
35	40	45	
ctt ggg acg ctg ctc cag cct acg gtc aac aag ttc tcc ctt cgg gtg			312
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val			
50	55	60	
ttc ggc agc cac aaa gca gtg gaa atc gag cag gag cgg gtg aag tca			360
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser			
65	70	75	80
gcg ggg gcc tgg atc atc cac ccc tac agc gac ttc cgg ttt tac tgg			408
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp			
85	90	95	
gac ctg atc atg ctg ctg ctg atg gtg ggg aac ctc atc gtc ctg cct			456
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro			
100	105	110	
gtg ggc atc acc ttc ttc aag gag gag aac tcc ccg cct tgg atc gtc			504
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val			
115	120	125	
ttc aac gta ttg tct gat act ttc ttc cta ctg gat ctg gtg ctc aac			552
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn			
130	135	140	
ttc cga acg ggc atc gtg gtg gag gag ggt gct gag atc ctg ctg gca			600
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala			
145	150	155	160
ccg cgg gcc atc cgc acg cgc tac ctg cgc acc tgg ttc ctg gtt gac			648
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp			
165	170	175	
ctc atc tct tct atc cct gtg gat tac atc ttc cta gtg gtg gag ctg			696
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu			
180	185	190	
gag cca cgg ttg gac gct gag gtc tac aaa acg gca cgg gcc cta cgc			744
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg			
195	200	205	
atc gtt cgc ttc acc aag atc cta agc ctg ctg agg ctg ctc cgc ctc			792

WO 00/29448

PCT/JP99/06412

171/233

Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu	
210 215 220	
tcc cgc ctc atc cgc tac ata cac cag tgg gag gag atc ttt cac atg	840
Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met	
225 230 235 240	
acc tat gac ctg gcc agt gct gtg gtt cgc atc ttc aac ctc att ggg	888
Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly	
245 250 255	
atg atg ctg ctg cta tgt cac tgg gat ggc tgt ctg cag ttc ctg gtg	936
Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val	
260 265 270	
ccc atg ctg cag gac ttc cct ccc gac tgc tgg gtc tcc atc aac cac	984
Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His	
275 280 285	
atg gtg gtg aga agt ccc cac agc tct gcc ttt cct ggg cct tct t	1030
Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser	
290 295 300	
agggctcttc tgcctgagta gcagggatgg ccacagggag caggaggtgg gagatgatca	1090
caacagaaaa taggagcgag gaggtgggga ggagggagga aaggggaagg agaccagaa	1150
gaagtgtcgt tgtgttgag ggagcaggca aaggaaggggt acctaccgg aagctgaggc	1210
ccccaagttg caatagagga cccttttgcc tcagggcccc ccagaaccaa acttaagtgc	1270
ctgccaggag gaaggcctgc agtagaaggg gcagacagaa agaccaaaga aggaaaagg	1330
gcaggcagag aatgaggtc cgaggggccc atgccagct ctgcaatata ctctgccct	1390
cagaaccact cgtggggccg ccagtattcc catgccctgt tcaaggccat gagccacatg	1450
ctgtgcattg gctatgggca gcaggcacct gtaggcatgc ccgacgtctg gctcaccatg	1510
ctcagcatga tcgtaggtgc cacatgctac gccatgttca tcggccatgc cacggcactc	1570
atccagtccc tggactcttc ccggcgtcag taccaggaga agtacaagca ggtggagcag	1630
tacatgtcct tccacaagct gccagcagac acgcggcagc gcatccacga gtactatgag	1690
caccgctacc agggcaagat gttegatgag gaaagcatcc tgggcgagct gagcgagccg	1750
cttcgcgagg agatcattaa cttcacctgt cggggcctgg tggcccacat gccgctgttt	1810
gcccattgcc accccagctt cgtcactgca gttctcacca agctgcgctt tgaggtcttc	1870
cagccggggg atctcgtggt gcgtgagggc tccgtgggga ggaagatgta cttcatccag	1930
catgggctgc tcagtgtgct ggcccgcggc gcccgggaca cagccctcac cgatggatcc	1990
tactttgggg agatctgcct gctaactagg ggccggcgca cagccagtgt tcgggctgac	2050
acctactgcc gcctttactc actcagcgtg gaccatttca atgctgtgct tgaggagttc	2110

WO 00/29448

PCT/JP99/06412

172/233

```

cccatgatgc gccgggcctt tgagactgtg gccatggatc ggctgctccg catcggcaag 2170
aagaattcca tactgcagcg gaagcgcctc gagccaagtc caggcagcag tgggtggcatc 2230
atggagcagc acttggtgca acatgacaga gacatggctc ggggtgttcg gggtcggggc 2290
ccgagcacag gagctcagct tagtggaaag ccagtactgt gggagccact ggtacatgcg 2350
ccccttcagg cagctgctgt gacctccaat gtggccattg ccctgactca tcagcggggc 2410
cctotgcccc tctccctga ctctccagcc accctccttg ctcgctctgc ttggcgctca 2470
gcaggtctct cagcttcccc gctgggtgcc gtccgagctg gcccatgggc atccacctcc 2530
cgccctgccc ccccacctgc ccgaacctg caccgcagcc tatcccgggc agggcgctcc 2590
caggtctccc tgctgggtcc ccctccagga ggaggtggac ggcggctagg acctcggggc 2650
cgcccactct cagcctccca accctctctg cctcagcggg caacaggcga tggctctcct 2710
gggcgtaagg gatcaggaag tgagcggctg cctccctcag ggctcctggc caaacctcca 2770
aggacagccc agccccccag gccaccagtg cctgagccag ccacaccccg ggggtctccag 2830
ctttctgcca acatgtaaaa cctttgagta catccagcct tagttcttgg ggtgcagtag 2890
tatgtaccca agggcagatg cctcttgggg aaggccatgg ggacctgaaa cattgcccc 2950
tggaatgtc gacctgtgc ggacattccg catactgcca tgaagacggt ctctgtgtcc 3010
tcagctcaag aatcctgtag cttgtcccat cataatccat tcaccggttc atcatgtgta 3070
ctgagcagct accatgttca aggtaaggag acaggaggag taggaggagg cagggcctct 3130
ccatgccagc ctctgtggtc cttgccccaa ccatcagcg caatacttga acctctccc 3190
aggtaggggc aggaggagcc acatgagaga gggagaagga ccgcgtttac ctttagagtt 3250
ttgttttgtt ttttcctct gagtttgctg ttggtgcagg aataaggga aggcccaagg 3310
tatccaagcc tggggaaggg caggccagcc agcacctctg ccttctcagg gacaagagta 3370
gtcctttacc accctcactc tgoctgtccc ctctcctact ctacagcatt aaagactgtg 3420
ggaccagg 3438

```

<210> 112

<211> 1144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)...(907)

<400> 112

```

caaggatctg gaaccctgag cctcgaagcg gaggatccct gtgtcccagc cgggc 55
atg gcc gac ccc cac cag ctt ttc gat gac aca agt tca gcc cag agc 103
Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser

```


WO 00/29448

PCT/JP99/06412

173/233

1	5	10	15	
cgg ggc tat ggg gcc cag cgg gca cct ggt ggc ctg agt tat cct gca	151			
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala				
20	25	30		
gcc tct ccc acg ccc cat gca gcc ttc ctg gct gac ccg gtg tcc aac	199			
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn				
35	40	45		
atg gcc atg gcc tat ggg agc agc ctg gcc gcg cag ggc aag gag ctg	247			
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu				
50	55	60		
gtg gat aag aac atc gac cgc ttc atc ccc atc acc aag ctc aag tat	295			
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr				
65	70	75	80	
tac ttt gct gtg gac acc atg tat gtg ggc aga aag ctg ggc ctg ctg	343			
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu				
85	90	95		
ttc ttc ccc tac cta cac cag gac tgg gaa gtg cag tac caa cag gac	391			
Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp				
100	105	110		
acc ccg gtg gcc ccc cgc ttt gac gtc aat gcc ccg gac ctc tac att	439			
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile				
115	120	125		
cca gca atg gct ttc atc acc tac gtt ttg gtg gct ggt ctt gcg ctg	487			
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu				
130	135	140		
ggg acc cag gat agg ttc tcc cca gac ctc ctg ggg ctg caa gcg agc	535			
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser				
145	150	155	160	
tea gcc ctg gcc tgg ctg acc ctg gag gtg ctg gcc atc ctg ctc agc	583			
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser				
165	170	175		
ctc tat ctg gtc act gtc aac acc gac ctc acc acc atc gac ctg gtg	631			
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val				
180	185	190		
gcc ttc ttg gcc tac aaa tat gtc ggg atg att ggc ggg gtc ctc atg	679			

WO 00/29448

PCT/JP99/06412

174/233

Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met	
195 200 205	
ggc ctg ctc ttc ggg aag att ggc tac tac ctg gtg ctg ggc tgg tgc	727
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys	
210 215 220	
tgc gta gcc atc ttt gtg ttc atg atc cgg acg ctg cgg ctg aag atc	775
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile	
225 230 235 240	
ttg gca gac gca gca gct gag ggg gtc cgg gtg cgt ggg gcc cgg aac	823
Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn	
245 250 255	
cag ctg cgc atg tac ctg acc atg gcg gtg gcg gcg gcg cag cct atg	871
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met	
260 265 270	
ctc atg tac tgg ctc acc ttc cac ctg gtg cgg tgagcgcgcc cgtga	920
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg	
275 280	
acctcccgcg gctgctgctg ctgctggggg ccactgtggc cgcgaactc atctcctgcc	980
tgcaggcccc aaggctcacc ctgtctggcc acaggcaccg cctccatccc atgtcccgc	1040
cagccccgcc cccaacccaa ggtgctgaga gatctccagc tgcacaggcc accgccccag	1100
ggcgtggccg ctgttacaga aacaataaac cctgatgggc atgg	1144
<210> 113	
<211> 2339	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (253)...(1719)	
<400> 113	
ctttactcag ggcacagagg gtctctgcgg ccgtagcggc cggggctgcg gtagccactt	60
tagatttggg caaggacttt agattcgggc tctgttctgt ttccgcgctc ctgcttcctg	120
ccgaggctgg ccaggcagc cgcgcttcga aggacgccg cgggagctgc ggagcatgag	180
tggagtggca gtgctaacgg ctggtgtctc gcaactgttg cctgtgaagg tacgtgaagc	240
tgaaagcctg ga atg gct gga aag ggg tca tca ggc agg cgg ccc ctg	288

WO 00/29448

PCT/JP99/06412

175/233

Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu																
1					5					10						
ctg	ctg	ggg	ctg	ctg	gtg	gcc	gta	gcc	act	gtc	cac	ctg	gtc	atc	tgt	336
Leu	Leu	Gly	Leu	Leu	Val	Ala	Val	Ala	Thr	Val	His	Leu	Val	Ile	Cys	
15					20					25						
ccc	tac	acc	aaa	gtg	gag	gag	agc	ttc	aac	ctg	cag	gcc	aca	cat	gac	384
Pro	Tyr	Thr	Lys	Val	Glu	Glu	Ser	Phe	Asn	Leu	Gln	Ala	Thr	His	Asp	
30					35					40						
ctg	ctc	tac	cac	tgg	caa	gac	ctg	gag	cag	tac	gac	cat	ctt	gag	ttc	432
Leu	Leu	Tyr	His	Trp	Gln	Asp	Leu	Glu	Gln	Tyr	Asp	His	Leu	Glu	Phe	
45					50					55					60	
ccc	gga	gtc	gtc	ccc	agg	acg	ttc	ctc	ggg	cca	gtg	gtg	atc	gca	gtg	480
Pro	Gly	Val	Val	Pro	Arg	Thr	Phe	Leu	Gly	Pro	Val	Val	Ile	Ala	Val	
65					70					75						
ttc	tcc	agc	ccc	gcg	gtt	tac	gtg	ctt	tcg	ctg	tta	gaa	atg	tcc	aag	528
Phe	Ser	Ser	Pro	Ala	Val	Tyr	Val	Leu	Ser	Leu	Leu	Glu	Met	Ser	Lys	
80					85					90						
ttt	tac	tct	cag	cta	ata	gtt	aga	gga	gtg	ctt	gga	ctc	ggc	gtg	att	576
Phe	Tyr	Ser	Gln	Leu	Ile	Val	Arg	Gly	Val	Leu	Gly	Leu	Gly	Val	Ile	
95					100					105						
ttt	gga	ctc	tgg	acg	tta	caa	aag	gaa	gtg	aga	cgg	cac	ttc	ggg	gcc	624
Phe	Gly	Leu	Trp	Thr	Leu	Gln	Lys	Glu	Val	Arg	Arg	His	Phe	Gly	Ala	
110					115					120						
atg	gtg	gcc	acc	atg	ttc	tgc	tgg	gtg	acg	gcc	atg	cag	ttc	cac	ctg	672
Met	Val	Ala	Thr	Met	Phe	Cys	Trp	Val	Thr	Ala	Met	Gln	Phe	His	Leu	
125					130					135					140	
atg	ttc	tac	tgc	acg	cgg	aca	ctg	ccc	aat	gtg	ctg	gcc	ctg	cct	gta	720
Met	Phe	Tyr	Cys	Thr	Arg	Thr	Leu	Pro	Asn	Val	Leu	Ala	Leu	Pro	Val	
145					150					155						
gtc	ctg	ctg	gcc	ctc	gcg	gcc	tgg	ctg	cgg	cac	gag	tgg	gcc	cgc	ttc	768
Val	Leu	Leu	Ala	Leu	Ala	Ala	Trp	Leu	Arg	His	Glu	Trp	Ala	Arg	Phe	
160					165					170						
atc	tgg	ctg	tca	gcc	ttc	gcc	atc	atc	gtg	ttc	agg	gtg	gag	ctg	tgc	816
Ile	Trp	Leu	Ser	Ala	Phe	Ala	Ile	Ile	Val	Phe	Arg	Val	Glu	Leu	Cys	
175					180					185						

WO 00/29448

PCT/JP99/06412

176/233

ctg ttc ctg ggc ctc ctg ctg ctg ctg gcc ttg ggc aac cga aag gtt	864
Leu Phe Leu Gly Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val	
190 195 200	
tct gta gtc aga gcc ctt cgc cac gcc gtc ccg gca ggg atc ctc tgt	912
Ser Val Val Arg Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys	
205 210 215 220	
tta gga ctg acg gtt gct gtg gac tct tat ttt tgg cgg cag ctc act	960
Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr	
225 230 235	
tgg ccg gaa gga aag gtg ctt tgg tac aac act gtc ctg aac aaa agc	1008
Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser	
240 245 250	
tcc aac tgg ggg acc tcc ccg ctg ctg tgg tac ttc tac tca gcc ctg	1056
Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu	
255 260 265	
ccc cgc ggc ctg ggc tgc agc ctg ctc ttc atc ccc ctg ggc ttg gta	1104
Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val	
270 275 280	
gac aga agg acg cac gcg ccg acg gtg ctg gca ctg ggc ttc atg gca	1152
Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala	
285 290 295 300	
ctc tac tcc ctc ctg cca cac aag gag cta cgc ttc atc atc tat gcc	1200
Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala	
305 310 315	
ttc ccc atg ctc aac atc acg gct gcc aga ggc tgc tcc tac ctg ctg	1248
Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu	
320 325 330	
aat aac tat aaa aag tct tgg ctg tac aaa gca ggg tct ctg ctt gtg	1296
Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val	
335 340 345	
atc gga cac ctc gtg gtg aat gcc gcc tac tca gcc acg gcc ctg tat	1344
Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr	
350 355 360	
gtg tcc cat ttc aac tac cca ggt ggc gtc gca atg cag agg ctg cac	1392
Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His	

WO 00/29448

PCT/JP99/06412

178/233

<211> 1756

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)...(650)

<400> 114

```

gtgtgccttg ccctccttcc gcacagcccg ggtttccgct tccctccggg cgcgagaaga      60
ggggagccag gccgagcccc ggccctaccg ccgcgcgcgc c atg tgg ccc oca      113
                                     Met Trp Pro Pro
                                     1
gac ccc gac ccc gac ccg gac ccc gag cct gcc ggc ggc tcc cgt ccc      161
Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly Gly Ser Arg Pro
   5              10              15              20
ggc ccc gcg gtc ccc ggg ctc cgc gcc ctg ctg ccg gcg cgg gct ttc      209
Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro Ala Arg Ala Phe
               25              30              35
ctc tgc tct ctc aaa ggc cgc ctc ctg ctg gcc gag tcg ggt ctc tca      257
Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu Ser Gly Leu Ser
               40              45              50
ttc atc act ttt atc tgc tat gtg gcg tcc tca gca tct gcc ttc ctc      305
Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala Ser Ala Phe Leu
               55              60              65
aca gcg cct ctg ctg gag ttc ctg ctg gcc ttg tac ttc ctc ttt gct      353
Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr Phe Leu Phe Ala
               70              75              80
gat gcc atg cag ctg aat gac aag tgg cag gcc ttg tgc tgg ccc atg      401
Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu Cys Trp Pro Met
               85              90              95              100
atg gac ttc ctg cgc tgt gtc acc gcg gcc ctc atc tac ttt gct atc      449
Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile Tyr Phe Ala Ile
               105              110              115
tcc atc acg gcc atc gcc aag tac tcg gat ggg gct tcc aaa gcc gct      497
Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala Ser Lys Ala Ala
               120              125              130

```

179/233

ggg gtg ttt ggc ttc ttt gct acc atc gtg ttt gca act gat ttc tac 545
 Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala Thr Asp Phe Tyr
 135 140 145
 ctg atc ttt aac gac gtg gcc aaa ttc ctc aaa caa ggg gac tct gca 593
 Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln Gly Asp Ser Ala
 150 155 160
 gat gag acc aca gcc cac aag aca gaa gaa gag aat tcc gac tcg gac 641
 Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn Ser Asp Ser Asp
 165 170 175 180
 tct gac tgaaggcctg gcgggtgcct tggcaacctg agccacacag gcc 690
 Ser Asp

tccacccctg cgcctcacag gggctcgtgg cgttgaggcg gaggcctgga cttctgagtt 750
 gcagaggggg ctgcggacac agcaggcccc ctacagcctc aggttctgcc tgagcccagc 810
 ctaccaggct tgcccctcag ctcagcactg ttgaccacgc tgcgtatgag ggcattcttg 870
 gtatcccaact ccttctcccc atttctgtcc cacaggcctt cagcccttta acgtctctgc 930
 caaaaaccag cacaaggaga caaagcagag ccttgtctgt atctgggcag caggtgttcc 990
 atgtgtctag gtggcggggg tcgggggtct tctgtttcac taacaggaac aaagacagaa 1050
 accatgacag ggctgccccg ccaggccccg gtgggtttgt ctgcacttgg tgctcctgcc 1110
 cacaccagcc acttttgtga caatgacct tccaagaatc tttggttcaa ggagcaccag 1170
 ttccctottc attcttgaag cagggagaaa ttgaccttg ccttgtcgcc caggaagtgg 1230
 ggctcggcac ccataactaa cacctccac ccttggaac catgtcttct ggggtgaga 1290
 tgaccattct gggcttaaga ctgtttcaaa gaagagctca tagactgact ggtccagaag 1350
 acagagggta caacagtggc atcacagtga cagtgtcatg gggagctggg cgggccagc 1410
 caaacctcc ttcttcctag agcccagcca gcaggcagga gtctctggac cctcaggaca 1470
 gtgaacttcc agacctcagg gcaggtctat gggccactgc aggagatgag accagccttc 1530
 tgtgttcacc taacgattta tactgtgtat ctgtctttga tgggaattttg taacttttta 1590
 tattttttta tgcaaaagca gcttcttaac agatggcatt ttctgtgact ctaggcctca 1650
 caaaagagcc agagttctgg acccatgttt ggagcatttg tagccttatt ctcttgctg 1710
 tgaatctctt acctgaaaa aaagccataa tgaattaagc caaaag 1756

<210> 115

<211> 1418

<212> DNA

<213> Homo sapiens

WO 00/29448

PCT/JP99/06412

180/233

<220>

<221> CDS

<222> (149)...(703)

<400> 115

```

attggtccta gcggggggcc gggggcggac accggcgcgg ggccggagca gcgcggctca      60
ggctgcggga aagcgggtgcg cgtgcagcgg ggtgggtgcc ctggtccgcg ggcgagctcg      120
agcagccaac cccggggcgcg tcgggggcc atg gac ggc ctg agg cag cgc gtg      172
                                Met Asp Gly Leu Arg Gln Arg Val
                                1              5
gag cac ttc ctg gag caa agg aac ctg gtc acc gaa gtg ctg ggg gcg      220
Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu Val Leu Gly Ala
      10              15              20
ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg gct gca gga gcc      268
Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu Ala Ala Gly Ala
      25              30              35              40
gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac gga gcg tct ctg      316
Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr Gly Ala Ser Leu
                                45              50              55
ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat gcc tca atc aaa      364
Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr Ala Ser Ile Lys
                                60              65              70
gct atc gag agc cca agc aag gac gac gac act gtg tgg ctc acc tac      412
Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val Trp Leu Thr Tyr
                                75              80              85
tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc ttc agc gat cta      460
Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe Phe Ser Asp Leu
                                90              95              100
ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag tgc gcc ttc ctg      508
Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys Cys Ala Phe Leu
      105              110              115              120
ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct ctc atg ctg tat      556
Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala Leu Met Leu Tyr
                                125              130              135
cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac ggg gcc gta gac      604
Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His Gly Ala Val Asp

```


gaaaatggct caggtggact ccgggctgga gctgtcctgg gggagcttgt ttgcggcagc	60
ggctgctgct gccactgctg tgetgggggc ccggtcgcca ggcaaaaagc cctcccacgt	120
ttgagggggag tc atg agc cgt ttc ctg aat gtg tta aga agt tgg ctg	168
Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu	
1 5 10	
gtt atg gtg tcc atc ata gcc atg ggg aac acg ctg cag agc ttc cga	216
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg	

WO 00/29448

PCT/JP99/06412

182/233

15	20	25	
gac cac act ttt ctc tat gaa aag ctc tac act ggc aag cca aac ctt			264
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu			
30	35	40	
gtg aat ggc ctc caa gct cgg acc ttt ggg atc tgg acg ctg ctc tca			312
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser			
45	50	55	60
tca gtg att cgc tgc ctc tgt gcc att gac att cac aac aag acg ctc			360
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu			
65	70	75	
tat cac atc aca ctc tgg acc ttc ctc ctt gcc ctg ggg cat ttc ctc			408
Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu			
80	85	90	
tct gag ttg ttt gtc tat gga act gca gct ccc acg att ggc gtc ctg			456
Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu			
95	100	105	
gca ccc ctg atg gtg gca agt ttc tcc atc ctg ggt atg ctg gtc ggg			504
Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly			
110	115	120	
ctc cgg tat cta gaa gta gaa cca gta tcc aga cag aag aag aga aac			552
Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn			
125	130	135	140
tgaggcca gcattatcac ctccaggact ttctcgtttt ccaccttggc catcttcttc			610
cttctgtctc tctcctcttt aatttctttt ctattccatc atctgccctt ttattoactt			670
ttagcctctt tttttaattt ttaaaattta aagatatgca tactgaaaag tatataacat			730
gtacgtacaa tttaaagaat aattttaaag tgaatactac gtaactccat ccaagtcaag			790
aaattgccag cttctcggaa gcccaactgtg tctccttccc ctacctgcaa cctcttccag			850
gctccctttt ccagccttcc cctttttccc ttttattttc atgccttgat ttgacttggtg			910
tggtgggaac atgtgaacta tgaaacttaa acctgctgcc caccagagc agctgtgacc			970
aagggctgcc tcaaggggtt gtccacgcag gttgggctcc tctctgctgc tggaccaag			1030
actotgaacc ttccaaggga caggcagttc ttctaagaag ggctcccctg tgtgtgagca			1090
agaccacagc tctccttcta tctacagatg catgaggggtt ggaagagtct gggctgtttt			1150
tagaccttct ggtcagctgt atttgtgtaa caacttttgt aataaataga aaaaccctct			1210
g			1211

gtatccgcgg	ccgtagcagc	cgggctggtc	ctgctgcgag	ccggcggccc	ggagtggggc		60
ggcggcatgt	accttcacaca	ttgagtattc	agaaagaagt	gatctgaact	ctgaccattc		120
tttatggata	cattaagtca	aatataagag	tctgactact	tgacacactg	gctcgagcaa		180
ac atg aac gtt gga gtt gcc cac agt gaa gtg aat cca aat acc cgt							227
Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg							
1	5	10	15				
gtc atg aac agc cgg ggt atg tgg ctg aca tat gca ttg gga gtt ggc							275
Val Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly							
20	25	30					
ttg ctt cat att gtc tta ctc agc att ccc ttc ttc agt gtt cct gtt							323
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val							
35	40	45					
gct tgg act tta aca aat att ata cat aat ctg ggg atg tac gta ttt							371
Ala Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe							
50	55	60					
ttg cat gca gtg aaa gga aca cct ttc gaa act cct gac cag ggt aaa							419
Leu His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys							
65	70	75					
gca agg ctc cta act cat tgg gaa caa ctg gac tat gga gta cag ttt							467
Ala Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe							
80	85	90	95				
aca tct tca cgg aag ttt ttc aca att tct cca ata att cta tat ttt							515
Thr Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe							
100	105	110					
ctg gca agt ttc tat acg aag tat gat cca act cac ttc atc cta aac							563
Leu Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn							
115	120	125					

WO 00/29448

PCT/JP99/06412

184/233

aca gct tct ctc ctg agt gta cta att ccc aaa atg cca caa cta cat 611
Thr Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His

130 135 140

ggg gtt cgg atc ttt gga att aat aag tat tgaaatgttt tgaaactga 660
Gly Val Arg Ile Phe Gly Ile Asn Lys Tyr

145 150

aaaaaaatatt tacagctact gaattttctta taaggaagga gtgggttagta aactgcactg 720
tttctctgat aatgtgaaat gagaagtatt tacattggag ggccaatggc tggctcttca 780
agtgtgtttt tgaagtgcag atttccatta aatgatgcct ctgtttaata cacctggtag 840
atttctgaag aggggcttta taagcaggct gggcaggccc agcttataag ttaaagggca 900
tcacagttag ggtgttagtag ataaattcaa ggaaataaga gatttgaag aaactaggac 960
cagcttaact tataatgaat gggcattgtg ttaagaaaag aacatttcca gtcattcagc 1020
tgtgtgttatt taaagcagac ttacatgtaa accggaatcc tctctataca agtttattaa 1080
agattatttt tattaccgt 1099

<210> 118

<211> 3489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (227)...(748)

<400> 118

gcgtgcattt ttctggagaa ctgcatgcat catgctctct ctgtgtgcat tttcctggac 60
aaaagcccat agtgcctatc agattctcaa agggactcct gactccagaa agtttaaaaa 120
ccattaggct taaggaagca catacctact ctgtactcca gggaccagggt gggaacagct 180
gagtgcaggg agtggctttc tctttcagac cctctcccgg agcccc atg gct gcc 235

Met Ala Ala

1

ttc ctg ata cag acc aag gac aac ccc atg aag gcc gtg ggt gtg ctg 283
Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val Gly Val Leu

5 10 15

gcc ggc acc atg gcc acc gtc gtg gcc atc act gtc ctc atc tcc acc 331
Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu Ile Ser Thr

20 25 30 35

WO 00/29448

PCT/JP99/06412

185/233

gcc acc ttc tgg cgc aac aag aag tct aac aag gtc ctg cca atg cgg	379
Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu Pro Met Arg	
40 45 50	
cgg gtg ctc cgc aag cgg ccc agc cct gcg ccc cgc acc atc cgc att	427
Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr Ile Arg Ile	
55 60 65	
gag tgg ctc aag tcc aag agc acc aaa gcc gct acc aag ttc atg ctc	475
Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys Phe Met Leu	
70 75 80	
aaa gag aaa cct ccc aat gag aac tgt aac aac aac agc cca gaa agc	523
Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser Pro Glu Ser	
85 90 95	
tct ctg ctc ccg aga gct ccg gct ctc cct cca cca ccc agc gtg gcg	571
Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro Ser Val Ala	
100 105 110 115	
ccc agc act ggc gca gcc cag tgg acc gtg cct act gtc tct ggc tct	619
Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val Ser Gly Ser	
120 125 130	
ctc act ccg cag ccg acc caa ccc ccg cca aaa ccc aaa act atg gga	667
Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys Thr Met Gly	
135 140 145	
agc ccc gtc cag tca act ctg atc tct gag ctc aag caa aag ttt gag	715
Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln Lys Phe Glu	
150 155 160	
aag aag agt gtg cac aac aag gct tac ttc tagtgtatgc cctat	760
Lys Lys Ser Val His Asn Lys Ala Tyr Phe	
165 170	
gaccccccat ctttctctcg cccctgaccc ccaccaccct gctgctcgga ctatgctccc	820
cttctctctgc tcttaaggt cactgacccc tgttttgcac aatggtataa tccccactgt	880
cctcatctct accgccacct tctggcgcaa caagaagttg cgtcttgaca gggctctagt	940
cagggccttg ggcaagacat tgggctctag gatgcaattg gcaaatacgt ccccgttact	1000
caaatccttg gcaactactac aatgccctcc attcttcagg gctgagaatt gacgagaagc	1060
cagctcacc atcccagacc tcacagtcctc tcaggtteta ctgggatctc atcatcatcc	1120
ttagtcaagc agcagggccc tggccacgtg gagcaacact gactagaatc tggatcctga	1180
cgcctgcagc tgagagcagg agcaggaaaa ggaggctcag cactgtctca ggctggaggt	1240

WO 00/29448

PCT/JP99/06412

186/233

cagcgaacct	cgtgggctgt	aggaaagcaa	atgtaggtaa	ggggagagca	aggatgcaca	1300
gaaaacacac	tgactgtggg	actgtgccag	gatgcatttg	gaaagataga	gcattctgtc	1360
tgggcagaga	ctgtggaccc	tggtatgcc	acgtgggaca	gaggacacag	aggtggaaga	1420
ttgatcttgc	caagagttag	ggcagatgtc	tccagccagg	actgccctga	gccgcaaaat	1480
gtcaaagctg	gagctataga	ggtagcccta	aaggcaacta	gaagagcatc	agggctgctc	1540
tctgaggagc	tgccccacca	gccatccttg	aagagacaat	tcagggcagt	tgatgaatat	1600
cagggctgag	atgtggttag	acttccgttt	ttatccagct	cttttctca	catcgcgtaa	1660
ccttgggaaa	gctgtttaaa	gtcgtgatc	atcctcttcc	tcactctgaa	atgaagaaag	1720
taggccctgt	ctacctcaca	tgcaggtcta	gggtgaggat	tgaagaaaat	agtgtgtatg	1780
agggctttaa	ccaagtgcaa	agcggcatga	atgcaaagta	tttttctgca	gccagttct	1840
gtgggtgcag	ctcttccaga	aagtattagg	agcctcacat	ctactctgcc	aagcgcccca	1900
gcaggcactg	tgtgtggctt	aggggtacc	actggatgat	ggcattgccg	tgaactcacac	1960
acctctactt	ctgttcttcc	ctcactccat	ccccgtacc	gtcctggcca	gctaccgtca	2020
gagagaacca	gagctccaag	tctttaattt	gccaagatga	agaaaatgag	ttctcaagga	2080
gggaatgctt	tgtttgaggc	cacacagcag	gttggttagca	aagatcttgt	ctagccaggg	2140
cagcccttat	cagcttgtga	caaccttccc	caggacagaa	gtcatacaag	gcctctgggg	2200
ttaatacaaa	taggttgtgc	cctgttttaa	ggaacctgct	atcaggaaat	ctacatgtgt	2260
gcacagagag	agaaaagtag	aacagttctt	tgcatttggc	tctacttact	aacaacccct	2320
ctagaataca	ttggtgattt	catttaaaga	gattgtatgc	atttgtggct	ttcctgattt	2380
ctgagtctgt	gtttggaggt	gttactgaga	tgtgccagtg	tgcagaatcc	ttgctggggg	2440
ttctacagtc	cccaacgtga	acagtattaa	gcaagagggtg	gactcgagca	atccaggagc	2500
ccagactgag	caaataagta	ctttccagcc	tgtgtttcag	gagaggactg	tgttgatca	2560
tgttggccct	ccacagggaa	tacagcatcc	ttacagcttg	catgcaatca	acctcttttg	2620
taaatggaaa	ataaagtctg	ttacccaaaag	gccatgctga	tccctgtctc	cctgttttca	2680
tttatgtttg	ctgacctgtg	gagaccagtc	tttctgacac	acagtgaagc	tcaacttgcc	2740
tcctggctgc	ttcagcaggt	ggatccattc	ttcgaccccc	agatgtgact	ctaaagaagg	2800
ctgaaaattt	ttgtccaaat	tgccatgcag	atatcttgaa	cagcaggaca	tttgagggcc	2860
ttgtctactg	gacttttctc	ccaaacagga	caagcccagg	cagggctgca	tggagaggaa	2920
tggaaacctg	agctagaatt	aattgcccac	tctcccaccc	taccagtgc	gcccggcaag	2980
ggcaggaatt	gggaggccta	gggtgggcat	gaaagcttgg	gaagcactgt	cgtctctcag	3040
acaggcgtcc	taaagacctc	taggctggaa	gcttgggctt	gcaagtggat	ccgggaccga	3100
gggtggtctc	ttggacaacc	ccaggaactt	ggaccaaggc	agagccaatc	ttgcaaaactg	3160
gccatggatg	gggaagtgcc	cggtagccag	catgagccac	actaggaaag	aggaggaggg	3220
tgcagccaaa	cttaaggcac	cggcaagtgt	tgtcagcact	ggaggagacc	ccgccagtgg	3280
ggtgaggcca	gccaaagccc	tgtgttacga	atggtggggc	aaggggctgt	ctgctaggtc	3340

WO 00/29448

PCT/JP99/06412

187/233

cagtaggaca ggcagagctc caggctggca ccattggtagg cctccagga aagagctggg 3400
aggcaggaat ggcacactgg gcaggcttgc ccattcctgg ccctgagaat ggagctgtag 3460
cctcatggac aataaatgga tgtgacacc 3489

<210> 119

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)...(252)

<400> 119

ctgacggacg cttcggccgt aacg atg atc gga gac atc ctg ctg ttc ggg 51
Met Ile Gly Asp Ile Leu Leu Phe Gly

1 5

acg ttg ctg atg aat gcc ggg gcg gtg ctg aac ttt aag ctg aaa aag 99
Thr Leu Leu Met Asn Ala Gly Ala Val Leu Asn Phe Lys Leu Lys Lys

10 15 20 25

aag gac acg cag ggc ttt ggg gag gag tcc agg gag ccc agc aca ggt 147
Lys Asp Thr Gln Gly Phe Gly Glu Glu Ser Arg Glu Pro Ser Thr Gly

30 35 40

gac aac atc cgg gaa ttc ttg ctg agc ctc aga tac ttt cga atc ttc 195
Asp Asn Ile Arg Glu Phe Leu Leu Ser Leu Arg Tyr Phe Arg Ile Phe

45 50 55

atc gcc ctg tgg aac atc ttc atg atg ttc tgc atg att gtg ctg ttc 243
Ile Ala Leu Trp Asn Ile Phe Met Met Phe Cys Met Ile Val Leu Phe

60 65 70

ggc tct tgaatcccag cgatgaaacc aggaactcac tttcccggga tgccgagtct c 300
Gly Ser

75

cattcctcca ttcctgatga cttcaagaat gtttttgacc agaaaaccga caaccttccc 360

agaaagtcca agctcgtggt ggggtgaaaa gtgttcgcca aggtgtgcat ggtttcccag 420

ccacgtccct gttttcaaag atagtctcac tttggtctct gaattgaaat gctgtctact 480

gaaagggttt caggagcgtt tatgtaaggg gctgtgatga aattgcattc cccatagata 540

aaagaaaaat catttctatc cagagatctg agcagaagga ttggcttggt agtttaacac 600

188/233

agccgtgttt ttggacattc agtgttactt gctgagtctg acagcctctg ggcccggcca 660
 ggggccctgt taacaaactg ctttcacatc ccaacagggt ctgcttggee actcagtga 720
 gctgcgatta accctaaagg ctttaaggaa cggggcacct gtaacagaga caccagcett 780
 cctgtataga cactaaattg ttagcaagag tgttgagcta gttcctggtg aagtgtttcc 840
 acagaagaca tgtggagcag ttgtggggat attaagggaa actttcctct gcottgaccc 900
 ctttggtaaa taaaatgact ttgggagcca t 931

<210> 120

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)...(547)

<400> 120

gtccccgag ttcggagcct aggagccccc cgcggctgcg ggcaggtgc cctcggcctg 60
 agtcggg atg gag ctg cct gct gtg aac ctg aag gtg att etc cta ggt 109
 Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly
 1 5 10
 cac tgg ctg ctg aca acc tgg ggc tgc att gta ttc tca ggc tcc tat 157
 His Trp Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr
 15 20 25 30
 gcc tgg gcc aac ttc acc atc ctg gcc ttg ggc gtg tgg gct gtg gct 205
 Ala Trp Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala
 35 40 45
 cag cgg gac tcc atc gac gcc ata agc atg ttt ctg ggt ggc ttg ctg 253
 Gln Arg Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu
 50 55 60
 gcc acc atc ttc ctg gac atc gtg cac atc agc atc ttc tac ccg cgg 301
 Ala Thr Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg
 65 70 75
 gtc agc etc acg gac acg ggc cgc ttt ggc gtg ggc atg gcc atc etc 349
 Val Ser Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu
 80 85 90
 agc ttg ctg etc aag ccg etc tcc tgc tgc ttc gtc tac cac atg tac 397

WO 00/29448

PCT/JP99/06412

189/233

Ser	Leu	Leu	Leu	Lys	Pro	Leu	Ser	Cys	Cys	Phe	Val	Tyr	His	Met	Tyr		
95						100					105				110		
cgg	gag	cgc	ggg	ggt	gag	ctc	ctg	gtc	cac	act	ggt	ttc	ctt	ggg	tct	445	
Arg	Glu	Arg	Gly	Gly	Glu	Leu	Leu	Val	His	Thr	Gly	Phe	Leu	Gly	Ser		
			115						120				125				
tct	cag	gac	cgt	agt	gcc	tac	cag	acg	att	gac	tca	gca	gag	gcg	ccc	493	
Ser	Gln	Asp	Arg	Ser	Ala	Tyr	Gln	Thr	Ile	Asp	Ser	Ala	Glu	Ala	Pro		
			130						135				140				
gca	gat	ccc	ttt	gca	gtc	cca	gag	ggc	agg	agt	caa	gat	gcc	cga	ggg	541	
Ala	Asp	Pro	Phe	Ala	Val	Pro	Glu	Gly	Arg	Ser	Gln	Asp	Ala	Arg	Gly		
			145						150				155				
tac	tgaagccagc	cacgctgcgc	ccggccctgc	cccgggcctt	cctcgtgcct	gggagg	600										
Tyr																	
tcgttctagg	gatgctcctg	acctccgtct	cttgaccta	agatggaatg	tgtccccagc	660											
tcagggattg	cctgaaccaa	gaggccagga	gccccatgg	gccgccagc	accatgcaca	720											
ctcctgtccc	gaactccctg	aggcctcccc	tcccttcagg	gcacccactg	gttcccaggc	780											
tggaaccagg	gtctctcttt	acctcctacc	ccatggtggc	accacagagg	ccctcagccg	840											
agtcctgcct	gagtgttgca	agctcaggcc	tttaaggact	gctgatgcc	cctcaggcct	900											
cccccaagtt	tgctgggctt	tggtggaagc	cctgagagct	tcaggctcctg	ctcagcccca	960											
ggagcagtct	ggcatgggag	tgaggccccg	tccttctcac	tgcttggtca	catggtgcct	1020											
agggatgcag	ggctggaggc	cagaggtgtc	agcaacactg	tgaccaccca	caacctccag	1080											
cctccctttt	cagagcacag	cattaaagtt	tggggaattc	tgt		1123											

<210> 121

<211> 636

<212> PRT

<213> Homo sapiens

<400> 121

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu		
1				5					10				15				
Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp		
			20					25					30				
Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln		
			35					40					45				

WO 00/29448

PCT/JP99/06412

190/233

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe			
50	55	60	
Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp			
65	70	75	80
Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr			
85	90	95	
Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser			
100	105	110	
Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly			
115	120	125	
Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp			
130	135	140	
Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu			
145	150	155	160
Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp			
165	170	175	
His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro			
180	185	190	
Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp			
195	200	205	
Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile			
210	215	220	
Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly			
225	230	235	240
Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu			
245	250	255	
Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro			
260	265	270	
Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly			
275	280	285	
Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala			
290	295	300	
Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly			
305	310	315	320
Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys			

WO 00/29448

PCT/JP99/06412

191/233

	325		330		335
Ser	Asp	Val	Thr	Ser	Tyr
Asp	Tyr	Asp	Tyr	Asp	Ala
Val	Leu	Thr	Glu	Ala	Gly
340			345		350
Asp	Tyr	Thr	Ala	Lys	Tyr
Met	Lys	Leu	Arg	Asp	Phe
Phe	Gly	Ser	Ile		
355			360		365
Ser	Gly	Ile	Pro	Leu	Pro
Pro	Pro	Pro	Pro	Asp	Leu
Leu	Pro	Lys	Met	Pro	
370			375		380
Tyr	Glu	Pro	Leu	Thr	Pro
Val	Leu	Tyr	Leu	Ser	Leu
Trp	Asp	Ala	Leu		
385			390		395
					400
Lys	Tyr	Leu	Gly	Glu	Pro
Ile	Lys	Ser	Glu	Lys	Pro
Ile	Asn	Met	Glu		
405			410		415
Asn	Leu	Pro	Val	Asn	Gly
Gly	Asn	Gly	Gln	Ser	Phe
Gly	Tyr	Ile	Leu		
420			425		430
Tyr	Glu	Thr	Ser	Ile	Thr
Ser	Ser	Gly	Ile	Leu	Ser
Gly	His	Val	His		
435			440		445
Asp	Arg	Gly	Gln	Val	Phe
Val	Asn	Thr	Val	Ser	Ile
Gly	Phe	Leu	Asp		
450			455		460
Tyr	Lys	Thr	Thr	Lys	Ile
Ala	Val	Pro	Leu	Ile	Gln
Gly	Tyr	Thr	Val		
465			470		475
					480
Leu	Arg	Ile	Leu	Val	Glu
Asn	Arg	Gly	Arg	Val	Asn
Tyr	Gly	Glu	Asn		
485			490		495
Ile	Asp	Asp	Gln	Arg	Lys
Gly	Leu	Ile	Gly	Asn	Leu
Tyr	Leu	Asn	Asp		
500			505		510
Ser	Pro	Leu	Lys	Asn	Phe
Arg	Ile	Tyr	Ser	Leu	Asp
Met	Lys	Lys	Ser		
515			520		525
Phe	Phe	Gln	Arg	Phe	Gly
Leu	Asp	Lys	Trp	Ser	Ser
Leu	Pro	Glu	Thr		
530			535		540
Pro	Thr	Leu	Pro	Ala	Phe
Phe	Leu	Gly	Ser	Leu	Ser
Ile	Ser	Ser	Thr		
545			550		555
					560
Pro	Cys	Asp	Thr	Phe	Leu
Lys	Leu	Glu	Gly	Trp	Glu
Lys	Gly	Val	Val		
565			570		575
Phe	Ile	Asn	Gly	Gln	Asn
Leu	Gly	Arg	Tyr	Trp	Asn
Ile	Gly	Pro	Gln		
580			585		590
Lys	Thr	Leu	Tyr	Leu	Pro
Gly	Pro	Trp	Leu	Ser	Ser
Gly	Ile	Asn	Gln		
595			600		605

WO 00/29448

PCT/JP99/06412

192/233

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620
 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 122
 <211> 318
 <212> PRT
 <213> Homo sapiens
 <400> 122

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1 5 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
 145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala

193/233

195	200	205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly		
210	215	220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val		
225	230	235
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe		
245	250	255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu		
260	265	270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His		
275	280	285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg		
290	295	300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp		
305	310	315

<210> 123

<211> 82

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Phe Thr Leu Tyr Ser Leu Leu Gln Ala Ala Leu Leu Cys Val		
1	5	10
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly		
20	25	30
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile		
35	40	45
Lys Ser Gln Leu Met Asn Leu Ile Arg Ser Val Arg Thr Val Met Arg		
50	55	60
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu		
65	70	75
Phe Gly		80

<210> 124

WO 00/29448

PCT/JP99/06412

194/233

<211> 247

<212> PRT

<213> Homo sapiens

<400> 124

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
1 5 10 15
Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
20 25 30
Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
35 40 45
Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
50 55 60
Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
65 70 75 80
Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
85 90 95
Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
100 105 110
Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala Gly Lys
115 120 125
Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Gln Ala
130 135 140
Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala Ala Asp
145 150 155 160
Gln Ala Gly Lys Glu Val Glu Lys Leu Gly Gln Gly Ala His His Ala
165 170 175
Ala Gly Gln Ala Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn
180 185 190
Gln Ala Ser Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser
195 200 205
Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
210 215 220
Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
225 230 235 240
Ser Val Ala Asn Ile Met Pro

WO 00/29448

PCT/JP99/06412

195/233

245

<210> 125

<211> 206

<212> PRT

<213> Homo sapiens

<400> 125

```

Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg Glu Asp Glu Lys
  1              5              10              15
Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys Asp Thr Glu Asn
              20              25              30
Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala Leu Leu Leu Leu
              35              40              45
Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala Ser Phe Ala Leu
              50              55              60
Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala Val Lys Leu Gly
              65              70              75              80
Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly Gly Leu Gly Gly
              85              90              95
Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys Gly Val Leu Ala
              100             105             110
Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg Val Thr Arg Leu
              115             120             125
Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly Arg Arg Leu Leu
              130             135             140
Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly Gly Met Gly Glu
              145             150             155             160
Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala Ala Trp Gly Val
              165             170             175
Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu Gly Gly Trp Gly
              180             185             190
Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys Asp Leu
              195             200             205

```

<210> 126

WO 00/29448

PCT/JP99/06412

196/233

<211> 432

<212> PRT

<213> Homo sapiens

<400> 126

```

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
  1             5             10             15
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
          20             25             30
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
          35             40             45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
          50             55             60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
          65             70             75             80
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
          85             90             95
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
          100            105            110
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
          115            120            125
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
          130            135            140
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
          145            150            155            160
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
          165            170            175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
          180            185            190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
          195            200            205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
          210            215            220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
          225            230            235            240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

```


Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys
1 5 10 15
Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala
20 25 30
Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly
35 40 45

WO 00/29448

PCT/JP99/06412

198/233

Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly
50 55 60
Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
65 70 75 80
Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
85 90 95
Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
100 105 110
Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
115 120 125
Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
130 135 140
Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
145 150 155 160
Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu Leu Arg Arg His
165 170 175
Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg Thr Ser Pro Gln
180 185 190
Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala Ser Gln Ala Ala
195 200 205
Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys Arg Pro Ala Thr
210 215 220
Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp Trp Ala Ser Leu
225 230 235 240
Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala Ala Trp Ala Ser
245 250 255
Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val Glu Asn Gly Leu
260 265 270
Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly Pro Gly Leu Thr
275 280 285
Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu Gly Pro Leu Gly
290 295 300
Val Arg
305

WO 00/29448

PCT/JP99/06412

199/233

<210> 128

<211> 555

<212> PRT

<213> Homo sapiens

<400> 128

```

Met Gln Ser Cys Glu Ser Ser Gly Asp Ser Ala Asp Asp Pro Leu Ser
  1              5              10              15
Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg Val Val Val Ile Gly Ala
      20              25              30
Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala Leu Leu Glu Gln Gly Phe
      35              40              45
Thr Asp Val Thr Val Leu Glu Ala Ser Ser His Ile Gly Gly Arg Val
      50              55              60
Gln Ser Val Lys Leu Gly His Ala Thr Phe Glu Leu Gly Ala Thr Trp
      65              70              75              80
Ile His Gly Ser His Gly Asn Pro Ile Tyr His Leu Ala Glu Ala Asn
      85              90              95
Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu Arg Ser Val Gly Arg Ile
      100             105             110
Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys Tyr Leu Thr Asn His Gly
      115             120             125
Arg Arg Ile Pro Lys Asp Val Val Glu Glu Phe Ser Asp Leu Tyr Asn
      130             135             140
Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe Arg His Asp Lys Pro Val
      145             150             155             160
Asn Ala Glu Ser Gln Asn Ser Val Gly Val Phe Thr Arg Glu Glu Val
      165             170             175
Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp Pro Glu Ala Thr Lys Arg
      180             185             190
Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu Lys Val Glu Ser Cys Glu
      195             200             205
Ser Ser Ser His Ser Met Asp Glu Val Ser Leu Ser Ala Phe Gly Glu
      210             215             220
Trp Thr Glu Ile Pro Gly Ala His His Ile Ile Pro Ser Gly Phe Met
      225             230             235             240

```

WO 00/29448

PCT/JP99/06412

200/233

Arg Val Val	Glu Leu Leu	Ala Glu Gly	Ile Pro Ala	His Val Ile	Gln
	245		250		255
Leu Gly Lys	Pro Val Arg	Cys Ile His	Trp Asp Gln	Ala Ser Ala	Arg
	260		265		270
Pro Arg Gly	Pro Glu Ile	Glu Pro Arg	Gly Glu Gly	Asp His Asn	His
	275		280		285
Asp Thr Gly	Glu Gly Gly	Gln Gly Gly	Glu Glu Pro	Arg Gly Gly	Arg
	290		295		300
Trp Asp Glu	Asp Glu Gln	Trp Ser Val	Val Val Glu	Cys Glu Asp	Cys
305		310		315	320
Glu Leu Ile	Pro Ala Asp	His Val Ile	Val Thr Val	Ser Leu Gly	Val
	325		330		335
Leu Lys Arg	Gln Tyr Thr	Ser Phe Phe	Arg Pro Gly	Leu Pro Thr	Glu
	340		345		350
Lys Val Ala	Ala Ile His	Arg Leu Gly	Ile Gly Thr	Thr Asp Lys	Ile
	355		360		365
Phe Leu Glu	Phe Glu Glu	Pro Phe Trp	Gly Pro Glu	Cys Asn Ser	Leu
	370		375		380
Gln Phe Val	Trp Glu Asp	Glu Ala Glu	Ser His Thr	Leu Thr Tyr	Pro
385		390		395	400
Pro Glu Leu	Trp Tyr Arg	Lys Ile Cys	Gly Phe Asp	Val Leu Tyr	Pro
	405		410		415
Pro Glu Arg	Tyr Gly His	Val Leu Ser	Gly Trp Ile	Cys Gly Glu	Glu
	420		425		430
Ala Leu Val	Met Glu Lys	Cys Asp Asp	Glu Ala Val	Ala Glu Ile	Cys
	435		440		445
Thr Glu Met	Leu Arg Gln	Phe Thr Gly	Asn Pro Asn	Ile Pro Lys	Pro
	450		455		460
Arg Arg Ile	Leu Arg Ser	Ala Trp Gly	Ser Asn Pro	Tyr Phe Arg	Gly
465		470		475	480
Ser Tyr Ser	Tyr Thr Gln	Val Gly Ser	Ser Gly Ala	Asp Val Glu	Lys
	485		490		495
Leu Ala Lys	Pro Leu Pro	Tyr Thr Glu	Ser Ser Lys	Thr Ala Pro	Met
	500		505		510
Gln Val Leu	Phe Ser Gly	Glu Ala Thr	His Arg Lys	Tyr Tyr Ser	Thr

WO 00/29448

PCT/JP99/06412

201/233

515	520	525
Thr His Gly Ala Leu Leu Ser Gly Gln Arg Glu Ala Ala Arg Leu Ile		
530	535	540
Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly Thr		
545	550	555

<210> 129

<211> 250

<212> PRT

<213> Homo sapiens

<400> 129

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg		
1	5	10
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu		
20	25	30
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser		
35	40	45
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln		
50	55	60
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg		
65	70	75
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu		
85	90	95
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu		
100	105	110
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln		
115	120	125
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn		
130	135	140
Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln		
145	150	155
Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu		
165	170	175
Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu		
180	185	190

Met	Gln	Ala	Pro	Ala	Phe	Arg	Asp	Lys	Lys	Gln	Gly	Val	Ser	Ala	Lys
1				5					10					15	
Asn	Gln	Gly	Ala	His	Asp	Pro	Asp	Tyr	Glu	Asn	Ile	Thr	Leu	Ala	Phe
			20					25					30		
Lys	Asn	Gln	Asp	His	Ala	Lys	Gly	Gly	His	Ser	Arg	Pro	Thr	Ser	Gln
		35						40				45			
Val	Pro	Ala	Gln	Cys	Arg	Pro	Pro	Ser	Asp	Ser	Thr	Gln	Val	Pro	Cys
	50					55					60				
Trp	Leu	Tyr	Arg	Ala	Ile	Leu	Ser	Leu	Tyr	Ile	Leu	Leu	Ala	Leu	Ala
65					70					75				80	
Phe	Val	Leu	Cys	Ile	Ile	Leu	Ser	Ala	Phe	Ile	Met	Val	Lys	Asn	Ala
				85					90					95	
Glu	Met	Ser	Lys	Glu	Leu	Leu	Gly	Phe	Lys	Arg	Glu	Leu	Trp	Asn	Val
			100					105					110		
Ser	Asn	Ser	Val	Gln	Ala	Cys	Glu	Glu	Arg	Gln	Lys	Arg	Gly	Trp	Asp
		115						120				125			
Ser	Val	Gln	Gln	Ser	Ile	Thr	Met	Val	Arg	Ser	Lys	Ile	Asp	Arg	Leu
	130					135					140				
Glu	Thr	Thr	Leu	Ala	Gly	Ile	Lys	Asn	Ile	Asp	Thr	Lys	Val	Gln	Lys
145					150				155					160	
Ile	Leu	Glu	Val	Leu	Gln	Lys	Met	Pro	Gln	Ser	Ser	Pro	Gln		

WO 00/29448

PCT/JP99/06412

203/233

165

170

<210> 131

<211> 1908

<212> DNA

<213> Homo sapiens

<400> 131

atgaccacgt	ggagcctccg	gcggaggccg	gcccgcacgc	tgggactcct	gctgctggtc	60
gtcttgggct	tcctggtget	tcgcaggctg	gactggagca	ccctggcccc	tctgcggtc	120
cgccatcgac	agctggggct	gcaggccqag	ggetggaact	tcctgctgga	ggattccacc	180
ttctggatct	tcgggggctc	catccactat	ttccgtgtgc	ccaggagta	ctggagggac	240
cgctgctga	agatgaaggc	ctgtggcttg	aacaccctca	ccacctatgt	tccgtggaac	300
ctgcatgagc	cagaaagagg	caaatttgac	ttctctggga	acctggacct	ggaggccttc	360
gtcctgatgg	ccgcagagat	cggtctgtgg	gtgattctgc	gtccaggccc	ctacatctgc	420
agtgagatgg	acctcggggg	cttgcccagc	tggctactcc	aagacctgg	catgaggctg	480
aggacaactt	acaagggtct	caccgaagca	gtggaccttt	atcttgacca	cctgatgtcc	540
aggggtggtg	cactccagta	caagcgtggg	ggacctatca	ttgccgtgca	ggtggagaat	600
gaatatggtt	cctataataa	agaccccgca	tacatgccct	acgtcaagaa	ggcactggag	660
gaccgtggca	ttgtggaact	gctcctgact	tcagacaaca	aggatgggct	gagcaagggg	720
attgtccagg	gagtcttggc	caccatcaac	ttgcagtcaa	cacacgagct	gcagctactg	780
accacctttc	tcttcaacgt	ccaggggact	cagcccaaga	tggatgatga	gtactggacg	840
gggtggtttg	actcgtgggg	aggccctcac	aatatcttgg	attctctctg	ggttttgaaa	900
accgtgtctg	ccattgtgga	cgccggctcc	tccatcaacc	tctacatgtt	ccacggaggc	960
accaactttg	gcttcatgaa	tggagccatg	cacttccatg	actacaagtc	agatgtcacc	1020
agctatgact	atgatgctgt	gctgacagaa	gcgggagatt	acacggccaa	gtacatgaag	1080
cttcgagact	tcttcggctc	catctcaggc	atccctctcc	ctccccacc	tgacctctct	1140
cccaagatgc	cgtatgagcc	cttaacgcca	gtcttgtacc	tgtctctgtg	ggacgccctc	1200
aagtacctgg	gggagccaat	caagtctgaa	aagcccatca	acatggagaa	cctgccagtc	1260
aatgggggaa	atggacagtc	cttcgggtac	attctctatg	agaccagcat	cacctcgtct	1320
ggcatcctca	gtggccacgt	gcctgatcgg	gggcagggtg	ttgtgaacac	agtatccata	1380
ggattcttgg	actacaagac	aacgaagatt	gctgtccccc	tgatccaggg	ttacaccgtg	1440
ctgaggatct	tgggtggagaa	tcgtggggga	gtcaactatg	gggagaatat	tgatgaccag	1500
cgcaaaggct	taattggaaa	tctctatctg	aatgattcac	ccctgaaaaa	cttcagaatc	1560
tatagcctgg	atatgaagaa	gagcttcttt	cagaggttcg	gcctggacaa	atggagtccc	1620
ctcccagaaa	cacccacatt	acctgctttc	ttcttgggta	gcttgtccat	cagctccacc	1680

WO 00/29448

PCT/JP99/06412

204/233

ccttgtgaca cctttctgaa gctggagggc tgggagaagg gggttgtatt catcaatggc	1740
cagaaccttg gacgttactg gaacattgga cccagaaga cgtttacct cccaggtccc	1800
tggttgagca gcggaatcaa ccaggtcatc gtttttgagg agacgatggc gggccctgca	1860
ttacagttca cggaaacccc ccacctgggc aggaaccagt acattaag	1908

<210> 132

<211> 954

<212> DNA

<213> Homo sapiens

<400> 132

atggttgagc tcatgttccc gctgttgetc ctcctttctgc ccttccttct gtatatgget	60
gcgccccaaa tcaggaaaat gctgtccagt ggggtgtgta catcaactgt tcagcttctc	120
gggaaagtag ttgtggtcac aggagctaat acagggtatcg ggaaggagac agccaaagag	180
ctggctcaga gaggagctcg agtatattta gcttgccggg atgtggaaaa gggggaattg	240
gtggccaaag agatccagac cacgacaggg aaccagcagg tgttggtgcg gaaactggac	300
ctgtctgata ctaagtctat tcgagctttt gctaagggtc tottagctga ggaaaagcac	360
ctccacgttt tgatcaacaa tgcaggagtg atgatgtgtc cgtactcgaa gacagcagat	420
ggctttgaga tgcacatagg agtcaaccac ttgggtcact tcctcctaac ccatctgctg	480
ctagagaaac taaaggaatc agcccatca aggatagtaa atgtgtcttc cctcgcacat	540
cacctgggaa ggatccactt ccataacctg caggggcgaga aattctacaa tgcaggcctg	600
gcctactgtc acagcaagct agccaacatc ctcttcaccc aggaactggc cgggagacta	660
aaaggctctg gcgttacgac gtattctgta caccctggca cagtccaatc tgaactgggt	720
cggcaactcat ctttcatgag atggatgtgg tggcttttct cttttttcat caagactcct	780
cagcagggag cccagaccag cctgcactgt gccttaacag aaggctctga gattctaagt	840
gggaatcatt tcagtgactg tcatgtggca tgggtctctg cccaagctcg taatgagact	900
atagcaaggc ggctgtggga cgtcagttgt gacctgctgg gcctcccaat agac	954

<210> 133

<211> 246

<212> DNA

<213> Homo sapiens

<400> 133

atggccttta ccctgtactc actgctgcag gcagccctgc tctgcgtcaa cgccatcgca	60
gtgctgcacg aggagcgatt cctcaagaac attggctggg gaacagacca ggggaattgg	120
ggatttgag aagagccggg aattaaatca cagctaataga acctatttcg atctgtaaga	180

WO 00/29448

PCT/JP99/06412

205/233

accgtgatga gagtgccatt gataatagta aactcaattg caattgtgtt acttttatta 240
tttgga 246

<210> 134

<211> 741

<212> DNA

<213> Homo sapiens

<400> 134

atgcatcttg cacgtctggt cggtcctgc tccctccttc tgetactggg ggccctgtct 60
ggatggggcg ccagcgatga cccattgag aaggctcattg aagggatcaa ccgagggctg 120
agcaatgcag agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 180
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag ccacaccggc 240
aaggagtgg acaaaggcgt ccaggggctc aaccacggca tggacaaggt tgcccatgag 300
atcaaccatg gtattggaca agcaggaaag gaagcagaga agcttggcca tgggggtcaac 360
aacgtgctg gacaggccgg gaaggaagca gacaaagcgg tccaaggggt ccacactggg 420
gtccaccagg ctgggaagga agcagagaaa ctgggccaag gggtaacca tgctgctgac 480
caggctggaa aggaagtgg gaagcttggc caaggtgcc accatgctgc tggccaggcc 540
gggaaggagc tgcagaatgc tcataatggg gtcaaccaag ccagcaagga ggccaaccag 600
ctgctgaatg gcaaccatca aagcggatct tccagccatc aaggaggggc cacaaccacg 660
ccgttagcct ctggggcctc ggtcaaacag cctttcatca accttccgc cctgtggagg 720
agcgtcgcca acatcatgcc c 741

<210> 135

<211> 618

<212> DNA

<213> Homo sapiens

<400> 135

atggccccc gccacctgc agtgcgagg atgagggag atgagaagcc cctgggtgctg 60
gagatgctga aggcggcgt gaaggacacg gaaaaccgcg tggccctcca tgccctgaca 120
cggccgccc ccctgctcct cctggcgccg gccagcagcg gcctgcgctt tgctcctggct 180
tccttcgccc tggccctcct cctgcgggtg ttcttggtg tggccgccc gaagctgggc 240
ctgcggggcc gatggggctc gctgcctccg ccgggtggcc tggggggccc ctgggtggcc 300
gtgcggggct ccggtgacgt gtgtggggtc ctggtctctg cccctggcac aaatgcaggg 360
gacggggccc gggtaaccgc cctgtctgtc tctcgtggc accgcgccc gggcgtgggc 420
aggaggctgc tggccttcgc ggaggcccgc gctcgggcct gggctggggg catgggggag 480

WO 00/29448

PCT/JP99/06412

206/233

ccccggggccc	ggctcgtggt	ccccgtggct	gtggccgcct	gggggggtggg	agggatgctg	540
gagggctgtg	gotaccaggc	cgaggggggc	tggggctgcc	tgggctacac	gctgggtagg	600
gaattcagca	aagacctg					618

<210> 136

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 136

atggacgcca	gatggtgggc	agtggtggtg	ctggctgcgt	tccctccct	aggggcaggt	60
ggggagactc	ccgaagcccc	tccggagtca	tggaccacgc	tatggttctt	ccgattttgtg	120
gtgaatgctg	ctggctatgc	cagctttatg	gtacctggct	acctcctggt	gcagtacttc	180
aggcggaaga	actacctgga	gaccggtagg	ggcctctgct	ttccctggt	gaaagcttgt	240
gtgtttggca	atgagcccaa	ggcctctgat	gaggttcccc	tggcgccccg	aacagaggcg	300
gcagagacca	ccccgatgtg	gcaggccctg	aagctgctct	tctgtgccac	agggctccag	360
gtgtcttata	tgacttgggg	tgtgctgcag	gaaagagtga	tgaccgcag	ctatggggcc	420
acagccacat	caccgggtga	gcgctttacg	gactcgagct	tcctgggtgct	aatgaaccga	480
gtgctggcac	tgattgtggc	tggcctctcc	tgtgttctct	gcaagcagcc	ccggcatggg	540
gcacccatgt	accggtactc	ctttgccagc	ctgtccaatg	tgcttagcag	ctggtgccaa	600
tacgaagctc	ttaagttcgt	cagcttcccc	accaggtgc	tggccaaggc	ctctaagggtg	660
atccctgtca	tgtgatggg	aaagcttgtg	tctcggcgca	gtacgaaca	ctgggagtag	720
ctgacagcca	cactcatctc	cattgggggc	agcatgttcc	tgctatccag	cggaccagag	780
ccccgcagct	ccccagccac	cacactctca	ggcctcatct	tactggcagg	ttatattgct	840
tttgacagct	tcacctcaaa	ctggcaggat	ggcctgtttg	cctataagat	gtcatcggtg	900
cagatgatgt	ttgggggtcaa	tttcttctcc	tgcctcttca	cagtgggctc	actgctagaa	960
cagggggccc	tactggaggg	aaccgcttc	atggggcgac	acagtgagtt	tgctgcccat	1020
ggcctgctac	tctccatctg	ctccgcatgt	ggccagctct	tcctctttta	caccattggg	1080
cagtttgggg	ctgccgtctt	caccatcatc	atgacctccc	gccaggcctt	tgccatcctt	1140
ctttcctgcc	ttctctatgg	ccacactgtc	actgtggtgg	gagggctggg	ggtggtgctg	1200
gtctttgctg	ccctcctgct	cagagtctac	gcgcggggcc	gtctaaagca	acgggggaaag	1260
aaggtgtgtc	ctgttgagtc	tcctgtgcag	aaggtt			1296

<210> 137

<211> 918

<212> DNA

207/233

<213> Homo sapiens

<400> 137

atgggggcacc	ggaccctggt	cctgccctgg	gtgctgctga	ccttgtgtgt	cactgcgggg	60
accccgagg	tgtgggttca	agttcggatg	gaggccaccg	agctctcgtc	cttcaccatc	120
cgttgtgggt	tcctggggtc	tggtcccatc	tcctgggtga	ctgtgagctg	ggggggcccc	180
gacggtgctg	gggggaccac	gctggctgtg	ttgcaccag	aacgtggcat	ccggcaatgg	240
gccctgctc	gccaggcccg	ctgggaaacc	cagagcagca	tctctctcat	cctggaaaggc	300
tctggggcca	gcagcccctg	cgccaacacc	acettctgct	gcaagtttgc	gtccttccct	360
gagggctcct	gggaggcctg	tgggagcctc	ccgccagct	cagaccagg	gctctctgcc	420
ccgccgaactc	ctgcccccat	tctgcgggca	gacctggccg	ggatcttggg	ggtctcagga	480
gtcctcctct	ttggctgtgt	ctacctcctt	catctgctgc	gcgacataa	gcaccgcct	540
gccctaggc	tcagccgtc	ccgcaccagc	cccaggcac	cgagagcacg	agcatgggca	600
ccaagccagg	cctcccaggc	tgctcttcac	gtcccttatg	ccaactatcaa	caccagctgc	660
cgcccagcta	ctttggacac	agctcaccac	catggggggc	cgtcctggtg	ggcgtaactc	720
cccaccacg	ctgcacaccg	gccccagggc	cctgccgcct	gggcctccac	acccatccct	780
gcacgtggca	gctttgtctc	tggtgagaat	ggactctacg	ctcaggcagg	ggagaggcct	840
cctcacactg	gtcccggcct	cactcttttc	cctgaccctc	ggggggcccag	ggccatggaa	900
ggacccttag	gagttcga					918

<210> 138

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 138

atgcaaagtt	gtgaatccag	tggtgacagt	gcggatgacc	ctctcagtcg	cggcctacgg	60
agaaggggac	agcctcgtgt	ggtggtgate	ggcgccggct	tggtggcct	ggctgcagcc	120
aaagcacttc	ttgagcaggg	tttcacggat	gtcactgtgc	ttgaggcttc	cagccacatc	180
ggaggccgtg	tgcagagtgt	gaaacttgga	cacgccacct	ttgagctggg	agccacctgg	240
atccatggct	cccattggga	ccctatctat	catctagcag	aagccaacgg	cctcctggaa	300
gagacaaccg	atggggaacg	cagcgtgggc	cgcatacagc	tctattccaa	gaatggcgtg	360
gcctgctacc	ttaccaacca	cggccgcagg	atccccaaag	acgtggttga	ggaattcagc	420
gatttataca	acgaggtcta	taacttgacc	caggagtctt	tccggcacga	taaaccagtc	480
aatgctgaaa	gtcaaaatag	cgtgggggtg	ttcaccgcag	aggaggtgcg	taaccgcac	540
aggaatgacc	ctgacgacc	agaggctacc	aagcgcctga	agctcgccat	gatccagcag	600
tacotgaagg	tggagagctg	tgagagcagc	tcacacagca	tggacgaggt	gtccctgagc	660

WO 00/29448

PCT/JP99/06412

208/233

gccttcgggg	agtggaccga	gateccccggc	gtcaccacaca	tcacccccctc	gggcttcctg	720
cgggttgttg	agctgctggc	ggagggcctc	cctgcccacg	tcacccagct	agggaaacct	780
gtccgctgca	ttcactggga	ccaggcctca	gcccgcacca	gaggccctga	gattgagccc	840
cggggtgagg	gcgaccacaa	tcacgacact	ggggaggggtg	gccaggggtg	agaggagccc	900
cgggggggca	ggtgggatga	ggatgagcag	tggtcgggtg	tggtggagtg	cgaggactgt	960
gagctgatcc	cggcggacca	tgtgattgtg	accgtgtcgc	taggtgtgct	aaagaggcag	1020
tacaccagtt	tcttcgggce	aggcctgccc	acagagaagg	tggtgccat	ccaccgctg	1080
ggcattggca	ccaccgacaa	gatctttctg	gaattcgagg	agcccttctg	gggcccctgag	1140
tgcaacagcc	tacagtttgt	gtgggaggac	gaagcggaga	gccacaccct	cacctacca	1200
cctgagctct	ggtaccgcaa	gatctgcggc	tttgatgtcc	tctacccgcc	tgagcgctac	1260
ggccatgtgc	tgagcggtg	gatctgcggg	gaggaggccc	tcgtcatgga	gaagtgtgat	1320
gacgaggcag	tggccgagat	ctgcacggag	atgctcgcgc	agttcacagg	gaaccccaac	1380
attccaaaac	ctcggcgaa	cttgcgctcg	gcctggggca	gcaaccctta	cttcgcggc	1440
tcctattcat	acacgcaggt	gggctccagc	ggggcggtg	tggagaagct	ggccaagccc	1500
ctgccgtaca	cggagagctc	aaagacagcg	cccatgcagg	tgctgttttc	cggtgaggcc	1560
accacccgca	agtactattc	caccaccac	ggtgctctgc	tgccggcca	gcgtgaggct	1620
gcccgcctca	ttgagatgta	ccgagacctc	ttccagcagg	ggacc		1665

<210> 139

<211> 750

<212> DNA

<213> Homo sapiens

<400> 139

atgggggtctc	agcattccgc	tgctgctcgc	ccctcctcct	gcaggcgaaa	gcaagaagat	60
gacagggacg	gtttgctggc	tgaacgagag	caggaagaag	ccattgctca	gttcccatat	120
gtggaattca	ccgggagaga	tagcatcacc	tgtctcacgt	gccaggggac	aggctacatt	180
ccaacagagc	aagtaaata	ggtgggtggc	ttgatccac	acagtgatca	gagattgcgc	240
cctcagcgaa	ctaagcaata	tgtcctcctg	tccatcctgc	tttgtctcct	ggcatctggt	300
ttggtggttt	tcttctgtt	tccgcattca	gtccttgtgg	atgatgacgg	catcaaagtg	360
gtgaaagtca	catttaataa	gcaagactcc	cttgtaattc	tcaccatcat	ggccaccctg	420
aaaatcagga	actocaaact	ctacacgggtg	gcagtgacca	gcctgtccag	ccagattcag	480
tacatgaaca	cagtggtcag	tacatatgtg	actactaacg	tctcccttat	tccacctcgg	540
agtgagcaac	tggtgaattt	taccgggaag	gccgagatgg	gaggaccgtt	ttcctatgtg	600
tactttctct	gcacgggtacc	tgagatcctg	gtgcacaaca	tagtgatctt	catgcgaact	660
tcagtgaaga	tttcatacat	tggcctcatg	accagagct	ccttgagagc	acatcactat	720

WO 00/29448

PCT/JP99/06412

209/233

gtggattgtg gaggaaattc cacagctatt 750

<210> 140

<211> 522

<212> DNA

<213> Homo sapiens

<400> 140

atgcaagcac cagccttcag ggacaagaaa caggggggtct cagccaagaa tcaaggtgcc	60
catgaccacag actatgagaa tatcaccttg gccttcaaaa atcaggacca tgcaaaggggt	120
ggatcatcac gacccacgag ccaagtccca gccagtgca ggccgcctc agactccacc	180
cagggtccct gctggttgta cagagccatc ctgagcctgt acatcctcct ggccctggcc	240
tttgtcctct gcatcatcct gtcagcctc atcatggtga agaattgctga gatgtccaag	300
gagctgctgg gctttaaaag ggagctttgg aatgtctcaa actccgtaca agcatgcgaa	360
gagagacaga agagaggctg ggattccgtt cagcagagca tcaccatggg caggagcaag	420
attgatagat tagagacgac attagcaggc ataaaaaaca ttgacacaaa ggtacagaaa	480
atcttgaggg tgctgcagaa aatgccacag tcctcacctc aa	522

<210> 141

<211> 3234

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)...(2039)

<400> 141

aatgagcgcc ggccggccgg ttgccaggc gaccagcgcg cggtccgcc ccccgcgcg	60
aggctccgc gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgttagag	120
aacaogcg atg acc acg tgg agc etc cgg cgg agg ccg gcc cgc acg ctg	170
Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu	
1 5 10	
gga etc ctg ctg ctg gtc gtc ttg ggc ttc ctg gtg ctt cgc agg ctg	218
Gly Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu	
15 20 25 30	
gac tgg agc acc ctg gtc cct ctg cgg etc cgc cat cga cag ctg ggg	266
Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly	

WO 00/29448

PCT/JP99/06412

210/233

35	40	45	
ctg cag gcc aag ggc tgg aac ttc atg ctg gag gat tcc acc ttc tgg			314
Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp			
50	55	60	
atc ttc ggg ggc tcc atc cac tat ttc cgt gtg ccc agg gag tac tgg			362
Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp			
65	70	75	
agg gac cgc ctg ctg aag atg aag gcc tgt ggc ttg aac acc ctc acc			410
Arg Asp Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr			
80	85	90	
acc tat gtt ccg tgg aac ctg cat gag cca gaa aga ggc aaa ttt gac			458
Thr Tyr Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp			
95	100	105	110
ttc tct ggg aac ctg gac ctg gag gcc ttc gtc ctg atg gcc gca gag			506
Phe Ser Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu			
115	120	125	
atc ggg ctg tgg gtg att ctg cgt cca ggc ccc tac atc tgc agt gag			554
Ile Gly Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu			
130	135	140	
atg gac ctc ggg ggc ttg ccc agc tgg cta ctc caa gac cct ggc atg			602
Met Asp Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met			
145	150	155	
agg ctg agg aca act tac aag ggc ttc acc gaa gca gtg gac ctt tat			650
Arg Leu Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr			
160	165	170	
ttt gac cac ctg atg tcc agg gtg gtg cca ctc cag tac aag cgt ggg			698
Phe Asp His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly			
175	180	185	190
gga cct atc att gcc gtg cag gtg gag aat gaa tat ggt tcc tat aat			746
Gly Pro Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn			
195	200	205	
aaa gac ccc gca tac atg ccc tac gtc aag aag gca ctg gag gac cgt			794
Lys Asp Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg			
210	215	220	
ggc att gtg gaa ctg ctc ctg act tca gac aac aag gat ggg ctg agc			842

WO 00/29448

PCT/JP99/06412

211/233

Gly	Ile	Val	Glu	Leu	Leu	Leu	Thr	Ser	Asp	Asn	Lys	Asp	Gly	Leu	Ser		
225						230						235					
aag	ggg	att	gtc	cag	gga	gtc	ttg	gcc	acc	atc	aac	ttg	cag	tca	aca	890	
Lys	Gly	Ile	Val	Gln	Gly	Val	Leu	Ala	Thr	Ile	Asn	Leu	Gln	Ser	Thr		
240						245						250					
cac	gag	ctg	cag	cta	ctg	acc	acc	ttt	ctc	ttc	aac	gtc	cag	ggg	act	938	
His	Glu	Leu	Gln	Leu	Leu	Thr	Thr	Phe	Leu	Phe	Asn	Val	Gln	Gly	Thr		
255						260						265			270		
cag	ccc	aag	atg	gtg	atg	gag	tac	tgg	acg	ggg	tgg	ttt	gac	tcg	tgg	986	
Gln	Pro	Lys	Met	Val	Met	Glu	Tyr	Trp	Thr	Gly	Trp	Phe	Asp	Ser	Trp		
			275						280						285		
gga	ggc	cct	cac	aat	atc	ttg	gat	tct	tct	gag	ggt	ttg	aaa	acc	gtg	1034	
Gly	Gly	Pro	His	Asn	Ile	Leu	Asp	Ser	Ser	Glu	Val	Leu	Lys	Thr	Val		
			290						295						300		
tct	gcc	att	gtg	gac	gcc	ggc	tcc	tcc	atc	aac	ctc	tac	atg	ttc	cac	1082	
Ser	Ala	Ile	Val	Asp	Ala	Gly	Ser	Ser	Ile	Asn	Leu	Tyr	Met	Phe	His		
305						310						315					
gga	ggc	acc	aac	ttt	ggc	ttc	atg	aat	gga	gcc	atg	cac	ttc	cat	gac	1130	
Gly	Gly	Thr	Asn	Phe	Gly	Phe	Met	Asn	Gly	Ala	Met	His	Phe	His	Asp		
320						325						330					
tac	aag	tca	gat	gtc	acc	agc	tat	gac	tat	gat	gct	gtg	ctg	aca	gaa	1178.	
Tyr	Lys	Ser	Asp	Val	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Val	Leu	Thr	Glu		
335						340						345			350		
gcc	ggc	gat	tac	acg	gcc	aag	tac	atg	aag	ctt	cga	gac	ttc	ttc	ggc	1226	
Ala	Gly	Asp	Tyr	Thr	Ala	Lys	Tyr	Met	Lys	Leu	Arg	Asp	Phe	Phe	Gly		
			355						360						365		
tcc	atc	tca	ggc	atc	cct	ctc	cct	ccc	cca	cct	gac	ctt	ctt	ccc	aag	1274	
Ser	Ile	Ser	Gly	Ile	Pro	Leu	Pro	Pro	Pro	Pro	Asp	Leu	Leu	Pro	Lys		
			370						375						380		
atg	ccg	tat	gag	ccc	tta	acg	cca	gtc	ttg	tac	ctg	tct	ctg	tgg	gac	1322	
Met	Pro	Tyr	Glu	Pro	Leu	Thr	Pro	Val	Leu	Tyr	Leu	Ser	Leu	Trp	Asp		
385						390						395					
gcc	ctc	aag	tac	ctg	ggg	gag	cca	atc	aag	tct	gaa	aag	ccc	atc	aac	1370	
Ala	Leu	Lys	Tyr	Leu	Gly	Glu	Pro	Ile	Lys	Ser	Glu	Lys	Pro	Ile	Asn		
400						405						410					

atg	gag	aac	ctg	cca	gtc	aat	ggg	gga	aat	gga	cag	tcc	ttc	ggg	tac	1418
Met	Glu	Asn	Leu	Pro	Val	Asn	Gly	Gly	Asn	Gly	Gln	Ser	Phe	Gly	Tyr	
415					420					425					430	
att	ctc	tat	gag	acc	agc	atc	acc	tcg	tct	ggc	atc	ctc	agt	ggc	cac	1466
Ile	Leu	Tyr	Glu	Thr	Ser	Ile	Thr	Ser	Ser	Gly	Ile	Leu	Ser	Gly	His	
					435					440					445	
gtg	cat	gat	cgg	ggg	cag	gtg	ttt	gtg	aac	aca	gta	tcc	ata	gga	ttc	1514
Val	His	Asp	Arg	Gly	Gln	Val	Phe	Val	Asn	Thr	Val	Ser	Ile	Gly	Phe	
					450					455					460	
ttg	gac	tac	aag	aca	acg	aag	att	gct	gtc	ccc	ctg	atc	cag	ggt	tac	1562
Leu	Asp	Tyr	Lys	Thr	Thr	Lys	Ile	Ala	Val	Pro	Leu	Ile	Gln	Gly	Tyr	
					465										475	
acc	gtg	ctg	agg	atc	ttg	gtg	gag	aat	cgt	ggg	cga	gtc	aac	tat	ggg	1610
Thr	Val	Leu	Arg	Ile	Leu	Val	Glu	Asn	Arg	Gly	Arg	Val	Asn	Tyr	Gly	
					480										490	
gag	aat	att	gat	gac	cag	cgc	aaa	ggc	tta	att	gga	aat	ctc	tat	ctg	1658
Glu	Asn	Ile	Asp	Asp	Gln	Arg	Lys	Gly	Leu	Ile	Gly	Asn	Leu	Tyr	Leu	
495					500						505				510	
aat	gat	tca	ccc	ctg	aaa	aac	ttc	aga	atc	tat	agc	ctg	gat	atg	aag	1706
Asn	Asp	Ser	Pro	Leu	Lys	Asn	Phe	Arg	Ile	Tyr	Ser	Leu	Asp	Met	Lys	
					515						520				525	
aag	agc	ttc	ttt	cag	agg	ttc	ggc	ctg	gac	aaa	tgg	agt	tcc	ctc	cca	1754
Lys	Ser	Phe	Phe	Gln	Arg	Phe	Gly	Leu	Asp	Lys	Trp	Ser	Ser	Leu	Pro	
					530						535				540	
gaa	aca	ccc	aca	tta	cct	gct	ttc	ttc	ttg	ggt	agc	ttg	tcc	atc	agc	1802
Glu	Thr	Pro	Thr	Leu	Pro	Ala	Phe	Phe	Leu	Gly	Ser	Leu	Ser	Ile	Ser	
					545						550				555	
tcc	acc	cct	tgt	gac	acc	ttt	ctg	aag	ctg	gag	ggc	tgg	gag	aag	ggg	1850
Ser	Thr	Pro	Cys	Asp	Thr	Phe	Leu	Lys	Leu	Glu	Gly	Trp	Glu	Lys	Gly	
					560						565				570	
gtt	gta	ttc	atc	aat	ggc	cag	aac	ctt	gga	cgt	tac	tgg	aac	att	gga	1898
Val	Val	Phe	Ile	Asn	Gly	Gln	Asn	Leu	Gly	Arg	Tyr	Trp	Asn	Ile	Gly	
575					580						585				590	
ccc	cag	aag	acg	ctt	tac	ctc	cca	ggt	ccc	tgg	ttg	agc	agc	gga	atc	1946
Pro	Gln	Lys	Thr	Leu	Tyr	Leu	Pro	Gly	Pro	Trp	Leu	Ser	Ser	Gly	Ile	

<222> (70)...(1026)

WO 00/29448

PCT/JP99/06412

214/233

<400> 142

agaaagagaa gccatagtcg gcgagcaacg ctggagcadc ccgctctggg gccgctgcag	60
ccggcagag atg gtt gag ctc atg ttc ccg ctg ttg ctc ctc ctt ctg ccc	111
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro	
1 5 10	
ttc ctt ctg tat atg gct gcg ccc caa atc agg aaa atg ctg tcc agt	159
Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser	
15 20 25 30	
ggg gtg tgt aca tca act gtt cag ctt cct ggg aaa gta gtt gtg gtc	207
Gly Val Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val	
35 40 45	
aca gga gct aat aca ggt atc ggg aag gag aca gcc aaa gag ctg gct	255
Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala	
50 55 60	
cag aga gga gct cga gta tat tta gct tgc cgg gat gtg gaa aag ggg	303
Gln Arg Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly	
65 70 75	
gaa ttg gtg gcc aaa gag atc cag acc acg aca ggg aac cag cag gtg	351
Glu Leu Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val	
80 85 90	
ttg gtg cgg aaa ctg gac ctg tct gat act aag tct att cga gct ttt	399
Leu Val Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe	
95 100 105 110	
gct aag ggc ttc tta gct gag gaa aag cac ctc cac gtt ttg atc aac	447
Ala Lys Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn	
115 120 125	
aat gca gga gtg atg atg tgt ccg tac tcc aag aca gca gat ggc ttt	495
Asn Ala Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe	
130 135 140	
gag atg cac ata gga gtc aac cac ttg ggt cac ttc ctc cta acc cat	543
Glu Met His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His	
145 150 155	
ctg ctg cta gag aaa cta aag gaa tca gcc cca tca agg ata gta aat	591
Leu Leu Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn	
160 165 170	

WO 00/29448

PCT/JP99/06412

215/233

gtg tct tcc ctc gca cat cac ctg gga agg atc cac ttc cat aac ctg	639
Val Ser Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu	
175 180 185 190	
cag ggc gag aaa ttc tac aat gca ggc ctg gcc tac tgt cac agc aag	687
Gln Gly Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys	
195 200 205	
cta gcc aac atc ctc ttc acc cag gaa ctg gcc cgg aga cta aaa ggc	735
Leu Ala Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly	
210 215 220	
tct ggc gtt acg acg tat tct gta cac cct ggc aca gtc caa tct gaa	783
Ser Gly Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu	
225 230 235	
ctg gtt cgg cac tca tct ttc atg aga tgg atg tgg tgg ctt ttc tcc	831
Leu Val Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser	
240 245 250	
ttt ttc atc aag act cct cag cag gga gcc cag acc agc ctg cac tgt	879
Phe Phe Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys	
255 260 265 270	
gcc tta aca gaa ggt ctt gag att cta agt ggg aat cat ttc agt gac	927
Ala Leu Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp	
275 280 285	
tgt cat gtg gca tgg gtc tct gcc caa gct cgt aat gag act ata gca	975
Cys His Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala	
290 295 300	
agg cgg ctg tgg gac gtc agt tgt gac ctg ctg ggc ctc cca ata gac	1023
Arg Arg Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp	
305 310 315	
taacagg cagtgccagt tggacccaag agaagactgc agcagactac acagtacttc	1080
ttgtcaaaat gattctcctt caagggtttt aaaaccttta gcacaaagag agcaaaacct	1140
tccagccttg cctgcttggt gtccagttaa aactcagtgt actgccagat tcgtctaaat	1200
gtctgtcatg tccagattta ctttgettct gttactgcca gagttactag agatatcata	1260
ataggataag aagacctca tatgacctgc acagctcatt ttccttctga aagaaactac	1320
tacctaggag aatctaagct atagcaggga tgatttatgc aaatttgaac tagcttcttt	1380
gttcacaatt cagttcctcc caaccaacca gtcttcactt caagagggcc aactgcaac	1440
ctcagcttaa catgaataac aaagactggc tcaggagcag ggcttgccca ggcattggtg	1500

WO 00/29448

PCT/JP99/06412

216/233

atcacccggag gtcagtagtt caagaccagc ctggccaaca tggtgaaacc ccacctctac 1560
 taaaaattgt gtatatcttt gtgtgtcttc ctgtttatgt gtgccaaagg agtattttca 1620
 caaagttcaa aacagccaca ataatcagag atggagcaaa ccagtgccat ccagtcttta 1680
 tgcaaatgaa atgctgcaaa gggaagcaga ttctgtatat gttggtaact acccaccaag 1740
 agcacatggg tagcagggaa gaagtaaaaa aagagaagga gaatactgga agataatgca 1800
 caaaatgaag ggactagtta aggattaact agccctttaa ggattaacta gttaaggatt 1860
 aatagcaaaa gatattaaat atgctaacat agctatggag gaattgaggg caagcaccca 1920
 ggactgatga ggtcttaaca aaaaccagtg tggcaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaaatcc taaaaacaaa caaacaaaaa aaacaattct tcattcagaa aaattatctt 2040
 agggactgat attggtaatt atgggtcaatt taataatatt ttggggcatt tccttacatt 2100
 gtcttgacaa gattaaaatg tctgtgcaa aattttgtat tttatttgga gacttcttat 2160
 caaaagtaat gctgccaaag gaagtetaag gaattagtag tgttcccatc acttgtttg 2220
 agtgtgctat tctaaaagat tttgatttcc tggaatgaca attatatttt aactttggtg 2280
 ggggaaagag ttataggacc acagtottca cttctgatac ttgtaaatta atcttttatt 2340
 gcacttgttt tgaccattaa gctatatgtt tagaaatggt cattttacgg aaaaattaga 2400
 aaaattctga taatagtga gaataaatga attaatgttt tacttaattt atattgaact 2460
 gtcaatgaca aataaaaatt ctttttgatt 2490

<210> 143

<211> 1465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)...(332)

<400> 143

gaaggcgccg gccgtggagg cgccacgtcc cttgcggcgg cgggagagaa atcgcttgga 60
 ctteggggcg gcctcggacg gcc atg gcc ttt acc ctg tac tca ctg ctg 110
 Met Ala Phe Thr Leu Tyr Ser Leu Leu
 1 5
 cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag gag 158
 Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu Glu
 10 15 20 25
 cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt gga 206
 Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly Gly

WO 00/29448

PCT/JP99/06412

217/233

30	35	40	
ttt gga gaa gag ccg gga att aaa tca cag cta atg aac ctt att cga			254
Phe Gly Glu Glu Pro Gly Ile Lys Ser Gln Leu Met Asn Leu Ile Arg			
45	50	55	
tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca att			302
Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser Ile			
60	65	70	
gca att gtg tta ctt tta tta ttt gga tgaatatcag tggagaaaat g			350
Ala Ile Val Leu Leu Leu Leu Phe Gly			
75	80		
gagactcaga agaggacatg ccagtagaag ttattacttt ggtcattatt ggaatattta			410
tatcttagct ggctgacctt gcacttgatc aaaatgtaaa gctgaaaata aaaccagggt			470
ttctatattat ctgttttttt ttttaattgtt gcacttgtag ttccattaca aaagatcaga			530
tcatgaaagg cagtaactct ccaggactgg aatatctgat tgctcagtgt taatagtagt			590
tcatgctgtg gtgagattgt taaaagggtg caagactggt gcttctcttt ttttagatat			650
ttttctatct ctcaactctc agggatgaaa ttcttttttca aagttttgaa gttccttgca			710
aacttagccat gatgtgagtg gttatcccta gataaaatta aaaggatttt taaaaagtaa			770
ttactgcaca taaaatgata aataggtaat ttgaataatt ttattttaag ctcttggtt			830
aattattttg tctattgtct cagctataaa ttcaaattta tacatactat tgagtattaa			890
tattctctga ttccaggag aattctgtca gtcacatgat gattatgttt ttgtttaaca			950
ttctttccat gcacttgta ttttattaat ttgcctgaat gatgagacca gaccagtgtc			1010
tacagatttt cattgtcaga aaaatctata agtctgccct tttacaatg atgatttaaa			1070
aaaaacaaca gcgtaaatat tagcccacaa gagcagtcct aaacaatcac aattacactg			1130
tactacccaa gaagactgtt tattgtgaag catttacctt tcaaaaaatc attacatttc			1190
tatttcttgg tggagcagca cattgtggag tgtgattctt aattcttcat tgagtttgtc			1250
aataggacat tgatgctgga taggttgtct tttgttttta tgtctcagac catcttgtga			1310
gattgtttgc ctatctcata atacagtttt atgcagaaag gttgaaacta tgtaaagtgt			1370
ttttatggaa attatcagtt acaatatttt aaagggtgtag aatggcatct ttgtttatag			1430
gagaacattt gtaaataaag ttaaatttct aagtc			1465

<210> 144

<211> 917

<212> DNA

<213> Homo sapiens

<220>

WO 00/29448

PCT/JP99/06412

218/233

<221> CDS

<222> (32)...(775)

<400> 144

tctctgcatac cttcccgacc ttcccagcaa t atg cat ctt gca cgt ctg gtc	52
Met His Leu Ala Arg Leu Val	
1 5	
ggc tcc tgc tcc ctc ctt ctg cta ctg ggg gcc ctg tct gga tgg gcg	100
Gly Ser Cys Ser Leu Leu Leu Leu Leu Gly Ala Leu Ser Gly Trp Ala	
10 15 20	
gcc agc gat gac ccc att gag aag gtc att gaa ggg atc aac cga ggg	148
Ala Ser Asp Asp Pro Ile Glu Lys Val Ile Glu Gly Ile Asn Arg Gly	
25 30 35	
ctg agc aat gca gag aga gag gtg ggc aag gcc ctg gat ggc atc aac	196
Leu Ser Asn Ala Glu Arg Glu Val Gly Lys Ala Leu Asp Gly Ile Asn	
40 45 50 55	
agt gga atc acg cat gcc gga agg gaa gtg gag aag gtt ttc aac gga	244
Ser Gly Ile Thr His Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly	
60 65 70	
ctt agc aac atg ggg agc cac acc ggc aag gag ttg gac aaa ggc gtc	292
Leu Ser Asn Met Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val	
75 80 85	
cag ggg ctc aac cac ggc atg gac aag gtt gcc cat gag atc aac cat	340
Gln Gly Leu Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His	
90 95 100	
ggt att gga caa gca gga aag gaa gca gag aag ctt ggc cat ggg gtc	388
Gly Ile Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val	
105 110 115	
aac aac gct gct gga cag gcc ggg aag gaa gca gac aaa gcg gtc caa	436
Asn Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln	
120 125 130 135	
ggg ttc cac act ggg gtc cac cag gct ggg aag gaa gca gag aaa ctt	484
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys Leu	
140 145 150	
ggc caa ggg gtc aac cat gct gct gac cag gct gga aag gaa gtg gag	532
Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu Val Glu	

gaaggaccaa aggcgaccgg tgcaggtgca cgacgccagc tcccttctgg ggggccgggg	60
cctggggggtt gcc atg gcc ccc agc cac ctg tca gtg cgg gag atg agg	109
Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg	
1 5 10	
gaa gat gag aag ccc ctg gtg ctg gag atg ctg aag gcc ggc gtg aag	157
Glu Asp Glu Lys Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys	
15 20 25	

WO 00/29448

PCT/JP99/06412

220/233

gac acg gaa aac cgc gtg gcc ctc cat gcc ttg aca cgg ccg ccg gcc	205
Asp Thr Glu Asn Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala	
30 35 40	
ctg ctc ctc ctg gcg gcg gcc agc agc ggc ctg cgc ttt gtc ctg gct	253
Leu Leu Leu Leu Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala	
45 50 55 60	
tcc ttc gcc ctg gcc ctc ctc ctg ccg gtg ttc ctg gct gtg gcc gcc	301
Ser Phe Ala Leu Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala	
65 70 75	
gtg aag ctg ggc ctg cgg gcc cga tgg ggc tcg ctg cct ccg ccg ggt	349
Val Lys Leu Gly Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly	
80 85 90	
ggc ctg ggg ggc ccc tgg gtg gcc gtg cgg ggc tcc ggt gac gtg tgt	397
Gly Leu Gly Gly Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys	
95 100 105	
ggg gtc ctg gct ctg gcc cct ggc aca aat gca ggg gac ggg gcc cgg	445
Gly Val Leu Ala Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg	
110 115 120	
gtc acc cgc ctg tct gtc tct cgc tgg cac cgc cgc cgg ggc gtg ggc	493
Val Thr Arg Leu Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly	
125 130 135 140	
agg agg ctg ctg gcc ttc gcg gag gcc cgg gct cgg gcc tgg gct ggg	541
Arg Arg Leu Leu Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly	
145 150 155	
ggc atg ggg gag ccc cgg gcc cgg ctc gtg gtc ccc gtg gct gtg gcc	589
Gly Met Gly Glu Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala	
160 165 170	
gcc tgg ggg gtg gga ggg atg ctg gag ggc tgt ggc tac cag gcc gag	637
Ala Trp Gly Val Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu	
175 180 185	
ggg ggc tgg ggc tgc ctg ggc tac acg ctg gtg agg gaa ttc agc aaa	685
Gly Gly Trp Gly Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys	
190 195 200	
gac ctg tgaagctaca gactgacagc cagggcaggg gagggaggag gggcgccag	740
Asp Leu	

221/233

205

cacctgatga tcgcctactg totgcggtt cttttacctg ctctccctca gtgagtcctc	800
aaccaccctg ggcccagaaa cagaggcctg cagaggggag gagcctggcc tctgtccacc	860
cgtcagcagt gtgaagtctg ttgtgtttga gcttctcaga gtggaatgac tccttttctt	920
tcctggccct cgggggcctc tcgaggtcag cctctccaac ccctacctca gctcctgtct	980
gcactgagaa acctccccgg gtgatgtctg caaagtctgt gctgtccgtg cccagggctg	1040
ggagagctat ctggggaggg ggagaggagg ccgagcagaa tacaccccag agttagggtt	1100
tgcgaactccg cctccctggg acctggattg ggtcagatgc ctgtccttg aggggacaag	1160
gttgactgct taggaggcgc gacgcacagg gctgccaggc ctggcccctc totgggaagg	1220
ttgagagctg agacgggcag ccctgtccct tcctccagat ccgtctggtt ttttacaccg	1280
tttgtaata aagcctgaaa ccgctt	1306

<210> 146

<211> 2022

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)...(1416)

<400> 146

cttccgctgg ccgctggctc gctggccgct cctggaggcg gcggcgggag cgcagggggc	60
gcgcggccccg gggactcgca ttccccggtt cccctccac cccacgcggc ctggacc	117
atg gac gcc aga tgg tgg gca gtg gtg ctg gct gcg ttc ccc tcc	165
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser	
1 5 10 15	
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc	213
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr	
20 25 30	
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc	261
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser	
35 40 45	
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac	309
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn	
50 55 60	
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt	357

222/233

Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys		
65					70				75					80			
gtg	ttt	ggc	aat	gag	ccc	aag	gcc	tct	gat	gag	gtt	ccc	ctg	gcg	ccc	405	
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro		
			85						90					95			
cga	aca	gag	gcg	gca	gag	acc	acc	ccg	atg	tgg	cag	gcc	ctg	aag	ctg	453	
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu		
			100						105					110			
ctc	ttc	tgt	gcc	aca	ggg	ctc	cag	gtg	tct	tat	ctg	act	tgg	ggg	gtg	501	
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val		
			115						120					125			
ctg	cag	gaa	aga	gtg	atg	acc	cgc	agc	tat	ggg	gcc	aca	gcc	aca	tca	549	
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser		
			130						135					140			
ccg	ggt	gag	cgc	ttt	acg	gac	tgc	cag	ttc	ctg	gtg	cta	atg	aac	cga	597	
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg		
			145						150					155		160	
gtg	ctg	gca	ctg	att	gtg	gct	ggc	ctc	tcc	tgt	gtt	ctc	tgc	aag	cag	645	
Val	Leu	Ala	Leu	Ile	Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln		
			165						170					175			
ccc	cgg	cat	ggg	gca	ccc	atg	tac	cgg	tac	tcc	ttt	gcc	agc	ctg	tcc	693	
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser		
			180						185					190			
aat	gtg	ctt	agc	agc	tgg	tgc	caa	tac	gaa	gct	ctt	aag	ttc	gtc	agc	741	
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser		
			195						200					205			
ttc	ccc	acc	cag	gtg	ctg	gcc	aag	gcc	tct	aag	gtg	atc	cct	gtc	atg	789	
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met		
			210						215					220			
ctg	atg	gga	aag	ctt	gtg	tct	cgg	cgc	agc	tac	gaa	cac	tgg	gag	tac	837	
Leu	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr		
			225						230					235		240	
ctg	aca	gcc	aca	ctc	atc	tcc	att	ggg	gtc	agc	atg	ttt	ctg	cta	tcc	885	
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser		
			245						250					255			

223/233

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc	933
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg	981
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt	1029
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa	1077
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	
305 310 315 320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag	1125
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	
325 330 335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag	1173
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	
340 345 350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc	1221
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr	
355 360 365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt	1269
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu	
370 375 380	
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg	1317
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val	
385 390 395 400	
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag	1365
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys	
405 410 415	
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt	1413
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val	
420 425 430	
tgagggt ggaaagggcc tgagggtga agtgaaatag gaccctccca ccacccctt	1470
ctgctgtaac ctctgaggga gctggctgaa agggcaaat gcaggtgttt tctcagtatc	1530

WO 00/29448

PCT/JP99/06412

224/233

acagaccagc tctgcagcag gggattgggg agcccaggag gcagccttcc cttttgcctt 1590
aagtcaccca tttccagta agcagtttat tctgagcccc gggggtagac agtcctcagt 1650
gaggggtttt ggggagtttg ggggtcaagag agcataggta ggttccacag ttactcttcc 1710
cacaagttcc cttaagtctt gccctagctg tgetctgcca cctccagac tcaactccct 1770
ctgcaaatac ctgcatttct taccctgggtg agaaaagcac aagcgggtgta ggctccaatg 1830
ctgctttccc aggaggggtga agatgggtgct gtgctgagga aaggggatgc agagccctgc 1890
ccagcaccac cacctcctat gctcctggat ccctaggctc tgttccatga gcctgttgca 1950
ggttttggtg ctttagaaat gtaacttttt gctcttataa tttatttta ttaaattaaa 2010
ttactgcagt gg 2022

<210> 147

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(995)

<400> 147

aaagacttcc tgcgatgaga acagagggcac aggtgccggc cctgcagccc ccagaacctg 60
gaactgtaggg ggcc atg ggg cac cgg acc ctg gtc ctg ccc tgg gtg ctg 110
Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu
1 5 10
ctg acc ttg tgt gtc act gcg ggg acc ccg gag gtg tgg gtt caa gtt 158
Leu Thr Leu Cys Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val
15 20 25
cgg atg gag gcc acc gag ctc tcg tcc ttc acc atc cgt tgt ggg ttc 206
Arg Met Glu Ala Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe
30 35 40
ctg ggg tct ggc tcc atc tcc ctg gtg act gtg agc tgg ggg ggc ccc 254
Leu Gly Ser Gly Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro
45 50 55 60
gac ggt gct ggg ggg acc acg ctg gct gtg ttg cac cca gaa cgt ggc 302
Asp Gly Ala Gly Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly
65 70 75
atc cgg caa tgg gcc cct gct cgc cag gcc cgc tgg gaa acc cag agc 350

WO 00/29448

PCT/JP99/06412

225/233

Ile Arg Gln Trp Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser	
80 85 90	
agc atc tct ctc atc ctg gaa ggc tot ggg gcc agc agc ccc tgc gcc	398
Ser Ile Ser Leu Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala	
95 100 105	
aac acc acc ttc tgc tgc aag ttt gcg tcc ttc cct gag ggc tcc tgg	446
Asn Thr Thr Phe Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp	
110 115 120	
gag gcc tgt ggg agc ctc ccg ccc agc tca gac cca ggg ctc tct gcc	494
Glu Ala Cys Gly Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala	
125 130 135 140	
ccg ccg act cct gcc ccc att ctg cgg gca gac ctg gcc ggg atc ttg	542
Pro Pro Thr Pro Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu	
145 150 155	
ggg gtc tca gga gtc ctc ctc ttt ggc tgt gtc tac ctc ctt cat ctg	590
Gly Val Ser Gly Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu	
160 165 170	
ctg cgc cga cat aag cac cgc cct gcc cct agg ctc cag ccg tcc cgc	638
Leu Arg Arg His Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg	
175 180 185	
acc agc ccc cag gca ccg aga gca cga gca tgg gca cca agc cag gcc	686
Thr Ser Pro Gln Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala	
190 195 200	
tcc cag get get ctt cac gtc cct tat gcc act atc aac acc agc tgc	734
Ser Gln Ala Ala Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys	
205 210 215 220	
cgc cca get act ttg gac aca get cac ccc cat ggg ggg ccg tcc tgg	782
Arg Pro Ala Thr Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp	
225 230 235	
tgg gcg tca ctc ccc acc cac get gca cac cgg ccc cag ggc cct gcc	830
Trp Ala Ser Leu Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala	
240 245 250	
gcc tgg gcc tcc aca ccc atc cct gca cgt ggc agc ttt gtc tct gtt	878
Ala Trp Ala Ser Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val	
255 260 265	

WO 00/29448

PCT/JP99/06412

226/233

gag aat gga ctc tac gct cag gca ggg gag agg cct cct cac act ggt 926
 Glu Asn Gly Leu Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly
 270 275 280
 ccc ggc ctc act ctt ttc cct gac cct cgg ggg ccc agg gcc atg gaa 974
 Pro Gly Leu Thr Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu
 285 290 295 300
 gga ccc tta gga gtt cga tgagagagac catgaggcca ctgggctt 1020
 Gly Pro Leu Gly Val Arg
 305
 tccccctccc aggcctcctg ggtgtcaccc ccttacttta attcttgggc ctccaataag 1080
 tgtcccatag gtgtctggcc aggccacct gctgcggatg tggctctgtg gcgtgtgtgg 1140
 gcacaggtgt gagtgtgtga gtgacagtta cccatttca gtcatttcct gctgcaacta 1200
 agtcagcaac acagttttctc tgatgtc 1227

<210> 148
 <211> 2210
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (204)...(1871)
 <400> 148

aggggacgcg aggcggagcg gggccccaca caggccgcgg cggctggctc gggcccctac 60
 ggtcccggcg gcggctggag gaggaagcca ggccgctggc ggaggaggag agacggagga 120
 ggccgagacc ggagcgccgc tcgccgcaga cttacttccc cggtcagca gggaaaggtt 180
 cctagaaggt gagcgcgac ggt atg caa agt tgt gaa tcc agt ggt gac agt 233
 Met Gln Ser Cys Glu Ser Ser Gly Asp Ser
 1 5 10
 gcg gat gac cct ctc agt cgc ggc cta cgg aga agg gga cag cct cgt 281
 Ala Asp Asp Pro Leu Ser Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg
 15 20 25
 gtg gtg gtg atc ggc gcc ggc ttg gct ggc ctg gct gca gcc aaa gca 329
 Val Val Val Ile Gly Ala Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala
 30 35 40
 ctt ctt gag cag ggt ttc acg gat gtc act gtg ctt gag gct tcc agc 377

WO 00/29448

PCT/JP99/06412

227/233

Leu Leu Glu Gln Gly Phe Thr Asp Val Thr Val Leu Glu Ala Ser Ser	
45 50 55	
cac atc gga ggc cgt gtg cag agt gtg aaa ctt gga cac gcc acc ttt	425
His Ile Gly Gly Arg Val Gln Ser Val Lys Leu Gly His Ala Thr Phe	
60 65 70	
gag ctg gga gcc acc tgg atc cat ggc tcc cat ggg aac cct atc tat	473
Glu Leu Gly Ala Thr Trp Ile His Gly Ser His Gly Asn Pro Ile Tyr	
75 80 85 90	
cat cta gca gaa gcc aac ggc ctc ctg gaa gag aca acc gat ggg gaa	521
His Leu Ala Glu Ala Asn Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu	
95 100 105	
cgc agc gtg ggc cgc atc agc ctc tat tcc aag aat ggc gtg gcc tgc	569
Arg Ser Val Gly Arg Ile Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys	
110 115 120	
tac ctt acc aac cac ggc cgc agg atc ccc aag gac gtg gtt gag gaa	617
Tyr Leu Thr Asn His Gly Arg Arg Ile Pro Lys Asp Val Val Glu Glu	
125 130 135	
ttc agc gat tta tac aac gag gtc tat aac ttg acc cag gag ttc ttc	665
Phe Ser Asp Leu Tyr Asn Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe	
140 145 150	
cgg cac gat aaa cca gtc aat gct gaa agt caa aat agc gtg ggg gtg	713
Arg His Asp Lys Pro Val Asn Ala Glu Ser Gln Asn Ser Val Gly Val	
155 160 165 170	
ttc acc cga gag gag gtg cgt aac cgc atc agg aat gac cct gac gac	761
Phe Thr Arg Glu Glu Val Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp	
175 180 185	
cca gag gct acc aag cgc ctg aag ctc gcc atg atc cag cag tac ctg	809
Pro Glu Ala Thr Lys Arg Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu	
190 195 200	
aag gtg gag agc tgt gag agc agc tca cac agc atg gac gag gtg tcc	857
Lys Val Glu Ser Cys Glu Ser Ser Ser His Ser Met Asp Glu Val Ser	
205 210 215	
ctg agc gcc ttc ggg gag tgg acc gag atc ccc ggc gct cac cac atc	905
Leu Ser Ala Phe Gly Glu Trp Thr Glu Ile Pro Gly Ala His His Ile	
220 225 230	

atc	ccc	tcg	ggc	ttc	atg	cgg	gtt	gtg	gag	ctg	ctg	gcg	gag	ggc	atc	953
Ile	Pro	Ser	Gly	Phe	Met	Arg	Val	Val	Glu	Leu	Leu	Ala	Glu	Gly	Ile	
235					240				245					250		
cct	gcc	cac	gtc	atc	cag	cta	ggg	aaa	cct	gtc	cgc	tgc	att	cac	tgg	1001
Pro	Ala	His	Val	Ile	Gln	Leu	Gly	Lys	Pro	Val	Arg	Cys	Ile	His	Trp	
				255					260					265		
gac	cag	gcc	tca	gcc	cgc	ccc	aga	ggc	cct	gag	att	gag	ccc	cgg	ggc	1049
Asp	Gln	Ala	Ser	Ala	Arg	Pro	Arg	Gly	Pro	Glu	Ile	Glu	Pro	Arg	Gly	
				270				275					280			
gag	ggc	gac	cac	aat	cac	gac	act	ggg	gag	ggc	ggc	cag	ggc	gga	gag	1097
Glu	Gly	Asp	His	Asn	His	Asp	Thr	Gly	Glu	Gly	Gly	Gln	Gly	Gly	Glu	
			285					290					295			
gag	ccc	cgg	ggg	ggc	agg	tgg	gat	gag	gat	gag	cag	tgg	tcg	gtg	gtg	1145
Glu	Pro	Arg	Gly	Gly	Arg	Trp	Asp	Glu	Asp	Glu	Gln	Trp	Ser	Val	Val	
	300					305					310					
gtg	gag	tgc	gag	gac	tgt	gag	ctg	atc	ccg	gcg	gac	cat	gtg	att	gtg	1193
Val	Glu	Cys	Glu	Asp	Cys	Glu	Leu	Ile	Pro	Ala	Asp	His	Val	Ile	Val	
315					320					325				330		
acc	gtg	tcg	cta	ggt	gtg	cta	aag	agg	cag	tac	acc	agt	ttc	ttc	cgg	1241
Thr	Val	Ser	Leu	Gly	Val	Leu	Lys	Arg	Gln	Tyr	Thr	Ser	Phe	Phe	Arg	
				335					340					345		
cca	ggc	ctg	ccc	aca	gag	aag	gtg	gct	gcc	atc	cac	cgc	ctg	ggc	att	1289
Pro	Gly	Leu	Pro	Thr	Glu	Lys	Val	Ala	Ala	Ile	His	Arg	Leu	Gly	Ile	
			350					355					360			
ggc	acc	acc	gac	aag	atc	ttt	ctg	gaa	ttc	gag	gag	ccc	ttc	tgg	ggc	1337
Gly	Thr	Thr	Asp	Lys	Ile	Phe	Leu	Glu	Phe	Glu	Glu	Pro	Phe	Trp	Gly	
			365				370					375				
cct	gag	tgc	aac	agc	cta	cag	ttt	gtg	tgg	gag	gac	gaa	gcg	gag	agc	1385
Pro	Glu	Cys	Asn	Ser	Leu	Gln	Phe	Val	Trp	Glu	Asp	Glu	Ala	Glu	Ser	
	380					385				390						
cac	acc	ctc	acc	tac	cca	cct	gag	ctc	tgg	tac	cgc	aag	atc	tgc	ggc	1433
His	Thr	Leu	Thr	Tyr	Pro	Pro	Glu	Leu	Trp	Tyr	Arg	Lys	Ile	Cys	Gly	
395					400					405				410		
ttt	gat	gtc	ctc	tac	ccg	cct	gag	cgc	tac	ggc	cat	gtg	ctg	agc	ggc	1481
Phe	Asp	Val	Leu	Tyr	Pro	Pro	Glu	Arg	Tyr	Gly	His	Val	Leu	Ser	Gly	

WO 00/29448

PCT/JP99/06412

229/233

415	420	425	
tgg atc tgc ggg gag gag gcc ctc gtc atg gag aag tgt gat gac gag			1529
Trp Ile Cys Gly Glu Glu Ala Leu Val Met Glu Lys Cys Asp Asp Glu			
430	435	440	
gca gtg gcc gag atc tgc acg gag atg ctg cgt cag ttc aca ggg aac			1577
Ala Val Ala Glu Ile Cys Thr Glu Met Leu Arg Gln Phe Thr Gly Asn			
445	450	455	
ccc aac att cca aaa cct cgg cga atc ttg cgc tgc gcc tgg ggc agc			1625
Pro Asn Ile Pro Lys Pro Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser			
460	465	470	
aac cct tac ttc cgc ggc tcc tat tca tac acg cag gtg ggc tcc agc			1673
Asn Pro Tyr Phe Arg Gly Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser			
475	480	485	490
ggg gcg gat gtg gag aag ctg gcc aag ccc ctg ccg tac acg gag agc			1721
Gly Ala Asp Val Glu Lys Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser			
495	500	505	
tca aag aca gcg ccc atg cag gtg ctg ttt tcc ggt gag gcc acc cac			1769
Ser Lys Thr Ala Pro Met Gln Val Leu Phe Ser Gly Glu Ala Thr His			
510	515	520	
cgc aag tac tat tcc acc acc cac ggt gct ctg ctg tcc ggc cag cgt			1817
Arg Lys Tyr Tyr Ser Thr Thr His Gly Ala Leu Leu Ser Gly Gln Arg			
525	530	535	
gag gct gcc cgc ctc att gag atg tac cga gac ctc ttc cag cag ggg			1865
Glu Ala Ala Arg Leu Ile Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly			
540	545	550	
acc tgagggctgt cctcgctgct gagaagagcc actaactcgt gacctccagc ct			1920
Thr			
555			
gcccttgct gccgtgtgct cctgccttcc tgatcctctg tagaaaggat ttttatcttc			1980
tgtagagcta gccgccctga ctgccttcag acctggccct gtagcttttc tttttctcca			2040
ggctgggccc tgagcaggtg ggccgttgag ttacctctgt gctggatccc gtgccccac			2100
ttgcctaccc tctgtcctgc cttgttattg taagtgcctt caatactttg cattttggga			2160
taataaaaaa ggctccctcc cctgcccctc agcttctctc tggttttctc			2210

<210> 149

ctcaagctgg	caggtggtcg	ggggagcggc	cggagaggag	ctgccggggag	ttcgtgccct	60
gcaggacatg	acaccagtgg	catatcacgg	cc atg ggg	tct cag cat	tcc gct	113
			Met Gly Ser	Gln His Ser Ala		
			1		5	
gct gct cgc	ccc tcc tcc	tgc agg cga	aag caa gaa	gat gac agg	gac	161
Ala Ala Arg	Pro Ser Ser	Cys Arg Arg	Lys Gln Glu	Asp Asp Arg	Asp	
	10	15		20		
ggt ttg ctg	gct gaa cga	gag cag gaa	gaa gcc att	gct cag ttc	cca	209
Gly Leu Leu	Ala Glu Arg	Glu Gln Glu	Glu Ala Ile	Ala Gln Phe	Pro	
	25	30		35		
tat gtg gaa	ttc acc ggg	aga gat agc	atc acc tgt	ctc acg tgc	cag	257
Tyr Val Glu	Phe Thr Gly	Arg Asp Ser	Ile Thr Cys	Leu Thr Cys	Gln	
	40	45		50	55	
ggg aca ggc	tac att cca	aca gag caa	gta aat gag	ttg gtg gct	ttg	305
Gly Thr Gly	Tyr Ile Pro	Thr Glu Gln	Val Asn Glu	Leu Val Ala	Leu	
	60	65		70		
atc cca cac	agt gat cag	aga ttg cgc	cct cag cga	act aag caa	tat	353
Ile Pro His	Ser Asp Gln	Arg Leu Arg	Pro Gln Arg	Thr Lys Gln	Tyr	
	75	80		85		
gtc ctc ctg	tcc atc ctg	ctt tgt ctc	ctg gca tct	ggg ttg gtg	gtt	401
Val Leu Leu	Ser Ile Leu	Leu Leu Cys	Leu Leu Ala	Ser Gly Leu	Val Val	
	90	95		100		
ttc ttc ctg	ttt ccg cat	tca gtc ctt	gtg gat gat	gac ggc atc	aaa	449
Phe Phe Leu	Phe Pro His	Ser Val Leu	Val Asp Asp	Asp Gly Ile	Lys	
	105	110		115		
gtg gtg aaa	gtc aca ttt	aat aag caa	gac tcc ctt	gta att ctc	acc	497
Val Val Lys	Val Thr Phe	Asn Lys Gln	Asp Ser Leu	Val Ile Leu	Thr	
120	125		130		135	

WO 00/29448

PCT/JP99/06412

231/233

atc atg gcc acc ctg aaa atc agg aac tcc aac ttc tac acg gtg gca	545
Ile Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala	
140 145 150	
gtg acc agc ctg tcc agc cag att cag tac atg aac aca gtg gtc agt	593
Val Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Ser	
155 160 165	
aca tat gtg act act aac gtc tcc ctt att cca cct cgg agt gag caa	641
Thr Tyr Val Thr Thr Asn Val Ser Leu Ile Pro Pro Arg Ser Glu Gln	
170 175 180	
ctg gtg aat ttt acc ggg aag gcc gag atg gga gga ccg ttt tcc tat	689
Leu Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr	
185 190 195	
gtg tac ttc ttc tgc acg gta cct gag atc ctg gtg cac aac ata gtg	737
Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val	
200 205 210 215	
atc ttc atg cga act tca gtg aag att tca tac att ggc ctc atg acc	785
Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr	
220 225 230	
cag agc tcc ttg gag aca cat cac tat gtg gat tgt gga gga aat tcc	833
Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser	
235 240 245	
aca gct att taacaactgc tattggttct tccacacagc gcctgtagaa gagagcac	890
Thr Ala Ile	
250	
agcatatgtt cccaaggcct gagttctgga cctaccccca cgtggtgtaa gcagaggagg	950
aattggttca ottaactccc agcaaacatc ctctgccac ttaggaggaa acacctccct	1010
atggtaccat ttatgtttct cagaaccagc agaatcagtg cctagcctgt gccagcaaa	1070
tagttggcac tcaataaaga tttgcagaat ttaatacaga tcttttcagc tgttcttagg	1130
gcattataaa tggaaatcat aacgtggttc taggttatca aaccatggag tgatgtggag	1190
ctaggattgt gagtgcctg caggccatta tcagtgcctc atctgtgcag aagtcgcagc	1250
agagagggac catccaaata cctaagagaa aacagacctc gtcaggatat gaatttgttt	1310
cagctgttcc caaaggcctg ggagcttttt gaaaagaaag aaaaaagtgt gttggctttt	1370
ttttttttta gaaagttaga attgttttta ccaagagtct atgtggggct tgattcaccc	1430
ttcatccatt ggctggaaca tggattgggg atttgataga aaaataaacc ctgcttttga	1490
ttc	1493

WO 00/29448

PCT/JP99/06412

232/233

<210> 150

<211> 1264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)...(550)

<400> 150

aatctacaag caccaggaag tcaag atg caa gca cca gcc ttc agg gac aag	52
Met Gln Ala Pro Ala Phe Arg Asp Lys	
1 5	
aaa cag ggg gtc tca gcc aag aat caa ggt gcc cat gac cca gac tat	100
Lys Gln Gly Val Ser Ala Lys Asn Gln Gly Ala His Asp Pro Asp Tyr	
10 15 20 25	
gag aat atc acc ttg gcc ttc aaa aat cag gac cat gca aag ggt ggt	148
Glu Asn Ile Thr Leu Ala Phe Lys Asn Gln Asp His Ala Lys Gly Gly	
30 35 40	
cat tca cga ccc acg agc caa gtc cca gcc cag tgc agg ccg ccc tca	196
His Ser Arg Pro Thr Ser Gln Val Pro Ala Gln Cys Arg Pro Pro Ser	
45 50 55	
gac tcc acc cag gtc ccc tgc tgg ttg tac aga gcc atc ctg agc ctg	244
Asp Ser Thr Gln Val Pro Cys Trp Leu Tyr Arg Ala Ile Leu Ser Leu	
60 65 70	
tac atc ctc ctg gcc ctg gcc ttt gtc ctc tgc atc atc ctg tca gcc	292
Tyr Ile Leu Leu Ala Leu Ala Phe Val Leu Cys Ile Ile Leu Ser Ala	
75 80 85	
ttc atc atg gtg aag aat gct gag atg tcc aag gag ctg ctg ggc ttt	340
Phe Ile Met Val Lys Asn Ala Glu Met Ser Lys Glu Leu Leu Gly Phe	
90 95 100 105	
aaa agg gag ctt tgg aat gtc tca aac tcc gta caa gca tgc gaa gag	388
Lys Arg Glu Leu Trp Asn Val Ser Asn Ser Val Gln Ala Cys Glu Glu	
110 115 120	
aga cag aag aga ggc tgg gat tcc gtt cag cag agc atc acc atg gtc	436
Arg Gln Lys Arg Gly Trp Asp Ser Val Gln Gln Ser Ile Thr Met Val	

WO 00/29448

PCT/JP99/06412

233/233

125	130	135	
agg agc aag att gat aga tta gag acg aca tta gca ggc ata aaa aac			484
Arg Ser Lys Ile Asp Arg Leu Glu Thr Thr Leu Ala Gly Ile Lys Asn			
140	145	150	
att gac aca aag gta cag aaa atc ttg gag gtg ctg cag aaa atg cca			532
Ile Asp Thr Lys Val Gln Lys Ile Leu Glu Val Leu Gln Lys Met Pro			
155	160	165	
cag tcc tca cct caa taaatgagag gacattgtgg cagccaaagc cac			580
Gln Ser Ser Pro Gln			
170			
aacttggaag atggggctgc acctgccaac gaagacggga aatgaccccc cccccagcc			640
tagtgtgaac ctgcccctcg tcccacgtat agaaaaacct cgagtcattg tgaatgagtg			700
tctcgagatt gctcgtgtgt gtgtacacct gcgtgcgtgt gtgtgcgtgt gtgcgcgtgt			760
gttcgtgtat gtgcgtgtgt gcgtgcgcgt gtgtgtgeat tttgcaaagg gtggacattt			820
cagtgtatct cccagaaagg tgatgaatga ataggactga gagtcacagt gaatgtggca			880
tgcattgctg tgcatgtga catatgtgag tctcggcattg tcacggtggg tggctgtgtc			940
tgagcacctc cagcagatgt cactctgagt gtgggtgttg gtgacatgca ttgcacgggc			1000
ctgtctccct gtttgtgtaa acatactaga gtatactgcg gcgtgttttc tgtctacca			1060
tgcatgggtg ggggagattt atctccgtac atgtgggtgt cgccatgtgt gccctgtcac			1120
tatctgtggc tgggtgaacg gctgtgtcat tatgagtggt cagagttatg ccaccctgtg			1180
tgctcagggc acatgcacac agacatttat ctctgcactc acattttgtg acttatgaag			1240
ataaataaag tcaagggaaa acag			1264

SEQUENCE LISTING

<110> Seishi Kato and Tomoko Kimura

<120> HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

<130> GIN-6727CPUS

<150> JP 10-326255

<151> 1998-11-17

<150> JP 10-364315

<151> 1998-12-22

<150> JP 11-69811

<151> 1999-03-16

<150> JP 11-119299

<151> 1999-04-27

<150> JP 11-138169

<151> 1999-05-19

<160> 150

<210> 1

<211> 647

<212> PRT

<213> Homo sapiens

<400> 1

```

Met Ala Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly Gly Gly
 1           5           10           15
Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Thr Glu
      20           25           30
Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro
      35           40           45
Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu Glu Ala
      50           55           60
Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly
      65           70           75           80
Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln
      85           90           95
Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val Pro Asp
      100          105          110
His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala
      115          120          125
Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu
      130          135          140
Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln
      145          150          155          160
Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val
      165          170          175
Cys Thr Val Leu Glu Gln Ala Leu Pro Cys Arg Ser Leu Cys Glu
      180          185          190
Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln
      195          200          205
Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly
      210          215          220
Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro

```

Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro
 225 230 235 240
 Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly
 245 250 255
 Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly
 260 265 270
 Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr
 275 280 285
 His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys
 290 295 300
 Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg
 305 310 315 320
 Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe
 325 330 335
 Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu
 340 345 350
 Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala
 355 360 365
 Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys
 370 375 380
 Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu
 385 390 395 400
 Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser
 405 410 415
 Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly
 420 425 430
 Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His
 435 440 445
 Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala
 450 455 460
 Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly
 465 470 475 480
 Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe
 485 490 495
 Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser
 500 505 510
 Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu
 515 520 525
 Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr
 530 535 540
 Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu Gln Ala
 545 550 555 560
 Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys Lys Ser
 565 570 575
 Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro
 580 585 590
 His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys Tyr Leu
 595 600 605
 Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp Ser Gly
 610 615 620
 Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr Asn Ser
 625 630 635 640
 Lys Gln Gly Glu Thr Thr Val
 645

<210> 2
 <211> 350
 <212> PRT
 <213> Homo sapiens

 <400> 2

Ser	Gln	Pro	Arg	Gly 85	Arg	Asp	Leu	Pro	Trp 90	Leu	Gly	Leu	Val	Gly 95	Pro
Ser	Gly	Leu	Trp 100	Thr	Ala	Asn	Thr	Leu	Cys 105	Cys	Phe	Trp	Lys 110	Ile	Pro
Leu	Pro	His 115	Pro	Cys	Leu	Ser	Pro 120	Ser	Ser	Pro	Pro	Thr 125	Leu	Arg	Ser
Gly	His 130	Pro	Ile	Pro	Phe	Gly 135	His	Gln	Pro	Asn	Arg 140	Leu	Ile	Arg	Gly
Trp 145	Lys	Leu	Gly	Gln	Arg 150	Arg	Arg	Val	Tyr	Pro 155	Leu	Val	Arg	Arg	Arg 160
Ala	Leu	Leu	Lys 165	Gly	Cys	Gly	Ala	Gly	Pro 170	Gly	Ala	Gly	Pro	Gly 175	Leu
Ala	Trp	Ala 180	Ala	Ala	Gly	Ala	Val	Val 185	Pro	Gly	Val	Leu	Gly 190	Ala	Leu
Gly	Pro	Ser 195	Trp	Pro	Ala	Val	Leu 200	Ala	Val	Pro	Val	Pro	Leu 205		

```
<210> 4
<211> 213
<212> PRT
<213> Homo'sapiens
```

[illegible]

```
<210> 5
<211> 595
<212> PRT
<213> Homo sapiens
```

```

<400> 5
Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu
  1             5             10             15
Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala

```

			20				25				30					
Val	Val	Leu	Ala	Ile	Leu	Ala	Arg	Asn	Ala	Glu	His	Ser	Leu	Pro	His	
		35					40					45				
Tyr	Leu	Gly	Ala	Leu	Glu	Arg	Leu	Asp	Tyr	Pro	Arg	Ala	Arg	Met	Ala	
	50					55					60					
Leu	Trp	Cys	Ala	Thr	Asp	His	Asn	Val	Asp	Asn	Thr	Thr	Glu	Met	Leu	
	65				70					75					80	
Gln	Glu	Trp	Leu	Ala	Ala	Val	Gly	Asp	Asp	Tyr	Ala	Ala	Val	Val	Trp	
			85						90					95		
Arg	Pro	Glu	Gly	Glu	Pro	Arg	Phe	Tyr	Pro	Asp	Glu	Glu	Gly	Pro	Lys	
			100					105					110			
His	Trp	Thr	Lys	Glu	Arg	His	Gln	Phe	Leu	Met	Glu	Leu	Lys	Gln	Glu	
			115				120					125				
Ala	Leu	Thr	Phe	Ala	Arg	Asn	Trp	Gly	Ala	Asp	Tyr	Ile	Leu	Phe	Ala	
	130					135					140					
Asp	Thr	Asp	Asn	Ile	Leu	Thr	Asn	Asn	Gln	Thr	Leu	Arg	Leu	Leu	Met	
	145				150					155					160	
Gly	Gln	Gly	Leu	Pro	Val	Val	Ala	Pro	Met	Leu	Asp	Ser	Gln	Thr	Tyr	
			165						170					175		
Tyr	Ser	Asn	Phe	Trp	Cys	Gly	Ile	Thr	Pro	Gln	Gly	Tyr	Tyr	Arg	Arg	
			180					185					190			
Thr	Ala	Glu	Tyr	Phe	Pro	Thr	Lys	Asn	Arg	Gln	Arg	Arg	Gly	Cys	Phe	
			195				200					205				
Arg	Val	Pro	Met	Val	His	Ser	Thr	Phe	Leu	Ala	Ser	Leu	Arg	Ala	Glu	
	210					215					220					
Gly	Ala	Asp	Gln	Leu	Ala	Phe	Tyr	Pro	Pro	His	Pro	Asn	Tyr	Thr	Trp	
	225				230					235					240	
Pro	Phe	Asp	Asp	Ile	Ile	Val	Phe	Ala	Tyr	Ala	Cys	Gln	Ala	Ala	Gly	
			245						250					255		
Val	Ser	Val	His	Val	Cys	Asn	Glu	His	Arg	Tyr	Gly	Tyr	Met	Asn	Val	
			260					265					270			
Pro	Val	Lys	Ser	His	Gln	Gly	Leu	Glu	Asp	Glu	Arg	Val	Asn	Phe	Ile	
		275					280					285				
His	Leu	Ile	Leu	Glu	Ala	Leu	Val	Asp	Gly	Pro	Arg	Met	Gln	Ala	Ser	
	290					295					300					
Ala	His	Val	Thr	Arg	Pro	Ser	Lys	Arg	Pro	Ser	Lys	Ile	Gly	Phe	Asp	
	305				310					315					320	
Glu	Val	Phe	Val	Ile	Ser	Leu	Ala	Arg	Arg	Pro	Asp	Arg	Arg	Glu	Arg	
			325						330					335		
Met	Leu	Ala	Ser	Leu	Trp	Glu	Met	Glu	Ile	Ser	Gly	Arg	Val	Val	Asp	
			340					345					350			
Ala	Val	Asp	Gly	Trp	Met	Leu	Asn	Ser	Ser	Ala	Ile	Arg	Asn	Leu	Gly	
		355					360					365				
Val	Asp	Leu	Leu	Pro	Gly	Tyr	Gln	Asp	Pro	Tyr	Ser	Gly	Arg	Thr	Leu	
	370				375											

Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Ser Gly
 545 550 555 560
 Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Arg
 565 570 575
 Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln Pro Arg
 580 585 590
 Asp Glu Leu
 595

<210> 6
 <211> 264
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Val Ala Ser Ala Lys Met Gly Arg Ala Gly Thr Met Ala Val Ala
 1 5 10 15
 Ala Glu Leu Arg Glu Leu Cys Pro Gly Val Asn Asn Gln Pro Tyr Leu
 20 25 30
 Cys Glu Ser Gly His Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr
 35 40 45
 Tyr Glu Leu Trp Trp Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe
 50 55 60
 Ser Cys Cys Cys Ala Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln
 65 70 75 80
 Gln Gln Gln Arg Gln Arg Glu Ile Asn Leu Leu Ala Tyr His Gly Ala
 85 90 95
 Cys His Gly Ala Gly Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg
 100 105 110
 Phe Leu Ser Thr Phe Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg
 115 120 125
 Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu
 130 135 140
 Thr Ala Ser Ser Glu Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro
 145 150 155 160
 Ala His Phe Glu Gly Thr Asn Val Glu Gly Val Ser Ser His Gln Ser
 165 170 175
 Ala Pro Pro His Gln Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala
 180 185 190
 Ser Thr Pro Pro Ser Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly
 195 200 205
 Ile Glu Leu Cys Pro Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys
 210 215 220
 Glu Val Arg Val Ser Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro
 225 230 235 240
 Cys Ala Leu Pro Pro Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu
 245 250 255
 Ser Ser Ser Glu Gly Asp Ile Pro
 260

<210> 7
 <211> 343
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp

1					5					10					15				
Glu	Asp	Leu	Gln	Gln	Asp	Phe	Gln	Asn	Ile	Gln	Glu	Thr	His	Arg	Leu				
		20						25				30							
Tyr	Arg	Leu	Lys	Leu	Glu	Glu	Leu	Thr	Lys	Leu	Gln	Asn	Asn	Cys	Thr				
		35				40						45							
Ser	Ser	Ile	Thr	Arg	Gln	Lys	Lys	Arg	Leu	Gln	Glu	Leu	Ala	Leu	Ala				
		50				55						60							
Leu	Lys	Lys	Cys	Lys	Pro	Ser	Leu	Pro	Ala	Glu	Ala	Glu	Gly	Ala	Ala				
		65		70						75				80					
Gln	Glu	Leu	Glu	Asn	Gln	Met	Lys	Glu	Arg	Gln	Gly	Leu	Phe	Phe	Asp				
		85						90						95					
Met	Glu	Ala	Tyr	Leu	Pro	Lys	Lys	Asn	Gly	Leu	Tyr	Leu	Ser	Leu	Val				
		100						105						110					
Leu	Gly	Asn	Val	Asn	Val	Thr	Leu	Leu	Ser	Lys	Gln	Ala	Lys	Phe	Ala				
		115						120				125							
Tyr	Lys	Asp	Glu	Tyr	Glu	Lys	Phe	Lys	Leu	Tyr	Leu	Thr	Ile	Ile	Leu				
		130				135						140							
Ile	Leu	Ile	Ser	Phe	Thr	Cys	Arg	Phe	Leu	Leu	Asn	Ser	Arg	Val	Thr				
145				150						155				160					
Asp	Ala	Ala	Phe	Asn	Phe	Leu	Leu	Val	Trp	Tyr	Tyr	Cys	Thr	Leu	Thr				
				165				170						175					
Ile	Arg	Glu	Ser	Ile	Leu	Ile	Asn	Asn	Gly	Ser	Arg	Ile	Lys	Gly	Trp				
		180						185						190					
Trp	Val	Phe	His	His	Tyr	Val	Ser	Thr	Phe	Leu	Ser	Gly	Val	Met	Leu				
		195				200						205							
Thr	Trp	Pro	Asp	Gly	Leu	Met	Tyr	Gln	Lys	Phe	Arg	Asn	Gln	Phe	Leu				
		210				215						220							
Ser	Phe	Ser	Met	Tyr	Gln	Ser	Phe	Val	Gln	Phe	Leu	Gln	Tyr	Tyr	Tyr				
225				230						235				240					
Gln	Ser	Gly	Cys	Leu	Tyr	Arg	Leu	Arg	Ala	Leu	Gly	Glu	Arg	His	Thr				
				245				250						255					
Met	Asp	Leu	Thr	Val	Glu	Gly	Phe	Gln	Ser	Trp	Met	Trp	Arg	Gly	Leu				
		260						265						270					
Thr	Phe	Leu	Leu	Pro	Phe	Leu	Phe	Phe	Gly	His	Phe	Trp	Gln	Leu	Phe				
		275						280				285							
Asn	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Gln	Asp	Pro	Gln	Cys	Lys	Glu				
		290				295						300							
Trp	Gln	Val	Leu	Met	Cys	Gly	Phe	Pro	Phe	Leu	Leu	Leu	Phe	Leu	Gly				
305				310						315				320					
Asn	Phe	Phe	Thr	Thr	Leu	Arg	Val	Val	His	His	Lys	Phe	His	Ser	Gln				
				325						330				335					
Arg	His	Gly	Ser	Lys	Lys	Asp													
		340																	

```
<210> 8
<211> 244
<212> PRT
<213> Homo sapiens
```

<400> 8															
Met	Asp	Ile	Leu	Val	Pro	Leu	Leu	Gln	Leu	Leu	Val	Leu	Leu	Leu	Thr
1				5					10					15	
Leu	Pro	Leu	His	Leu	Met	Ala	Leu	Leu	Gly	Cys	Trp	Gln	Pro	Leu	Cys
			20					25					30		
Lys	Ser	Tyr	Phe	Pro	Tyr	Leu	Met	Ala	Val	Leu	Thr	Pro	Lys	Ser	Asn
		35					40					45			
Arg	Lys	Met	Glu	Ser	Lys	Lys	Arg	Glu	Leu	Phe	Ser	Gln	Ile	Lys	Gly
	50					55					60				
Leu	Thr	Gly	Ala	Ser	Gly	Lys	Val	Ala	Leu	Leu	Glu	Leu	Gly	Cys	Gly
	65				70					75					80
Thr	Gly	Ala	Asn	Phe	Gln	Phe	Tyr	Pro	Pro	Gly	Cys	Arg	Val	Thr	Cys

				85					90					95					
Leu	Asp	Pro	Asn	Pro	His	Phe	Glu	Lys	Phe	Leu	Thr	Lys	Ser	Met	Ala				
			100					105					110						
Glu	Asn	Arg	His	Leu	Gln	Tyr	Glu	Arg	Phe	Val	Val	Ala	Pro	Gly	Glu				
		115					120					125							
Asp	Met	Arg	Gln	Leu	Ala	Asp	Gly	Ser	Met	Asp	Val	Val	Val	Cys	Thr				
	130					135					140								
Leu	Val	Leu	Cys	Ser	Val	Gln	Ser	Pro	Arg	Lys	Val	Leu	Gln	Glu	Val				
	145				150					155					160				
Arg	Arg	Val	Leu	Arg	Pro	Gly	Gly	Val	Leu	Phe	Phe	Trp	Glu	His	Val				
				165					170					175					
Ala	Glu	Pro	Tyr	Gly	Ser	Trp	Ala	Phe	Met	Trp	Gln	Gln	Val	Phe	Glu				
			180					185					190						
Pro	Thr	Trp	Lys	His	Ile	Gly	Asp	Gly	Cys	Cys	Leu	Thr	Arg	Glu	Thr				
		195					200					205							
Trp	Lys	Asp	Leu	Glu	Asn	Ala	Gln	Phe	Ser	Glu	Ile	Gln	Met	Glu	Arg				
	210					215					220								
Gln	Pro	Pro	Pro	Leu	Lys	Trp	Leu	Pro	Val	Gly	Pro	His	Ile	Met	Gly				
	225				230					235					240				
Lys	Ala	Val	Lys																

<210> 9
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 9

Met	Lys	Leu	Lys	Leu	Lys	Asn	Val	Phe	Leu	Ala	Tyr	Phe	Leu	Val	Ser				
	1			5					10					15					
Ile	Ala	Gly	Leu	Leu	Tyr	Ala	Leu	Val	Gln	Leu	Gly	Gln	Pro	Cys	Asp				
		20						25					30						
Cys	Leu	Pro	Pro	Leu	Arg	Ala	Ala	Ala	Glu	Gln	Leu	Arg	Gln	Lys	Asp				
		35					40					45							
Leu	Arg	Ile	Ser	Gln	Leu	Gln	Ala	Glu	Leu	Arg	Arg	Pro	Pro	Pro	Ala				
	50					55					60								
Pro	Ala	Gln	Pro	Pro	Glu	Pro	Glu	Ala	Leu	Pro	Thr	Ile	Tyr	Val	Val				
	65				70					75				80					
Thr	Pro	Thr	Tyr	Ala	Arg	Pro	Leu	Trp	Val	Gln	Tyr	Pro	Gln	Asp	Val				
				85					90					95					
Thr	Thr	Phe	Asn	Ile	Asp	Asp	Gln	Tyr	Leu	Leu	Gly	Asp	Ala	Leu	Leu				
			100					105					110						
Val	His	Pro	Val	Ser	Asp	Ser	Gly	Ala	His	Gly	Val	Gln	Val	Tyr	Leu				
		115					120					125							
Pro	Gly	Gln	Gly	Glu	Val	Trp	Tyr	Asp	Ile	Gln	Ser	Tyr	Gln	Lys	His				
	130					135						140							
His	Gly	Pro	Gln	Thr	Leu	Tyr	Leu	Pro	Val	Thr	Leu	Ser	Ser	Ile	Pro				
	145				150					155					160				
Val	Phe	Gln	Arg	Gly	Gly	Thr	Ile	Val	Pro	Arg	Trp	Met	Arg	Val	Arg				
			165					170						175					
Arg	Ser	Ser	Glu	Cys	Met	Lys	Asp	Asp	Pro	Ile	Thr	Leu	Phe	Val	Ala				
			180					185						190					
Leu	Ser	Pro	Gln	Gly	Thr	Ala	Gln	Gly	Glu	Leu	Phe	Leu	Asp	Asp	Gly				
		195					200					205							
His	Thr	Phe	Asn	Tyr	Gln	Thr	Arg	Gln	Glu	Phe	Leu	Leu	Arg	Arg	Phe				
	210					215					220								
Ser	Phe	Ser	Gly	Asn	Thr	Leu	Val	Ser	Ser	Ser	Ala	Asp	Pro	Glu	Gly				
	225				230					235					240				
His	Phe	Glu	Thr	Pro	Ile	Trp	Ile	Glu	Arg	Val	Val	Ile	Ile	Gly	Ala				
				245					250					255					
Gly	Lys	Pro	Ala	Ala	Val	Val	Leu	Gln	Thr	Lys	Gly	Ser	Pro	Glu	Ser				

260 265 270
 Arg Leu Ser Phe Gln His Asp Pro Glu Thr Ser Val Leu Val Leu Arg
 275 280 285
 Lys Pro Gly Ile Asn Val Ala Ser Asp Trp Ser Ile His Leu Arg
 290 295 300

<210> 10
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg
 1 5 10 15
 Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
 20 25 30
 Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
 35 40 45
 Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
 50 55 60
 Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
 65 70 75 80
 Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
 85 90 95
 Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
 100 105 110
 Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
 115 120 125
 Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
 130 135 140
 Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys Leu Ala
 145 150 155 160

<210> 11
 <211> 1941
 <212> DNA
 <213> Homo sapiens

<400> 11
 atggctgagg agggaggcgcc taagaagtcc cgggcccggcg gcggtggcgc gagctgggaa 60
 ctttgtgccg gggcgctctc ggcccggctg acggaggagg gcagcgggga cgccggtggc 120
 cgccgcgcgc cgccagttga ccccccgcga ttggcgcgcc agctgctgct gctgctttgg 180
 ctgctggagg ctccgctgct gctgggggtc cgggcccagg cgccgggcca ggggccaggc 240
 caggggcccg ggccggggca gcaaccgccc ccgcccctc agcagcaaca gagcgggcag 300
 cagtacaacg gcgagcgggg catctccgtc ccggaccacg gctattgcca gcccatctcc 360
 atcccgtgt gcacggacat cgcgtacaac cagaccatca tgcccaacct gctggggccac 420
 acgaaccagg aggaacgcgg cctggagggtg caccagttct accctctagt gaaagtgcag 480
 tgttccgctg agctcaagtt ctccctgtgc tccatgtacg cgcccgtgtg caccgtgcta 540
 gaggaggcgc tgcgcacctg ccgctccctg tgcgagcgcg cgcccgagg ctgcgaggcg 600
 ctcatgaaca agttcggctt ccagtggcca gacacgctca agtgtgagaa gttcccggtg 660
 cacggcgccc gcgagctgtg cgtgggccag aacacgtccc acaagggcac cccgacgccc 720
 tcgctgcttc cagagttctg gaccagcaac cctcagcacg gcggcggagg gcaccgtggc 780
 ggcttcccgg ggggcgcccg cgcgtcggag cgaggcaagt tctcctgccc gcgcgcctc 840
 aaggtgccct cctacctcaa ctaccacttc ctgggggaga aggactgcgg cgcaccttgt 900
 gagccgacca aggtgtatgg gctcatgtac ttccggccc aggagctgcg cttctcgcgc 960
 acctggattg gcatttggtc agtgcgtgtc tgcgcctcca cgctcttcac ggtgcttacg 1020
 tacctggtgg acatgcggcg cttcagctac ccggagcggc ccatcatctt cttgtccggc 1080
 tgttacacgg ccgtggccgt ggcctacatc gccggcttcc tcttgaaga ccgagtgggtg 1140
 tgtaatgaca agttcgccga ggacggggca cgcactgtgg cgcagggcac caagaaggag 1200
 ggctgcacca tcctcttcat gatgctctac ttcttcagca tggccagctc catctggtgg 1260
 gtgatcctgt cgctcacctg gttcctggcg gctggcatga agtggggcca cgaggccatc 1320

gaagccaact	cacagtat	tcacctggcc	gcctgggctg	tgccggccat	caagaccatc	1380
accatcctgg	cgctgggcca	ggtggacggc	gatgtgctga	gcgagagtgtg	cttcgtgggg	1440
cttaacaacg	tggacgcgct	gcgtggcttc	gtgctggcgc	ccctcttcgt	gtacctgttt	1500
atcggcacgt	cctttctgct	ggccggcttt	gtgtcgctct	tccgcatecg	caccatcatg	1560
aagcacgatg	gcaccaagac	cgagaagctg	gagaagctca	tggtgcgcat	tggcgtcttc	1620
agcgtgctgt	acactgtgcc	agccaccatc	gtcatcgctt	gctacttcta	cgagcaggcc	1680
ttccggggacc	agtgggaacg	cagctgggtg	gccagagctt	gcaagagcta	cgctatcccc	1740
tgccctcacc	tccaggcggg	cggaggcgcc	ccgccgcacc	cgcccatgag	cccggacttc	1800
acggtcttca	tgattaaagta	ccttatgacg	ctgatcgtgg	gcacacagtc	gggcttctgg	1860
atctgggtccg	gcaagaccct	caactcctgg	aggaagttct	acacgaggct	caccaacagc	1920
aaacaagggg	agactacagt	c				1941

<210> 12
 <211> 1050
 <212> DNA
 <213> Homo sapiens

<400> 12						
atgcaccctg	cagccttccc	gcttctctgtg	gttgtggccg	ctgtgctgtg	gggagcggcc	60
ccgaccggg	ggctcattcg	agcgacctcg	gaccacaatg	ccagcatgga	ctttgcagac	120
cttccagctc	tggttggggc	taccttgagc	caggaggggc	tccaggggtt	ccttgtggag	180
gctcaccag	acaatgcctg	cagccccatt	gccccaccac	ccccagcccc	ggtcaatggg	240
tcagtcttta	ttgcgctgct	tcgaagattc	gactgcaact	ttgacctcaa	ggtcctaaat	300
gccagaagg	ctggatatgg	tgccgctgta	gtacacaatg	tgaattccaa	tgaacttctg	360
aacatggtgt	ggaatagtga	ggaaatccag	cagcagatct	ggatcccgtc	tgtatttatt	420
ggggagagaa	gctccgagta	cctgcgtgcc	ctctttgtct	acgagaagg	ggctcgggtg	480
cttctgggtc	cagacaatac	cttccccttg	ggctattacc	tcaccccttt	cacagggatt	540
gtgggactgc	tggttttggc	catgggagca	gtaatgatag	ctcgttgtat	ccagcaccgg	600
aaacggctcc	agcgggaatc	acttaccaaa	gagcaactga	aacagattcc	tacacatgac	660
tatcagaagg	gagaccaagta	tgatgtctgt	gccatttgcc	tgatgaata	tgaggatggg	720
gacaagctgc	gggtactccc	ctgtgctcat	gcctaccaca	gccgctgcgt	ggacccctgg	780
ctcactcaga	cccgggaagac	ctgccccatt	tgcaagcagc	ctgttcacgc	gggtcctggg	840
gacgaagacc	aagaggaaga	aactcaagg	caagaggagg	gtgatgaagg	ggagccaagg	900
gaccaccctg	cctcagaagg	gaccccaatt	ttgggttcta	gccccactct	tccccactcc	960
tttggttcct	tagccccagc	tccccttggt	tttctggggc	cttcaacaga	tccccactg	1020
tccccctcct	cttcccctgt	tatcctggtc				1050

<210> 13
 <211> 618
 <212> DNA
 <213> Homo sapiens

<400> 13						
atggggctgg	gtcagcccca	ggcctgggtg	ctgggtctgc	ccacagctgt	ggtctatggc	60
tccctggctc	tcttcaccac	catcctgcac	aatgtcttcc	tgctctacta	tgtggacacc	120
tttgtctcag	tgtacaagat	caacaaaatg	gccttctggg	tggagagagc	agtgtttctc	180
ctctggaaca	gcctcaatga	ccccctcttc	ggttggctca	gtgaccggca	gttccctcagc	240
tccagcccc	ggggaagaga	tctaccctgg	cttggcttgg	ttggccccctc	tggactgtgg	300
actgcaaaca	ccctctgctg	cttctggaag	attcctttgc	cccatccctg	cttgagcccg	360
tcatcaccctc	caaccttgag	aagtgggcat	cccataccct	ttggccatca	gcccacacagg	420
ctaataagg	ggtggaaatt	ggggcagagg	aggagagtgt	accactgggt	caggcgccgg	480
gctctcctca	agggctgtgg	tgctggcccc	ggtgcaggcc	ctgggctggc	atgggcgct	540
gctggcgctg	tcgttctctg	cgttctgggt	gcctggggcc	ccagctggcc	tgcagttctt	600
gctgtgcctg	tgctctca					618

<210> 14
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 14

atgcactatt	atagatactc	taacgccaa	gtcagctgct	ggtacaagta	cctccttttc	60
agctacaaca	tcattcttctg	gttggctgga	gttgtcttcc	ttggagtcgg	gctgtgggca	120
tggagcga	aggggtgtgct	gtccgacctc	accaaagtga	cccggatgca	tggaaatcgac	180
cctgtggtgc	tggctctgat	gggtggcgtg	gtgatgttca	ccctgggggtt	cgccggctgc	240
gtgggggctc	tgcgggagaa	tatctgcttg	ctcaacttta	accagtgtctg	tggcgcatat	300
ggccctgaag	actgggacct	caacgtctac	ttcaattgca	gcgggtgccag	ctacagccga	360
gagaagtgcg	gggtccctt	ctcctgctgc	gtgccagatc	ctgcgcaaaa	agttgtgaac	420
acacagtgtg	gatatgatgt	caggattcag	ctgaagagca	agtgggatga	gtccatcttc	480
acgaaaggct	gcatccaggc	gctggaaagc	tggctcccgc	ggaacattta	cattgtggct	540
ggcgtcttca	tcgccatctc	gctgttgtag	atatttggca	tcttctctgga	aaggacgctg	600
atctcagaca	tcgaggcagt	gaaggccggc	catcacttc			639

<210> 15
 <211> 1785
 <212> DNA
 <213> Homo sapiens

<400> 15						
atgcgcgctg	cccgcgcgcg	gccgctgctc	cagctgctgc	tcctgctggg	gccgtggtg	60
gaggctgcgg	gcgttgccga	gtcgcgcgtg	cccgcgcgtg	tccttgccat	cctggccgcg	120
aatgccgaac	actcgtctgc	ccactacctg	ggcgtctctg	agcggctgga	ctacccccgg	180
gccaggatgg	ccctctgggt	tgccacggac	cacaatgtgg	acaacaccac	agagatgctg	240
caggagtggc	tggcgcgtgt	ggcgatgac	tatgctgctg	tggctctggag	gcctgagggc	300
gagcccaggt	tctacccaga	tgaagaggg	cccaagcact	ggaccaaaga	aaggcaccag	360
tttctgatgg	agctgaagca	ggaagccctc	acctttgcc	ggaactgggg	ggccgactat	420
atcctgtttg	cagacacaga	caacattctg	accaacaatc	agactctgcg	gcttctcatg	480
gggcaggggg	ttccagtgg	ggccccaatg	ctggactccc	agacctacta	ctccaacttc	540
tgggtgtggga	tcacccccca	gggctactac	cgccgcacag	ccgagtactt	ccccaccaag	600
aaccgccagc	gccggggctg	cttccgtgtc	cccatggtec	actccacctt	ccttgcatcc	660
ctgcgggctg	aaggggcaga	ccagcttgc	ttctaccgcg	cacatcccaa	ctacacttgg	720
cctttcgacg	acatcatcgt	cttcgcctat	gcctgccagg	ctgctgggg	ctccgtccac	780
gtgtgcaatg	agcaccgtta	tgggtacatg	aatgtgccgg	tgaatccca	ccaggggctg	840
gaagacgaga	gggtcaactt	catccacctg	atcttagaag	cactagtgg	cggccccgcg	900
atgcaggcct	cagctcatgt	gactcggccc	tctaagaggc	ccagcaagat	agggtttgac	960
gaggctctttg	tcattcagct	ggctcgcagg	cctgaccgtc	gggaacgc	gctcgcctcg	1020
ctctgggaga	tggagatctc	tgggaggggt	gtggacgctg	tggatggctg	gatgctcaac	1080
agcagtgcc	tcagggaacct	cggcgtagac	ctgctcccgg	gctaccagga	cccttactcg	1140
ggccgcactc	tgaccaagg	cgaggtgggc	tgttctctca	gccattactc	catctgggaa	1200
gaggtggttg	ccaggggcct	ggccccgggtc	ctgggtgttg	aggatgacgt	gcgctttgag	1260
agcaacttca	gggggcggct	ggagcggctg	atggaggatg	tggaggcaga	gaaactgtct	1320
tgggaacctga	tctacctcgg	acggaagcag	gtgaaccttg	agaaggagac	ggccgtggag	1380
gggctgccgg	gcctggtgg	ggctgggtac	tctactgga	cgctggccta	tgccctgcgt	1440
ctggcgggtg	cccgcgaagct	gctggcctca	cagcctctgc	gccgcatgct	gcccgtggac	1500
gagttcctgc	ccatcatgtt	cgaccagcac	cccaacgagc	agtacaaggc	acacttcttg	1560
ccacgggacc	tgggtggcctt	ctccgcccag	cccctgctcg	ctgcccctac	ccactatgcc	1620
ggggacgccg	agtggctcag	tgacacggag	acatcctctc	catgggatga	tgacagcggc	1680
cgcctcatca	gctggagcgg	ctcccaaaa	accctgcgca	gccccgcct	ggacctgact	1740
ggcagcagcg	ggcacagcct	ccaacccag	ccccgagatg	agctc		1735

<210> 16
 <211> 792
 <212> DNA
 <213> Homo sapiens

<400> 16						
atgggtggcct	cagcgaagat	gggccgggca	gggacatgg	cggtggcagc	agagcttcga	60
gagctgtgcc	caggagtga	caaccagccc	tacctctgtg	agagtggtea	ctgctgcggg	120
gagactggct	gctgcaccta	ctactatgag	ctctgggtgg	tctggctgct	ctggactgtc	180
ctcatcctct	ttagctgctg	ttgcgccttc	cgccaccgac	gagctaaact	caggctgcaa	240
caacagcagc	ggcagcgtga	aatcaacttg	ttggcctatc	atggggcatg	ccatggggct	300
ggtcctttcc	ctaccgggttc	actgcttgac	cttcgcttcc	tcagcacctt	caagccccc	360

gcctacgagg	atgtggttca	ccgcccaggc	acaccacccc	ccccttatac	tgtggcecca	420
ggccgcccc	tgactgcttc	cagtgaacaa	acctgctggt	cctcctcacc	cagctgcect	480
gcccactttg	aaggaacaaa	tgtggaaggt	gtttcctccc	accagagtgc	cccccccat	540
caggaggggtg	agcccggggc	aggggtgacc	cctgcctcca	cacccccctc	ctgcctctat	600
cgccgtttta	ctggcgactc	cggtattgag	ctctgccctt	gtcctgcctc	cggtaggggt	660
gagccagtca	aggaggtgag	ggttagtgcc	accctgccag	atctggagga	ctactccccg	720
tgtgcactac	cccagagtc	tgtaccgcag	atctttccca	tggggctgtc	ttccagtga	780
ggggacatcc	ca					792

<210> 17
 <211> 1029
 <212> DNA
 <213> Homo sapiens

<400> 17						
atgcagcccc	cgccccggg	cccgtgggc	gactgcctgc	gggactggga	ggatctacag	60
caggacttcc	agaacatcca	ggagacccat	cggctctacc	gcctgaagct	ggaggagctg	120
accaaacttc	agaacaattg	caccagctcc	atcacgcggc	agaagaagcg	gctccaggag	180
ctggccctcg	ccctgaagaa	atgcaaacc	tccctcccag	cagaggccga	gggggccgca	240
caggagctgg	agaaccagat	gaaagagcgc	caaggcctct	tctttgacat	ggaggcctat	300
ttgcctaaga	agaatggatt	gtacctgagc	ctgggtctgg	ggaacgtcaa	cgtcacgctc	360
ctgagcaagc	aggctaagtt	tgcctacaag	gacgagtatg	agaagttcaa	gctctacctc	420
accatcatcc	tcatcctcat	ctccttcaact	tgccgcttcc	tgctcaactc	cagggtgaca	480
gatgctgcct	tcaacttcct	gctggtctgg	tactactgca	ccctgaccat	ccgggagagc	540
atcctcatca	acaacggctc	ccggatcaaa	ggctgggtgg	tggtccatca	ctacgtgtcc	600
accttccctgt	cgggagtcac	gctgacgtgg	cccgacggtc	tcatgtacca	gaaattcccg	660
aaccaattcc	tctccttttc	catgtaccag	agcttcgtgc	agtttctcca	gtactactac	720
cagagcggct	gcctctaccg	cctgcgggcg	ctgggcgagc	ggcacacccat	ggacctcact	780
gtggagggct	tccagtcctg	gatgtggcgg	ggcctcacct	tctgtctgcc	ttttcttttc	840
tttgagacact	tctggcagct	ttttaacgcg	ctgacgttgt	tcaacctggc	ccaggacctt	900
cagtgcgaagg	agtggcaggt	gcttatgtgc	ggctttccct	tcctcctcct	tttcctcggc	960
aatttcttca	ccacctgag	ggttgtgcac	cacaagtttc	acagtcagcg	gcacgggagc	1020
aagaaggat						1029

<210> 18
 <211> 732
 <212> DNA
 <213> Homo sapiens

<400> 18						
atggacatcc	tggtcccact	cctgcagctg	ctgggtgctgc	ttcttaccct	gccccgcac	60
ctcatggctc	tgtgtggctg	ctggcagccc	ctgtgcaaaa	gctacttccc	ctacctgatg	120
gocgtgctga	ctcccaagag	caaccgcaag	atggagagca	agaaacggga	gctcttcagc	180
cagataaagg	ggcttacagg	agcctccggg	aaagtggccc	tactggagct	gggctgcgga	240
accggagcca	actttcagtt	ctacccaccg	ggctgcaggg	tcacctgcct	agacccaaat	300
ccccactttg	agaagttcct	gacaaagagc	atggctgaga	acaggcacct	ccaatatgag	360
cggtttgttg	tggctcctgg	agaggacatg	agacagctgg	ctgatggctc	catggatgtg	420
gtgggtctgca	ctctggtgct	gtgctctgtg	cagagcccaa	ggaaggctct	gcaggaggtc	480
cggagagtac	tgagaccggg	aggtgtgctc	tttttctggg	agcatgtggc	agaaccatat	540
ggaagctggg	ccttcatgtg	gcagcaagtt	ttcgagccca	cctggaaaca	cattggggat	600
ggctgctgcc	tcaccagaga	gacctggaag	gatcttgaga	acgcccagtt	ctccgaaatc	660
caaattggaac	gacagccccc	tcccttgaag	tggctacctg	ttgggccccca	catcatggga	720
aaggctgtca	aa					732

<210> 19
 <211> 909
 <212> DNA
 <213> Homo sapiens

<400> 19						
atgaagctga	agctgaagaa	cgtgtttctc	gcctacttcc	tggtgtcgat	cgccggcctc	60

```

ctctacgcgc tggtagagct cggccagcca tgtgactgcc ttctctccct gcgggcagca 120
gccgagcagc tacggcagaa ggatctgagg atttcccagc tgcaagcgga actccgacgg 180
ccacccccctg cccctgccca gcccctgaa cccgaggccc tgccctactat ctatgttggt 240
acccccacct atgccaggcc cctgtgggtg cagtaccctc aggatgtgac taccttcaat 300
atagatgac agtacttgct tgggagtcg ttgctggttc accctgtatc agactctgga 360
gcccatgggtg tccaggctta tctgcctggc caaggggagg tgtggtatga cattcaaagc 420
taccagaagc atcatggtcc ccagaccctg tacctgcctg taactctaag cagtatccct 480
gtgttccagc gtggaggagc aatcgtgcct cgatggatgc gagtgcggcg gtcttcagaa 540
tgtatgaagg atgaccccat cactctcttt gttgcactta gccctcaggg tacagctcaa 600
ggagagctct ttctggatga tgggcacacg ttcaactatc agactcgcca agagttcctg 660
ctgcgtcgat tctcattctc tggcaacacc cttgtctcca gctcagcaga cctgaagga 720
cactttgaga caccaatctg gattgagcgg gtggtgataa taggggctgg aaagccagca 780
gctgtggtag tccagacaaa aggatctcca gaaagccgcc tgtccttcca gcatgacct 840
gagacctctg tgttggctct gcgcaagcct ggcataatg ttgcatctga ttggagtatt 900
cacctgcga 909

```

<210> 20
 <211> 480
 <212> DNA
 <213> Homo sapiens

```

<400> 20
atggacaagc tgaagaaggt gctgagcggg caggacacgg aggaccggag cggcctgtcc 60
gaggttggtg aggcattctc attaagctgg agtaccagga taaaaggctt cattgcgtgt 120
tttgcctatg gaattctctg ctactgctg ggtactgttc tgctgtgggt gccaggaag 180
ggactacacc tcttcgcagt gttttataacc tttgtaata tcgcatcaat tgggagtacc 240
atcttctca tgggaccagt gaaacagctg aagcgaatgt ttgagcctac tcgtttgatt 300
gcaactatca tgggtgctgt gtgttttgca cttaccctgt gttctgcctt ttggtggcat 360
aacaagggac ttgcacttat cttctgcatt ttgcagctct tggcattgac gtggtacagc 420
ctttccttca taccatttgc aagggatgct gtgaagaagt gttttgccgt gtgtcttgca 480

```

<210> 21
 <211> 4485
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (189)...(2132)

```

<400> 21
gaatcgcaag tttccgcggc ggcggcggct gcggtacgca gaacaggagc cgggggagcg 60
ggccgaaaagc ggcttgggct cgacggaggg caccgcgcga gaggtctccc tggccgcagg 120
gggagccgcc gccggccgtg cccctggcag cccagcgga gcggcgccaa gagaggagcc 180
gagaaagt atg gct gag gag gag gcg cct aag aag tcc cgg gcc gcc ggc 230
      Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly
          1           5           10
ggt ggc gcg agc tgg gaa ctt tgt gcc ggg gcg ctc tcg gcc cgg ctg 278
Gly Gly Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu
      15           20           25           30
acg gag gag ggc agc ggg gac gcc ggt ggc cgc cgc cgc ccg cca gtt 326
Thr Glu Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val
          35           40           45
gac ccc cgg cga ttg gcg cgc cag ctg ctg ctg ctg ctt tgg ctg ctg 374
Asp Pro Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu
          50           55           60
gag gct ccg ctg ctg ctg ggg gtc cgg gcc cag gcg gcg ggc cag ggg 422
Glu Ala Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly
          65           70           75
cca ggc cag ggg ccc ggg ccg ggg cag caa ccg ccg ccg cct cag 470
Pro Gly Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln

```


gttgggaagag actgaagata tgggttataa aatgttaatt ctaattgcat acggatgcct 3230
 ggcaaccttg cctttgagaa tgagacagcc tgcgcttaga ttttaccggt ctgtaaaatg 3290
 gaaatgttga ggtcacctgg aaagctttgt taaggagtgt atgtttgctt tccttaacaa 3350
 gacagcaaaa cgtaaacaga aattgaaaaac ttgaaggata tttcagtgtc atggacttcc 3410
 tcaaaatgaa gtgctatttt cttattttta atcaaataac tagacatata tcagaaactt 3470
 taaaatgtaa aagttgtaca ctttcaacat tttattacga ttattattca gcagcacatt 3530
 ctgagggggg aacaattcac accaccaata ataacctggt aagatttcag gaggtaaaga 3590
 aggtggaata attgacgggg agatagcgcc tgaaataaac aaaatatggg catgcatgct 3650
 aaagggaaaa tgtgtgcagg tctactgcat taaatcctgt gtgctcctct tttggattta 3710
 cagaaatgtg tcaaatgtaa atctttcaaa gccatttaaa aatattcact ttagttctct 3770
 gtgaagaaga ggagaaaagc aatcctcctg attgtattgt tttaaacttt aagaatttat 3830
 caaaatgccg gtacttagga cctaaattta tctatgtctg tcatacgcta aaatgatatt 3890
 ggtctttgaa tttgggtatac atttattctg ttcactatca caaaatcatc tatattttata 3950
 gaggaataga agtttatata tatataatac catattttta atttcacaaa taaaaaatte 4010
 aaagttttgt acaaaattat atggattttg tgcctgaaaa taatagagct tgagctgtct 4070
 gaactatttt acattttatg gtgtctcata gccaatccca cagtgtaaaa attcaggaat 4130
 tcaatgaaaa aagtctaccc ttaaaccctc agatcagctt ttccaaagaa ttactctgtt 4190
 tgcattgttg tgattgacat ttgtgaagtc ccaagaaaag atctgttttc atgacagtag 4250
 aaaatagaag tttgcaaatt atttctttac tcaaagagga ttaaaagaga actctaattt 4310
 taatattaaa gctttctttt ctttcaggga ataaatttac atgacttttt atattatgga 4370
 ggtttatttt taaatcatca cttttctcat attttttaga ggtattgtct tatctcttcc 4430
 ataatcttgg atattacaaa accctaaata ggcaatcaat aaatggttaa ctggc 4485

<210> 22

<211> 1509

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (253)...(1305)

<400> 22

ttttccgcgt tttatccccg taccagaaaa ggatacattht agtgccctccc acccagctcc 60
 actaaacggg ttggatatct cattctttga gttgggtgttc cttccccggc gcccccatgt 120
 agctgggaag tgggacctgg ggggtggttg acccctggga tcctaaagga ggggcagggg 180
 ggggcgcagaa ctccgcttct gctccttgct accaggacgc gcggcctcct cagcctcttt 240
 cctcccgctg cc atg cac cct gca gcc ttc ccg ctt cct gtg gtt gtg gcc 291
 Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala
 1 5 10
 gct gtg ctg tgg gga gcg gcc ccg acc cgg ggg ctc att cga gcg acc 339
 Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr
 15 20 25
 tcg gac cac aat gcc agc atg gac ttt gca gac ctt cca gct ctg ttt 387
 Ser Asp His Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe
 30 35 40 45
 ggg gct acc ttg agc cag gag ggc ctc cag ggg ttc ctt gtg gag gct 435
 Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala
 50 55 60
 cac cca gac aat gcc tgc agc ccc att gcc cca cca ccc cca gcc ccg 483
 His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro
 65 70 75
 gtc aat ggg tca gtc ttt att gcg ctg ctt cga aga ttc gac tgc aac 531
 Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn
 80 85 90
 ttt gac ctc aag gtc cta aat gcc cag aag gct gga tat ggt gcc gct 579
 Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala
 95 100 105
 gta gta cac aat gtg aat tcc aat gaa ctt ctg aac atg gtg tgg aat 627
 Val Val His Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn

110	115										120					125					
agt gag gaa atc cag cag cag atc tgg atc ccg tct gta ttt att ggg																675					
Ser Glu Glu Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly																					
130										135					140						
gag aga agc tcc gag tac ctg cgt gcc ctc ttt gtc tac gag aag ggg																723					
Glu Arg Ser Ser Glu Tyr Leu Arg Ala Leu Phe Val Tyr Lys Gly																					
145										150					155						
gct cgg gtg ctt ctg gtt cca gac aat acc ttc ccc ttg ggc tat tac																771					
Ala Arg Val Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr																					
160										165					170						
ctc atc cct ttc aca ggg att gtg gga ctg ctg gtt ttg gcc atg gga																819					
Leu Ile Pro Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly																					
175										180					185						
gca gta atg ata gct cgt tgt atc cag cac ccg aaa ccg ctc cag ccg																867					
Ala Val Met Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg																					
190	195										200					205					
aat cga ctt acc aaa gag caa ctg aaa cag att cct aca cat gac tat																915					
Asn Arg Leu Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr																					
210										215					220						
cag aag gga gac cag tat gat gtc tgt gcc att tgc ctg gat gaa tat																963					
Gln Lys Gly Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr																					
225										230					235						
gag gat ggg gac aag ctg cgg gta ctc ccc tgt gct cat gcc tac cac																1011					
Glu Asp Gly Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His																					
240										245					250						
agc cgc tgc gtg gac ccc tgg ctc act cag acc ccg aag acc tgc ccc																1059					
Ser Arg Cys Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro																					
255										260					265						
att tgc aag cag cct gtt cat cgg ggt cct ggg gac gaa gac caa gag																1107					
Ile Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu																					
270	275										280					285					
gaa gaa act caa ggg caa gag gag ggt gat gaa ggg gag cca agg gac																1155					
Glu Glu Thr Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp																					
290										295					300						
cac cct gcc tca gaa agg acc cca ctt ttg ggt tct agc ccc act ctt																1203					
His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu																					
305										310					315						
ccc acc tcc ttt ggt tcc tta gcc cca gct ccc ctt gtt ttt cct ggg																1251					
Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly																					
320										325					330						
cct tca aca gat ccc cca ctg tcc cct ccc tct tcc cct gtt atc ctg																1299					
Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu																					
335										340					345						
gtc taataacccc ccacacatac acctctggtg acctatttgc acagaccg																1350					
Val																					
350																					
tcgtcttccc tccagtccttc tgagggatag gggacattcc atcccaagct tctcccttac																1410					
ccacacctat ccttttgagg ggctttgggg tggggctggg gcaagcagag ggactgggtc																1470					
ttcacttctt gggctaataa aattgtttct ttgtggact																1509					

```
<210> 23
<211> 3059
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (230) ... (850)
```

<400> 23
cctggctccc gccagccgtg ggattagqct tcgccggcta cgattgcggc ccccatcttc 60

tgactttttcc	tcgtgtgacc	catctttttca	aatttccctta	cctgaggaag	gagcccgatt	120
acaaggatat	ttacctgctc	ctaccctgat	ctagggacga	ggatgggaag	accgcctgtg	180
gccatgagcc	ctccccggtg	ctcctggggc	taaggctggg	gctgcagcc	atg ggg ctg	238
					Met Gly Leu	
					1	
ggt cag ccc cag gcc tgg ttg ctg ggt ctg ccc	aca gct gtg gtc tat	286				
Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala Val Val Tyr						
5 10 15						
ggc tcc ctg gct ctc ttc acc acc atc ctg cac aat gtc ttc ctg ctc	334					
Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val Phe Leu Leu						
20 25 30 35						
tac tat gtg gac acc ttt gtc tca gtg tac aag atc aac aaa atg gcc	382					
Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn Lys Met Ala						
40 45 50						
ttc tgg gtc gga gag aca gtg ttt ctc ctc tgg aac agc ctc aat gac	430					
Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser Leu Asn Asp						
55 60 65						
ccc ctc ttc ggt tgg ctc agt gac cgg cag ttc ctc agc tcc cag ccc	478					
Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser Ser Gln Pro						
70 75 80						
cgg gga aga gat cta ccc tgg ctt ggc ttg gtt ggc ccc tct gga ctg	526					
Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro Ser Gly Leu						
85 90 95						
tgg act gca aac acc ctc tgc tgc ttc tgg aag att cct ttg ccc cat	574					
Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro Leu Pro His						
100 105 110 115						
ccc tgc ttg agc ccg tca tca ccc cca acc ttg aga agt ggg cat ccc	622					
Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser Gly His Pro						
120 125 130						
ata ccc ttt ggc cat cag ccc aac agg cta ata agg ggg tgg aaa ttg	670					
Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly Trp Lys Leu						
135 140 145						
ggg cag agg agg aga gtg tac cca ctg gtc agg cgc cgg gct ctc ctc	718					
Gly Gln Arg Arg Val Tyr Pro Leu Val Arg Arg Arg Ala Leu Leu						
150 155 160						
aag ggc tgt ggt gct ggc ccg ggt gca ggc cct ggg ctg gca tgg gcc	766					
Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu Ala Trp Ala						
165 170 175						
gct gct ggc gct gtc gtt cct ggc gtt ctg ggt gcc ctg ggc ccc agc	814					
Ala Ala Gly Ala Val Pro Gly Val Leu Gly Ala Leu Gly Pro Ser						
180 185 190 195						
tgg cct gca gtt ctt gct gtg cct gtg cct cta tgatggcttc ctg	860					
Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu						
200 205						
acgctcgtgg acctgcacca ccatgccttg ctggccgacc tgccctcttc agcccacgac	920					
cgcacccacc tcaacttcta ctgctccctc ttcagcgagg ccggctccct ctctgtcttt	980					
gcacccctatg ccttttggaa caaggaggat ttctctcct tccgcgcttt ctgctgaca	1040					
ctggctgtca gctctgggt gggctttctg ggggccacac agctgctgag gcggcggtt	1100					
gaggcgggccc gaaaggaccc aggggtgctca ggcttggttg tggatagcgg cctgtgtgga	1160					
gaggagctgc ttgtaggcag tgaggaggcg gacagcatca ccttggggccg gtatctccgg	1220					
cagctggcac gccatcgaa cttcctgttg ttctgtagca tggacctggt gcaggtcttc	1280					
cactgccact tcaacagcaa cttcttccct ctcttccctg agcatctgtt gtcgacat	1340					
atctcccttt ccacgggctc catcctgttg ggctctcct atgtcgctcc ccatctcaac	1400					
aacctctact tctgtccct gtgcgggcgc tggggcgctc acggggtggt gcgggggctc	1460					
ttcctgtca agctgggact tagcctgctc atgttggttg ccggcccggg caacctcagc	1520					
ctgctgtgcc ttttcattgc cagcaaccgc gctcttact agggcacctg taagctgtg	1580					
accttggttg tcaactgacct ggtagacgag gacctggtgc tgaaccaccg caagcaggca	1640					
gcctcggcac tctcttttg catggttgcc ttggtgacca agccaggcca gacctttgcc	1700					
ccgctgctgg gcacctggct gctctgttcc tacacaggctc atgacctctt ccagcagtc	1760					
ctcataaccc ctgtggggag tgcccatccc tggccagagc cccagctcc agccctgca	1820					
caggccccga cgctccgcca gggctgcttc tacctgctgg tgctggtgcc catcacctgt	1880					

145						150						155						
atc	ttc	acg	aaa	ggc	tgc	atc	cag	gcg	ctg	gaa	agc	tgg	ctc	ccg	cgg	590		
Ile	Phe	Thr	Lys	Gly	Cys	Ile	Gln	Ala	Leu	Glu	Ser	Trp	Leu	Pro	Arg			
160						165						170						
aac	att	tac	att	gtg	gct	ggc	gtc	ttc	atc	gcc	atc	tcg	ctg	ttg	cag	638		
Asn	Ile	Tyr	Ile	Val	Ala	Gly	Val	Phe	Ile	Ala	Ile	Ser	Leu	Leu	Gln			
175						180						185						190
ata	ttt	ggc	atc	ttc	ctg	gca	agg	acg	ctg	atc	tca	gac	atc	gag	gca	686		
Ile	Phe	Gly	Ile	Phe	Leu	Ala	Arg	Thr	Leu	Ile	Ser	Asp	Ile	Glu	Ala			
195						200						205						
gtg	aag	gcc	ggc	cat	cac	ttc	tgaggagcag	agttgaggga	gccgagctga	gcc						740		
Val	Lys	Ala	Gly	His	His	Phe												
210																		
acgctgggag	gccagagcct	ttctctgcc	tcagccctac	gtccagaggg	agaggagccg											800		
acacccccag	agccagtgcc	ccatcttaag	catcagcgtg	acgtgacctc	tctgtttctg											860		
cttgctgggtg	ctgaagacca	aggggtcccc	ttgttaacctg	cccaaacttg	tgactgcatc											920		
cctctggagt	ctacccagag	acagagaatg	tgtctttatg	tgggagtggg	gactctgaaa											980		
gacagagagg	gctcctgtgg	ctgccaggag	ggcttgactc	agacccccctg	cagctcaagc											1040		
atgtctgcag	gacaccttg	tccccctctc	actggcatcc	agacatctgc	tttgggtcat											1100		
ccacatctgt	gggtggggcg	tgggtagagg	gacccacagg	cgtggacagg	gcactctctc											1160		
ccatcaagca	aagcagctg	ggggctggcc	cgtaacggga	ggcggacgtg	gccccgctgg											1220		
gcctctgagt	gccagcgcag	tctgctggga	catgcacata	tcaggggttg	tttgaggat											1280		
cctcagccat	gttcaagtga	agtaagcctg	agccagtgcg	tggactgggtg	ccacgggagt											1340		
gccttgctcca	ctgtccccct	gtgtccacca	gctattctcc	tggcgccgga	actgcctctg											1400		
gtcttgatag	cattaagccc	tgatggcgcc	ggtggcgcg	tgggcatggt	tcttcaactga											1460		
gagccggctc	tcccttttct	aaagtgtgta	aatagtttat	ttataggggt	aagaatgttc											1520		
tcacaccatt	tcacttctc	tccctctctc	ccagcattct	cctctgagca	gccttagata											1580		
gtgtccattg	ctggagccga	cccccttgagt	cccccttgagt	gtcttaagaa	ccagccaca											1640		
acagcctctc	ttctctctcc	acatactgea	gcctccctcc	atgcatacca	catacaagca											1700		
ctccccact	cccagcgtg	gcctcactgt	cttctgggtc	tgggtgctact	gaaattgtca											1760		
cccagaattt	gaatcctgac	cctccccact	gcaagcccag	ggagccccag	cccaagatgg											1820		
ccagcctgaa	actgttggcc	agggctcctc	ttgtggccat	gtacccaggg	ctggctggcc											1880		
tggcatttgc	ctctcccccg	agacagccgt	tcttctgcaa	ccacaccccc	tgcctagcca											1940		
caaccccagg	ctgcagctgc	tcagaagctc	caggcatttt	gtttctgggt	accgccccta											2000		
atgggatata	ggtgatcact	ggtccacct	tctgtccagg	gcttttctgg	gctgtctctt											2060		
ggaaatgaag	tcttaagtac	tgaataactc	ccctggggat	agctggggca	tttgtctagc											2120		
tgggctactt	tctaacactt	tgccatagct	cagaccactt	ctcatcgttc	agggatggac											2180		
tgcaacctta	atttacttgc	cggagtgtac	attctagtgt	ggtgtatact	ggtggctggt											2240		
gatgatgatt	tttttttttt	tttttttacac	aattctctgt	agactaggag	aagaatgctt											2300		
gtgttttttcg	gaagtgtgat	gcttctcttt	gactgccaaa	ctctttttatg	gaatatatct											2360		
ttatatt																		

```
<210> 25
<211> 2355
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (20)...(1807)
```

[illegible]

cac His	tcg Ser 45	ctg Leu	ccc Pro	cac His	tac Tyr	ctg Leu 50	ggc Gly	gct Ala	ctg Leu	gag Glu	cgg Arg 55	ctg Leu	gac Asp	tac Tyr	ccc Pro	196
cgg Arg 60	gcc Ala	agg Arg	atg Met	gcc Ala	ctc Leu 65	tgg Trp	tgt Cys	gcc Ala	acg Thr	gac Asp 70	cac His	aat Asn	gtg Val	gac Asp	aac Asn 75	244
acc Thr	aca Thr	gag Glu	atg Met	ctg Leu 80	cag Gln	gag Glu	tgg Trp	ctg Leu	gcg Ala 85	gct Ala	gtg Val	ggc Gly	gat Asp 90	gac Asp	tat Tyr	292
gct Ala	gct Ala	gtg Val	gtc Val 95	tgg Trp	agg Arg	cct Pro	gag Glu	ggc Gly 100	gag Glu	ccc Pro	agg Arg	ttc Phe 105	tac Tyr	cca Pro	gat Asp	340
gaa Glu	gag Glu	ggt Gly 110	ccc Pro	aag Lys	cac His	tgg Trp	acc Thr 115	aaa Lys	gaa Glu	agg Arg	cac His	cag Gln 120	ctt Phe	ctg Leu	atg Met	388
gag Glu	ctg Leu 125	aag Lys	cag Gln	gaa Glu	gcc Ala	ctc Leu 130	acc Thr	ttt Phe	gcc Ala	agg Arg	aac Asn 135	tgg Trp	ggg Gly	gcc Ala	gac Asp	436
tat Tyr 140	atc Ile	ctg Leu	ttt Phe	gca Ala	gac Asp 145	aca Thr	gac Asp	aac Asn	att Ile 150	ctg Leu	acc Thr	aac Asn	aat Asn	cag Gln	act Thr 155	484
ctg Leu	cgg Arg	ctt Leu	ctc Leu	atg Met 160	ggg Gly	cag Gln	ggg Gly	ctt Leu	cca Pro 165	gtg Val	gtg Val	gcc Ala	cca Pro	atg Met 170	ctg Leu	532
gac Asp	tcc Ser	cag Gln	acc Thr 175	tac Tyr	tac Tyr	tcc Ser	aac Asn	ttc Phe 180	tgg Trp	tgt Cys	ggg Gly	atc Ile 185	acc Thr	ccc Pro	cag Gln	580
ggc Gly	tac Tyr 190	tac Tyr	cgc Arg	cgc Arg	aca Thr	gcc Ala	gag Glu 195	tac Tyr	ttc Phe	ccc Pro	acc Thr 200	aag Lys	aac Asn	cgc Arg	cag Gln	628
cgc Arg 205	cgg Arg	ggc Gly	tgc Cys	ttc Phe	cgt Arg	gtc Val 210	ccc Pro	atg Met	gtc Val	cac His	tcc Ser 215	acc Thr	ttc Phe	ctt Leu	gca Ala	676
tcc Ser 220	ctg Leu	cgg Arg	gct Ala	gaa Glu 225	ggg Gly	gca Ala	gac Asp	cag Gln	ctt Leu	gct Ala 230	ttc Phe	tac Tyr	ccg Pro	cca Pro	cat His 235	724
ccc Pro	aac Asn	tac Tyr	act Thr 240	tgg Trp	cct Pro	ttc Phe	gac Asp	gac Asp	atc Ile 245	atc Ile	gtc Val	ttc Phe	gcc Ala	tat Tyr 250	gcc Ala	772
tgc Cys	cag Gln	gct Ala	gct Ala 255	ggg Gly	gtc Val	tcc Ser	gtc Val	cac His 260	gtg Val	tgc Cys	aat Asn	gag Glu 265	cac His	cgt Arg	tat Tyr	820
ggg Gly	tac Tyr 270	atg Met	aat Asn	gtg Val	ccg Pro	gtg Val	aaa Lys 275	tcc Ser	cac His	cag Gln	ggg Gly 280	ctg Leu	gaa Glu	gac Asp	gag Glu	868
agg Arg	gtc Val 285	aac Asn	ttc Phe	atc Ile	cac His	ctg Leu 290	atc Ile	tta Leu	gaa Glu	gca Ala 295	cta Leu	gtg Val	gac Asp	ggc Gly	ccc Pro	916
cgc Arg 300	atg Met	cag Gln	gcc Ala	tca Ser	gct Ala 305	cat His	gtg Val	act Thr	cgg Arg 310	ccc Pro	tct Ser	aag Lys	agg Arg	ccc Pro	agc Ser 315	964
aag Lys	ata Ile	ggg Gly	ttt Phe	gac Asp 320	gag Glu	gtc Val	ttt Phe	gtc Val	atc Ile 325	agc Ser	ctg Leu	gct Ala	cgc Arg	agg Arg 330	cct Pro	1012
gac Asp	cgt Arg	cgg Arg	gaa Glu 335	cgc Arg	atg Met	ctc Leu	gcc Ala	tcg Ser 340	ctc Leu	tgg Trp	gag Glu	atg Met	gag Glu 345	atc Ile	tct Ser	1060
ggg Gly	agg Arg	gtg Val	gtg Val 350	gac Asp	gct Ala	gtg Val	gat Gly 355	ggc Gly	tgg Trp	atg Met	ctc Leu 360	aac Asn	agc Ser	agt Ser	gcc Ala	1108
atc	agg	aac	ctc	ggc	gta	gac	ctg	ctc	ccg	ggc	tac	caq	gac	cct	tac	1156

Ile	Arg	Asn	Leu	Gly	Val	Asp	Leu	Leu	Pro	Gly	Tyr	Gln	Asp	Pro	Tyr	
365						370					375					
tgc	ggc	cgc	act	ctg	acc	aag	ggc	gag	gtg	ggc	tgc	ttc	ctc	agc	cat	1204
Ser	Gly	Arg	Thr	Leu	Thr	Lys	Gly	Glu	Val	Gly	Cys	Phe	Leu	Ser	His	
380						385				390					395	
tac	tcc	atc	tgg	gaa	gag	gtg	gtt	gcc	agg	ggc	ctg	gcc	cgg	gtc	ctg	1252
Tyr	Ser	Ile	Trp	Glu	Glu	Val	Val	Ala	Arg	Gly	Leu	Ala	Arg	Val	Leu	
				400				405						410		
gtg	ttt	gag	gat	gac	gtg	cgc	ttt	gag	agc	aac	ttc	agg	ggg	cgg	ctg	1300
Val	Phe	Glu	Asp	Asp	Val	Arg	Phe	Glu	Ser	Asn	Phe	Arg	Gly	Arg	Leu	
				415				420					425			
gag	cgg	ctg	atg	gag	gat	gtg	gag	gca	gag	aaa	ctg	tct	tgg	gac	ctg	1348
Glu	Arg	Leu	Met	Glu	Asp	Val	Glu	Ala	Glu	Lys	Leu	Ser	Trp	Asp	Leu	
				430				435					440			
atc	tac	ctc	gga	cgg	aag	cag	gtg	aac	cct	gag	aag	gag	acg	gcc	gtg	1396
Ile	Tyr	Leu	Gly	Arg	Lys	Gln	Val	Asn	Pro	Glu	Lys	Glu	Thr	Ala	Val	
						450										
gag	ggg	ctg	ccg	ggc	ctg	gtg	gtg	gct	ggg	tac	tcc	tac	tgg	acg	ctg	1444
Glu	Gly	Leu	Pro	Gly	Leu	Val	Val	Ala	Gly	Tyr	Ser	Tyr	Trp	Thr	Leu	
460						465				470					475	
gcc	tat	gcc	ctg	cgt	ctg	gcg	ggt	gcc	cgc	aag	ctg	ctg	gcc	tca	cag	1492
Ala	Tyr	Ala	Leu	Arg	Leu	Ala	Gly	Ala	Arg	Lys	Leu	Leu	Ala	Ser	Gln	
					480					485					490	
cct	ctg	cgc	cgc	atg	ctg	ccc	gtg	gac	gag	ttc	ctg	ccc	atc	atg	ttc	1540
Pro	Leu	Arg	Arg	Met	Leu	Pro	Val	Asp	Glu	Phe	Leu	Pro	Ile	Met	Phe	
				495				500						505		
gac	cag	cac	ccc	aac	gag	cag	tac	aag	gca	cac	ttc	tgg	cca	cgg	gac	1588
Asp	Gln	His	Pro	Asn	Glu	Gln	Tyr	Lys	Ala	His	Phe	Trp	Pro	Arg	Asp	
				510				515						520		
ctg	gtg	gcc	ttc	tcc	gcc	cag	ccc	ctg	ctc	gct	gcc	cct	acc	cac	tat	1636
Leu	Val	Ala	Phe	Ser	Ala	Gln	Pro	Leu	Leu	Ala	Ala	Pro	Thr	His	Tyr	
					525											
gcc	ggg	gac	gcc	gag	tgg	ctc	agt	gac	acg	gag	aca	tcc	tct	cca	tgg	1684
Ala	Gly	Asp	Ala	Glu	Trp	Leu	Ser	Asp	Thr	Glu	Thr	Ser	Ser	Pro	Trp	
540						545				550					555	
gat	gat	gac	agc	ggc	cgc	ctc	atc	agc	tgg	agc	ggc	tcc	caa	aag	acc	1732
Asp	Asp	Asp	Ser	Gly	Arg	Leu	Ile	Ser	Trp	Ser	Gly	Ser	Gln	Lys	Thr	
					560					565					570	
ctg	cgc	agc	ccc	cgc	ctg	gac	ctg	act	ggc	agc	agc	ggg	cac	agc	ctc	1780
Leu	Arg	Ser	Pro	Arg	Leu	Asp	Leu	Thr	Gly	Ser	Ser	Gly	His	Ser	Leu	
				575				580						585		
caa	ccc	cag	ccc	cga	gat	gag	ctc	taggtccagg	tgatgactgc	aaagca						1830
Gln	Pro	Gln	Pro	Arg	Asp	Glu	Leu									
				590			595									
gtgtccagga	gcaggccact	actgccccaga	gagcagagga	ggaggttggt	ggcagggact											1890
gcagatcctg	tcagacctgg	ccaccacctt	gggcatggcc	actctgccct	ctggacctgt											1950
ctttcatcgg	gagaaaccac	tcagagatgg	atcccatctc	ctaaaggctct	cacagcaaag											2010
gagcaggact	cccaggcccc	tgtacctctg	ctggcctgat	tcagggcctt	gtggccccca											2070
gcttctgttt	caagctgggc	agaccccagg	atcccttccc	tccctaagga	ctcagctgag											2130
gggccccctct	gcccccttct	acctccacct	cagcaccctc	ccccagcttg	atgtttgggt											2190
ctccccagca	ccctcctccc	tggccggtgc	aaagtacagg	gaggtaaagc	aggacccttg											2250
cagacatggt	gcccagcaca	cagtaggccc	tcaataaaag	ccatttgcac	tttaaataata											2310
tatatgtatg	tatatatatg	tatatatata	tatatatata	tatgt												2355

<210> 26
 <211> 1024
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (27)...(821)

<400> 26

```

cggatggaag ctccggccgc ggagtg atg gtg gcc tca gcg aag atg ggc cgg      53
               Met Val Ala Ser Ala Lys Met Gly Arg
               1               5

gca ggg acc atg gcg gtg gca gca gag ctt cga gag ctg tgc cca gga      101
Ala Gly Thr Met Ala Val Ala Ala Glu Leu Arg Glu Leu Cys Pro Gly
10               15               20               25
gtg aac aac cag ccc tac ctc tgt gag agt ggt cac tgc tgc ggg gag      149
Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His Cys Cys Gly Glu
               30               35               40
act ggc tgc tgc acc tac tac tat gag ctc tgg tgg ttc tgg ctg ctc      197
Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Leu
               45               50               55
tgg act gtc ctc atc ctc ttt agc tgc tgt tgc gcc ttc cgc cac cga      245
Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala Phe Arg His Arg
               60               65               70
cga gct aaa ctc agg ctg caa caa cag cag cgg cag cgt gaa atc aac      293
Arg Ala Lys Leu Arg Leu Gln Gln Gln Gln Arg Gln Arg Glu Ile Asn
               75               80               85
ttg ttg gcc tat cat ggg gca tgc cat ggg gct ggt cct ttc cct acc      341
Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly Pro Phe Pro Thr
90               95               100               105
ggg tca ctg ctt gac ctt cgc ttc ctc agc acc ttc aag ccc cca gcc      389
Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala
               110               115               120
tac gag gat gtg gtt cac cgc cca ggc aca cca ccc ccc cct tat act      437
Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro Pro Pro Tyr Thr
               125               130               135
gtg gcc cca ggc cgc ccc ttg act gct tcc agt gaa caa acc tgc tgt      485
Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu Gln Thr Cys Cys
               140               145               150
tcc tcc tca tcc agc tgc cct gcc cac ttt gaa gga aca aat gtg gaa      533
Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly Thr Asn Val Glu
               155               160               165
ggg gtt tcc tcc cac cag agt gcc ccc ccc cat cag gag ggt gag ccc      581
Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln Glu Gly Glu Pro
170               175               180               185
ggg gca ggg gtg acc cct gcc tcc aca ccc ccc tcc tgc cgc tat cgc      629
Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser Cys Arg Tyr Arg
               190               195               200
cgt tta act ggc gac tcc ggt att gag ctc tgc cct tgt cct gcc tcc      677
Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro Cys Pro Ala Ser
               205               210               215
ggg gag ggt gag cca gtc aag gag gtg agg gtt agt gcc acc ctg cca      725
Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser Ala Thr Leu Pro
               220               225               230
gat ctg gag gac tac tcc ccg tgt gca cta ccc cca gag tct gta ccg      773
Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro Glu Ser Val Pro
               235               240               245
cag atc ttt ccc atg ggg ctg tct tcc agt gaa ggg gac atc cca      818
Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Glu Gly Asp Ile Pro
250               255               260
ta agtagttttg agagggtgga tgggttactt gccaccaga aacagcccta      870
gtcccaactc cttgcgttcc ttggccct cctgcctac ctagaatctg cctgaaagg      930
ctggagaggg gcagtattgg gggactgtgc tagctttacc cccgcaggac atacacagga      990
gcctttgatc tcattaaaga gatgtgaacc agct      1024

```

<210> 27

<211> 1237

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (24)...(1055)

<400> 27

```
tactggctac tggcgctgca gcc atg cag ccc ccg ccc ccg ggc ccg ctg ggc      53
                Met Gln Pro Pro Pro Pro Gly Pro Leu Gly
                1          5          10
gac tgc ctg cgg gac tgg gag gat cta cag cag gac ttc cag aac atc      101
Asp Cys Leu Arg Asp Trp Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile
                15          20          25
cag gag acc cat cgg ctc tac cgc ctg aag ctg gag gag ctg acc aaa      149
Gln Glu Thr His Arg Leu Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys
                30          35          40
ctt cag aac aat tgc acc agc tcc atc acg cgg cag aag aag cgg ctc      197
Leu Gln Asn Asn Cys Thr Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu
                45          50          55
cag gag ctg gcc ctc gcc ctg aag aaa tgc aaa ccc tcc ctc cca gca      245
Gln Glu Leu Ala Leu Ala Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala
                60          65          70
gag gcc gag ggg gcc gca cag gag ctg gag aac cag atg aaa gag cgc      293
Glu Ala Glu Gly Ala Ala Gln Glu Leu Glu Asn Gln Met Lys Glu Arg
                75          80          85
caa ggc ctc ttc ttt gac atg gag gcc tat ttg cct aag aag aat gga      341
Gln Gly Leu Phe Phe Asp Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly
                95          100          105
ttg tac ctg agc ctg gtt ctg ggg aac gtc aac gtc acg ctc ctg agc      389
Leu Tyr Leu Ser Leu Val Leu Gly Asn Val Asn Val Thr Leu Leu Ser
                110          115          120
aag cag gct aag ttt gcc tac aag gac gag tat gag aag ttc aag ctc      437
Lys Gln Ala Lys Phe Ala Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu
                125          130          135
tac ctc acc atc atc ctc atc ctc atc tcc ttc act tgc cgc ttc ctg      485
Tyr Leu Thr Ile Ile Leu Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu
                140          145          150
ctc aac tcc agg gtg aca gat gct gcc ttc aac ttc ctg ctg gtc tgg      533
Leu Asn Ser Arg Val Thr Asp Ala Ala Phe Asn Phe Leu Leu Val Trp
                155          160          165
tac tac tgc acc ctg acc atc cgg gag agc atc ctc atc aac aac ggc      581
Tyr Tyr Cys Thr Leu Thr Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly
                175          180          185
tcc cgg atc aaa ggc tgg tgg gtg ttc cat cac tac gtg tcc acc ttc      629
Ser Arg Ile Lys Gly Trp Trp Val Phe His His Tyr Val Ser Thr Phe
                190          195          200
ctg tcg gga gtc atg ctg acg tgg ccc gac ggt ctc atg tac cag aaa      677
Leu Ser Gly Val Met Leu Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys
                205          210          215
ttc cgg aac caa ttc ctc tcc ttt tcc atg tac cag agc ttc gtg cag      725
Phe Arg Asn Gln Phe Leu Ser Phe Ser Met Tyr Gln Ser Phe Val Gln
                220          225          230
ttt ctc cag tac tac tac cag agc ggc tgc ctc tac cgc ctg cgg gcg      773
Phe Leu Gln Tyr Tyr Tyr Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala
                235          240          245
ctg ggc gag cgg cac acc atg gac ctc act gtg gag ggc ttc cag tcc      821
Leu Gly Glu Arg His Thr Met Asp Leu Thr Val Glu Gly Phe Gln Ser
                255          260          265
tgg atg tgg cgg ggc ctc acc ttc ctg ctg cct ttt ctt ttc ttt gga      869
Trp Met Trp Arg Gly Leu Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly
```

270						275						280									
cac	ttc	tgg	cag	ctt	ttt	aac	gcg	ctg	acg	ttg	ttc	aac	ctg	gcc	cag	917					
His	Phe	Trp	Gln	Leu	Phe	Asn	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Gln						
285						290						295									
gac	cct	cag	tgc	aag	gag	tgg	cag	gtg	ctt	atg	tgc	ggc	ttt	ccc	ttc	965					
Asp	Pro	Gln	Cys	Lys	Glu	Trp	Gln	Val	Leu	Met	Cys	Gly	Phe	Pro	Phe						
300						305						310									
ctc	ctc	ctt	ttc	ctc	ggc	aat	ttc	ttc	acc	acc	ctg	agg	gtt	gtg	cac	1013					
Leu	Leu	Leu	Phe	Leu	Gly	Asn	Phe	Phe	Thr	Thr	Leu	Arg	Val	Val	His						
315						320						325						330			
cac	aag	ttt	cac	agt	cag	cgg	cac	ggg	agc	aag	aag	gat	tgaggctg		1060						
His	Lys	Phe	His	Ser	Gln	Arg	His	Gly	Ser	Lys	Lys	Asp									
335						340															
ggccttccccc						tgccggcccca						gaggggcttc						tgtctctgtgt	ggttggtgggag	gggatgggag	1120
gcgcccctcg						agtgtgcgtg						tatacaggggg						tctcttctat	tctcccttgg	gttttatggg	1180
cgctgtgggc						cctgaaggaa						gacctgggcc						cagtgccttc	aataaagaga	gqcccaq	1237

```
<210> 28
<211> 1331
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (39) ... (773)
```

<400> 28																	
agtgtccccag cggaagcaca gctcagagct ggtctgcc											atg gac atc ctg gtc cca						56
											Met Asp Ile Leu Val Pro						
											1 5						
ctc	ctg	cag	ctg	ctg	gtg	ctg	ctt	ctt	acc	ctg	ccc	ctg	cac	ctc	atg	104	
Leu	Leu	Gln	Leu	Leu	Val	Leu	Leu	Leu	Thr	Leu	Pro	Leu	His	Leu	Met		
											10 15 20						
gct	ctg	ctg	ggc	tgc	tgg	cag	ccc	ctg	tgc	aaa	agc	tac	ttc	ccc	tac	152	
Ala	Leu	Leu	Gly	Cys	Trp	Gln	Pro	Leu	Cys	Lys	Ser	Tyr	Phe	Pro	Tyr		
											25 30 35						
ctg	atg	gcc	gtg	ctg	act	ccc	aag	agc	aac	cgc	aag	atg	gag	agc	aag	200	
Leu	Met	Ala	Val	Leu	Thr	Pro	Lys	Ser	Asn	Arg	Lys	Met	Glu	Ser	Lys		
											40 45 50						
aaa	cgg	gag	ctc	ttc	agc	cag	ata	aag	ggg	ctt	aca	gga	gcc	tcc	ggg	243	
Lys	Arg	Glu	Leu	Phe	Ser	Gln	Ile	Lys	Gly	Leu	Thr	Gly	Ala	Ser	Gly		
											55 60 65 70						
aaa	gtg	gcc	cta	ctg	gag	ctg	ggc	tgc	gga	acc	gga	gcc	aac	ttt	cag	296	
Lys	Val	Ala	Leu	Leu	Glu	Leu	Gly	Cys	Gly	Thr	Gly	Ala	Asn	Phe	Gln		
											75 80 85						
ttc	tac	cca	ccg	ggc	tgc	agg	gtc	acc	tgc	cta	gac	cca	aat	ccc	cac	344	
Phe	Tyr	Pro	Pro	Gly	Cys	Arg	Val	Thr	Cys	Leu	Asp	Pro	Asn	Pro	His		
											90 95 100						
ttt	gag	aag	ttc	ctg	aca	aag	agc	atg	gct	gag	aac	agg	cac	ctc	caa	392	
Phe	Glu	Lys	Phe	Leu	Thr	Lys	Ser	Met	Ala	Glu	Asn	Arg	His	Leu	Gln		
											105 110 115						
tat	gag	cgg	ttt	gtg	gtg	gct	cct	gga	gag	gac	atg	aga	cag	ctg	gct	440	
Tyr	Glu	Arg	Phe	Val	Val	Ala	Pro	Gly	Glu	Asp	Met	Arg	Gln	Leu	Ala		
											120 125 130						
gat	ggc	tcc	atg	gat	gtg	gtg	gtc	tgc	act	ctg	gtg	ctg	tgc	tct	gtg	488	
Asp	Gly	Ser	Met	Asp	Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val		
											135 140 145 150						
cag	agc	cca	agg	aag	gtc	ctg	cag	gag	gtc	cgg	aga	gta	ctg	aga	ccg	536	
Gln	Ser	Pro	Arg	Lys	Val	Leu	Gln	Glu	Val	Arg	Arg	Val	Leu	Arg	Pro		
											155 160 165						
gga	ggt	gtg	ctc	ttt	ttc	tgg	gaq	cat	qtg	qca	qaa	cca	tat	qqa	agc	584	

Gly	Gly	Val	Leu	Phe	Phe	Trp	Glu	His	Val	Ala	Glu	Pro	Tyr	Gly	Ser	
			170					175					180			
tgg	gcc	ttc	atg	tgg	cag	caa	gtt	ttc	gag	ccc	acc	tgg	aaa	cac	att	632
Trp	Ala	Phe	Met	Trp	Gln	Gln	Val	Phe	Glu	Pro	Thr	Trp	Lys	His	Ile	
		185					190					195				
ggg	gat	ggc	tgc	tgc	ctc	acc	aga	gag	acc	tgg	aag	gat	ctt	gag	aac	680
Gly	Asp	Gly	Cys	Cys	Leu	Thr	Arg	Glu	Thr	Trp	Lys	Asp	Leu	Glu	Asn	
	200					205					210					
gcc	cag	ttc	tcc	gaa	atc	caa	atg	gaa	cga	cag	ccc	cct	ccc	ttg	aag	728
Ala	Gln	Phe	Ser	Glu	Ile	Gln	Met	Glu	Arg	Gln	Pro	Pro	Pro	Leu	Lys	
	215				220					225				230		
tgg	cta	cct	gtt	ggg	ccc	cac	atc	atg	gga	aag	gct	gtc	aaa	taatctttc		779
Trp	Leu	Pro	Val	Gly	Pro	His	Ile	Met	Gly	Lys	Ala	Val	Lys			
			235					240								
caagctccaa	ggcactcatt	tgctccttcc	ccagcctcca	attagaacaa	gccacccacc											839
agcctatcta	tcttccactg	agagggacct	agcagaatga	gagaagacat	tcatgtacca											899
cctactagtc	cctctctccc	caacctctgc	cagggcaatc	tctaacttca	atccccgctt											959
cgacagtga	aaagctctac	ttctacgctg	acccaggag	gaaacactag	gaccctgttg											1019
tatcctcaac	tgcaagtttc	tggaactagtc	tcccaacggt	tgctcccaa	tgttgctccct											1079
ttccttcgtt	cccatggtaa	agctcctctc	gctttcctcc	tgaggctaca	cccatgctgc											1139
tctaggaact	ggtcacaaaa	gtcatggtgc	ctgcatccct	gccaagcccc	cctgaccctc											1199
tctccccact	accaccttct	tcttgagctg	ggggcaccag	ggagaatcag	agatgctggg											1259
gatgccagag	caagactcaa	agaggcagag	gttttggtct	caaatatattt	ttaataaata											1319
gacgaaacca	cg															1331

<210> 29
 <211> 1932
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (38)...(949)

<400> 29	
agacccccgcc	tgctcgggcg
	cgggcgggcg
	cgcgggcc
	atg aag ctg aag ctg aag
	Met Lys Leu Lys Leu Lys
	1 5
aac gtg ttt ctc gcc tac ttc ctg gtg tgc atc gcc ggc ctc ctc tac	103
Asn Val Phe Leu Ala Tyr Phe Leu Val Ser Ile Ala Gly Leu Leu Tyr	
	10 15 20
gcg ctg gta cag ctc ggc cag cca tgt gac tgc ctt cct ccc ctg cgg	151
Ala Leu Val Gln Leu Gly Gln Pro Cys Asp Cys Leu Pro Pro Leu Arg	
	25 30 35
gca gca gcc gag cag cta cgg cag aag gat ctg agg att tcc cag ctg	199
Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp Leu Arg Ile Ser Gln Leu	
	40 45 50
caa gcg gaa ctc cga cgg cca ccc cct gcc cct gcc cag ccc cct gaa	247
Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala Pro Ala Gln Pro Pro Glu	
	55 60 65 70
ccc gag gcc ctg cct act atc tat gtt gtt acc ccc acc tat gcc agg	295
Pro Glu Ala Leu Pro Thr Ile Tyr Val Val Thr Pro Thr Tyr Ala Arg	
	75 80 85
ccc ctg tgg gtg cag tac cct cag gat gtg act acc ttc aat ata gat	343
Pro Leu Trp Val Gln Tyr Pro Gln Asp Val Thr Thr Phe Asn Ile Asp	
	90 95 100
gat cag tac ttg ctt ggg gat gcg ttg ctg gtt cac cct gta tca gac	391
Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu Val His Pro Val Ser Asp	
	105 110 115
tct gga gcc cat ggt gtc cag gtc tat ctg cct ggc caa ggg gag gtg	439
Ser Gly Ala His Gly Val Gln Val Tyr Leu Pro Gly Gln Gly Glu Val	

```

120      125      130
tgg tat gac att caa agc tac cag aag cat cat ggt ccc cag acc ctg      487
Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His His Gly Pro Gln Thr Leu
135      140      145      150
tac ctg cct gta act cta agc agt atc cct gtg ttc cag cgt gga ggg      535
Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro Val Phe Gln Arg Gly Gly
155      160      165
aca atc gtg cct cga tgg atg cga gtg cgg cgg tct tca gaa tgt atg      583
Thr Ile Val Pro Arg Trp Met Arg Val Arg Arg Ser Ser Glu Cys Met
170      175      180
aag gat gac ccc atc act ctc ttt gtt gca ctt agc cct cag ggt aca      631
Lys Asp Asp Pro Ile Thr Leu Phe Val Ala Leu Ser Pro Gln Gly Thr
185      190      195
gct caa gga gag ctc ttt ctg gat gat ggg cac acg ttc aac tat cag      679
Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly His Thr Phe Asn Tyr Gln
200      205      210
act cgc caa gag ttc ctg ctg cgt cga ttc tca ttc tct ggc aac acc      727
Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe Ser Phe Ser Gly Asn Thr
215      220      225      230
ctt gtc tcc agc tca gca gac cct gaa gga cac ttt gag aca cca atc      775
Leu Val Ser Ser Ser Ala Asp Pro Glu Gly His Phe Glu Thr Pro Ile
235      240      245
tgg att gag cgg gtg gtg ata ata ggg gct gga aag cca gca gct gtg      823
Trp Ile Glu Arg Val Val Ile Ile Gly Ala Gly Lys Pro Ala Ala Val
250      255      260
gta ctc cag aca aaa gga tct cca gaa agc cgc ctg tcc ttc cag cat      871
Val Leu Gln Thr Lys Gly Ser Pro Glu Ser Arg Leu Ser Phe Gln His
265      270      275
gac cct gag acc tct gtg ttg gtc ctg cgc aag cct ggc atc aat gtg      919
Asp Pro Glu Thr Ser Val Leu Val Leu Arg Lys Pro Gly Ile Asn Val
280      285      290
gca tct gat tgg agt att cac ctg cga taacccaagg gatgttctgg gtta      970
Ala Ser Asp Trp Ser Ile His Leu Arg
295      300
gggggaggga aggggagcat tagtgctgag agatattctt tcttctgcct tggagttcgg      1030
ccctccccag acttcactta tgctagtcta agaccagat tctgccaaca tttgggcagg      1090
atgagagggc tgacctggg ctccaaattc ctcttgatgat ctccctacct ctccactcc      1150
attgatacca actctttccc ttcattcccc caacatcctg ttgctctaac tggagcacat      1210
tcacttacga acaccaggaa accacagggc ccttgctgcc ctttctcttt cccttattta      1270
ggagccctga actccccag agtctatcca ttcatgcctc ttgtatgttg atgccacttc      1330
ttggaagaag atgagggcaa tgagttaggg ctctttttcc ccttccctcc caccagattg      1390
ctctcccacc tttcatttct tctccaggc tttactcccc tttttatgcc ccaccgatac      1450
actgggacca ccccttacct cggacaggat gaatggatca aaggagtgag gttgctaaag      1510
aacatccctt tccctctcat tctacccttt tctctcccc gattccttgt agagctgctg      1570
caattcttag aggggcagtt ctacctctc tgtccctcgg cagaaagacg tttccacacc      1630
tcttagggga tgcgcattaa acttcttttg ccccttctt gtccctttg aggggcactt      1690
aagatggaga aatcagttgt ggtttcagt aatcatggtc acctgtattt attgctagga      1750
gaagcctgag ggtgggggga gatgatcatg tgtgctcggg gttggctgga agccctgggt      1810
ggggggttgg gggaggacta atggggagtc ggggaatatt tgtgggtatt tttttactt      1870
cctcttggtt ccagctgtg acacgttttg atcaaaggag aaacaataaa gggataaacc      1930
at
1932

```

```

<210> 30
<211> 1124
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73)...(555)

```


<400> 30																
ggaagagccg tcaacttagc gagcgcaaca ggctgccgct gaggagctgg agctgggtggg																60
gactggggccg ca atg gac aag ctg aag aag gtg ctg agc ggg cag gac acg																111
Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr																
1 5 10																
gag gac cgg agc ggc ctg tcc gag gtt gtt gag gca tct tca tta agc																159
Glu Asp Arg Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser																
15 20 25																
tgg agt acc agg ata aaa ggc ttc att gcg tgt ttt gct ata gga att																207
Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile																
30 35 40 45																
ctc tgc tca ctg ctg ggt act gtt ctg ctg tgg gtg ccc agg aag gga																255
Leu Cys Ser Leu Leu Gly Thr Val Leu Trp Val Pro Arg Lys Gly																
50 55 60																
cta cac ctc ttc gca gtg ttt tat acc ttt ggt aat atc gca tca att																303
Leu His Leu Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile																
65 70 75																
ggg agt acc atc ttc ctc atg gga cca gtg aaa cag ctg aag cga atg																351
Gly Ser Thr Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met																
80 85 90																
ttt gag cct act cgt ttg att gca act atc atg gtg ctg ttg tgt ttt																399
Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe																
95 100 105																
gca ctt acc ctg tgt tct gcc ttt tgg tgg cat aac aag gga ctt gca																447
Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala																
110 115 120 125																
ctt atc ttc tgc att ttg cag tct ttg gca ttg acg tgg tac agc ctt																495
Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu																
130 135 140																
tcc ttc ata cca ttt gca agg gat gct gtg aag aag tgt ttt gcc gtg																543
Ser Phe Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val																
145 150 155																
tgt ctt gca taattcatgg ccagtttttat gaagcttttg aaggcactat ggacagaa																600
Cys Leu Ala																
160																
gctgggtggac agtttttgtaa ctatcttcga aacctctgtc ttacagacat gtgcctttta																660
tcttgacagca atgtgttgct tgtgattcga acatttgagg gttacttttg gaagcaacaa																720
tacattctcg aacctgaatg tcagtagcac aggatgagaa gtgggttctg tatcttgtgg																780
agtggaatct tctcatgta cctgtttcct ctctggatgt tgtcccaactg aattcccatg																840
aatacaaaccc tattcagcaa cagcacataa gccttggggtg caagtgattc ccagggtggca																900
aaaggcagcc ccatcagaga tcacggggagc aacagtaagg gacagagttt tgggggtccac																960
ttgtccctca gcatggaagc catcacctgt gtccctgcata gagtgaagtct acttctactc																1020
tggcatctga gaacaagtga ccttgcttta gacaagcccc tggagagcct ggccatggag																1080
tgaggtagaa aagaagcact ttttggtggt atatgctggt tctg																1124

```
<210> 31
<211> 1445
<212> PRT
<213> Homo sapiens
```

<400> 31															
Met	Gln	Gly	Pro	Pro	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	Cys	Val	Cys
1				5					10					15	
Thr	Ala	Ala	Leu	Ala	Val	Ala	Pro	Gly	Pro	Arg	Phe	Leu	Val	Thr	Ala
			20					25					30		
Pro	Gly	Ile	Ile	Arg	Pro	Gly	Gly	Asn	Val	Thr	Ile	Gly	Val	Glu	Leu
		35					40					45			
Leu	Glu	His	Cys	Pro	Ser	Gln	Val	Thr	Val	Lys	Ala	Glu	Leu	Leu	Lys
	50					55					60				
Thr	Ala	Ser	Asn	Leu	Thr	Val	Ser	Val	Leu	Glu	Ala	Glu	Gly	Val	Phe
65					70					75					80

Glu 85	Lys	Gly	Ser	Phe	Lys	Thr	Leu	Thr	Leu	Pro	Ser	Leu	Pro	Leu	Asn
Ser 100	Ala	Asp	Glu	Ile	Tyr	Glu	Leu	Arg	Val	Thr	Gly	Arg	Thr	Gln	Asp
Glu 115	Ile	Leu	Phe	Ser	Asn	Ser	Thr	Arg	Leu	Ser	Phe	Glu	Thr	Lys	Arg
Ile 130	Ser	Val	Phe	Ile	Gln	Thr	Asp	Lys	Ala	Leu	Tyr	Lys	Pro	Lys	Gln
Glu 145	Val	Lys	Phe	Arg	Ile	Val	Thr	Leu	Phe	Ser	Asp	Phe	Lys	Pro	Tyr
Lys	Thr	Ser	Leu	Asn	Ile	Leu	Ile	Lys	Asp	Pro	Lys	Ser	Asn	Leu	Ile
Gln	Gln	Trp	Leu	Ser	Gln	Gln	Ser	Asp	Leu	Gly	Val	Ile	Ser	Lys	Thr
Phe	Gln	Leu	Ser	Ser	His	Pro	Ile	Leu	Gly	Asp	Trp	Ser	Ile	Gln	Val
Gln 210	Val	Asn	Asp	Gln	Thr	Tyr	Tyr	Gln	Ser	Phe	Gln	Val	Ser	Glu	Tyr
Val 225	Leu	Pro	Lys	Phe	Glu	Val	Thr	Leu	Gln	Thr	Pro	Leu	Tyr	Cys	Ser
Met	Asn	Ser	Lys	His	Leu	Asn	Gly	Thr	Ile	Thr	Ala	Lys	Tyr	Thr	Tyr
Gly	Lys	Pro	Val	Lys	Gly	Asp	Val	Thr	Leu	Thr	Phe	Leu	Pro	Leu	Ser
Phe	Trp	Gly	Lys	Lys	Lys	Asn	Ile	Thr	Lys	Thr	Phe	Lys	Ile	Asn	Gly
Ser 290	Ala	Asn	Phe	Ser	Phe	Asn	Asp	Glu	Glu	Met	Lys	Asn	Val	Met	Asp
Ser 305	Ser	Asn	Gly	Leu	Ser	Glu	Tyr	Leu	Asp	Leu	Ser	Phe	Pro	Gly	Pro
Val	Glu	Ile	Leu	Thr	Thr	Val	Thr	Glu	Ser	Val	Thr	Gly	Ile	Ser	Arg
Asn	Val	Ser	Thr	Asn	Val	Phe	Phe	Lys	Gln	His	Asp	Tyr	Ile	Ile	Glu
Phe	Phe	Asp	Tyr	Thr	Thr	Val	Leu	Lys	Pro	Ser	Leu	Asn	Phe	Thr	Ala
Thr 370	Val	Lys	Val	Thr	Arg	Ala	Asp	Gly	Asn	Gln	Leu	Thr	Leu	Glu	Glu
Arg 385	Arg	Asn	Asn	Val	Val	Ile	Thr	Val	Thr	Gln	Arg	Asn	Tyr	Thr	Glu
Tyr	Trp	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Gln	Lys	Met	Glu	Ala	Val	Gln
Lys	Ile	Asn	Tyr	Thr	Val	Pro	Gln	Ser	Gly	Thr	Phe	Lys	Ile	Glu	Phe
Pro	Ile	Leu	Glu	Asp	Ser	Ser	Glu	Leu	Gln	Leu	Lys	Ala	Tyr	Phe	Leu
Gly 450	Ser	Lys	Ser	Ser	Met	Ala	Val	His	Ser	Leu	Phe	Lys	Ser	Pro	Ser
Lys 465	Thr	Tyr	Ile	Gln	Leu	Lys	Thr	Arg	Asp	Glu	Asn	Ile	Lys	Val	Gly
Ser	Pro	Phe	Glu	Leu	Val	Val	Ser	Gly	Asn	Lys	Arg	Leu	Lys	Glu	Leu
Ser	Tyr	Met	Val	Val	Ser	Arg	Gly	Gln	Leu	Val	Ala	Val	Gly	Lys	Gln
Asn	Ser	Thr	Met	Phe	Ser	Leu	Thr	Pro	Glu	Asn	Ser	Trp	Thr	Pro	Lys
Ala 530	Cys	Val	Ile	Val	Tyr	Tyr	Ile	Glu	Asp	Asp	Gly	Glu	Ile	Ile	Ser
Asp 545	Val	Leu	Lys	Ile	Pro	Val	Gln	Leu	Val	Phe	Lys	Asn	Lys	Ile	Lys
Leu	Tyr	Trp	Ser	Lys	Val	Lys	Ala	Glu	Pro	Ser	Glu	Lys	Val	Ser	Leu

				565				570				575				
Arg	Ile	Ser	Val	Thr	Gln	Pro	Asp	Ser	Ile	Val	Gly	Ile	Val	Ala	Val	
			580							585				590		
Asp	Lys	Ser	Val	Asn	Leu	Met	Asn	Ala	Ser	Asn	Asp	Ile	Thr	Met	Glu	
			595				600							605		
Asn	Val	Val	His	Glu	Leu	Glu	Leu	Tyr	Asn	Thr	Gly	Tyr	Tyr	Leu	Gly	
			610				615							620		
Met	Phe	Met	Asn	Ser	Phe	Ala	Val	Phe	Gln	Glu	Cys	Gly	Leu	Trp	Val	
625							630				635				640	
Leu	Thr	Asp	Ala	Asn	Leu	Thr	Lys	Asp	Tyr	Ile	Asp	Gly	Val	Tyr	Asp	
			645							650				655		
Asn	Ala	Glu	Tyr	Ala	Glu	Arg	Phe	Met	Glu	Glu	Asn	Glu	Gly	His	Ile	
			660				665							670		
Val	Asp	Ile	His	Asp	Phe	Ser	Leu	Gly	Ser	Ser	Pro	His	Val	Arg	Lys	
			675				680							685		
His	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Leu	Asp	Thr	Asn	Met	Gly	Ser	Arg	
			690				695							700		
Ile	Tyr	Gln	Glu	Phe	Glu	Val	Thr	Val	Pro	Asp	Ser	Ile	Thr	Ser	Trp	
705							710				715				720	
Val	Ala	Thr	Gly	Phe	Val	Ile	Ser	Glu	Asp	Leu	Gly	Leu	Gly	Leu	Thr	
			725							730				735		
Thr	Thr	Pro	Val	Glu	Leu	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Ile	Phe	Leu	
			740				745							750		
Asn	Leu	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Glu	Phe	Ala	Leu	Glu	Ile	
			755				760							765		
Thr	Ile	Phe	Asn	Tyr	Leu	Lys	Asp	Ala	Thr	Glu	Val	Lys	Val	Ile	Ile	
			770				775							780		
Glu	Lys	Ser	Asp	Lys	Phe	Asp	Ile	Leu	Met	Thr	Ser	Ser	Glu	Ile	Asn	
785							790				795				800	
Ala	Thr	Gly	His	Gln	Gln	Thr	Leu	Leu	Val	Pro	Ser	Glu	Asp	Gly	Ala	
			805							810				815		
Thr	Val	Leu	Phe	Pro	Ile	Arg	Pro	Thr	His	Leu	Gly	Glu	Ile	Pro	Ile	
			820				825							830		
Thr	Val	Thr	Ala	Leu	Ser	Pro	Thr	Ala	Ser	Asp	Ala	Ile	Thr	Gln	Met	
			835				840							845		
Ile	Leu	Val	Lys	Ala	Glu	Gly	Ile	Glu	Lys	Ser	Tyr	Ser	Gln	Ser	Ile	
			850				855				860					
Leu	Leu	Asp	Leu	Thr	Asp	Asn	Arg	Leu	Gln	Ser	Thr	Leu	Lys	Thr	Leu	
865							870				875				880	
Ser	Phe	Ser	Phe	Pro	Pro	Asn	Thr	Val	Thr	Gly	Ser	Glu	Arg	Val	Gln	
			885							890				895		
Ile	Thr	Ala	Ile	Gly	Asp	Val	Leu	Gly	Pro	Ser	Ile	Asn	Gly	Leu	Ala	
			900							905				910		
Ser	Leu	Ile	Arg	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	Asn	
			915				920							925		
Phe	Ala	Pro	Asn	Ile	Tyr	Ile	Leu	Asp	Tyr	Leu	Thr	Lys	Lys	Lys	Gln	
			930				935							940		
Leu	Thr	Asp	Asn	Leu	Lys	Glu	Lys	Ala	Leu	Ser	Phe	Met	Arg	Gln	Gly	
945							950				955				960	
Tyr																

Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
 1060 1065 1070
 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
 1075 1080 1085
 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
 1090 1095 1100
 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
 1105 1110 1115 1120
 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
 1125 1130 1135
 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
 1140 1145 1150
 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
 1155 1160 1165
 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
 1170 1175 1180
 Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
 1185 1190 1195 1200
 Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
 1205 1210 1215
 Pro Val Lys Phe Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr
 1220 1225 1230
 Ala Glu Leu Ala Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn
 1235 1240 1245
 Gly Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys
 1250 1255 1260
 Ala Ser Gly Ser Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala
 1265 1270 1275 1280
 Phe Asp Leu Asp Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His
 1285 1290 1295
 Val Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly
 1300 1305 1310
 Met Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser
 1315 1320 1325
 Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His
 1330 1335 1340
 Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys
 1345 1350 1355 1360
 Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp
 1365 1370 1375
 Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val
 1380 1385 1390
 Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser
 1395 1400 1405
 Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His
 1410 1415 1420
 His His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe
 1425 1430 1435 1440
 Met Glu Leu Trp Leu
 1445

<210> 32
 <211> 582
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
 1 5 10 15
 Leu Gln Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
 20 25 30

Arg	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Leu	Glu	Asp	Val	Val	Ile	Glu	Arg
		35					40					45			
Tyr	His	Ile	Pro	Arg	Ala	Cys	Pro	Arg	Glu	Val	Gln	Met	Gly	Asp	Phe
	50					55					60				
Val	Arg	Tyr	His	Tyr	Asn	Gly	Thr	Phe	Glu	Asp	Gly	Lys	Lys	Phe	Asp
	65				70					75				80	
Ser	Ser	Tyr	Asp	Arg	Asn	Thr	Leu	Val	Ala	Ile	Val	Val	Gly	Val	Gly
				85					90					95	
Arg	Leu	Ile	Thr	Gly	Met	Asp	Arg	Gly	Leu	Met	Gly	Met	Cys	Val	Asn
			100					105					110		
Glu	Arg	Arg	Arg	Leu	Ile	Val	Pro	Pro	His	Leu	Gly	Tyr	Gly	Ser	Ile
		115					120					125			
Gly	Leu	Ala	Gly	Leu	Ile	Pro	Pro	Asp	Ala	Thr	Leu	Tyr	Phe	Asp	Val
	130					135					140				
Val	Leu	Leu	Asp	Val	Trp	Asn	Lys	Glu	Asp	Thr	Val	Gln	Val	Ser	Thr
	145				150					155				160	
Leu	Leu	Arg	Pro	Pro	His	Cys	Pro	Arg	Met	Val	Gln	Asp	Gly	Asp	Phe
				165					170					175	
Val	Arg	Tyr	His	Tyr	Asn	Gly	Thr	Leu	Leu	Asp	Gly	Thr	Ser	Phe	Asp
			180					185					190		
Thr	Ser	Tyr	Ser	Lys	Gly	Gly	Thr	Tyr	Asp	Thr	Tyr	Val	Gly	Ser	Gly
		195					200					205			
Trp	Leu	Ile	Lys	Gly	Met	Asp	Gln	Gly	Leu	Leu	Gly	Met	Cys	Pro	Gly
	210					215					220				
Glu	Arg	Arg	Lys	Ile	Ile	Ile	Pro	Pro	Phe	Leu	Ala	Tyr	Gly	Glu	Lys
	225				230					235				240	
Gly	Tyr	Gly	Thr	Val	Ile	Pro	Pro	Gln	Ala	Ser	Leu	Val	Phe	His	Val
				245					250					255	
Leu	Leu	Ile	Asp	Val	His	Asn	Pro	Lys	Asp	Ala	Val	Gln	Leu	Glu	Thr
			260					265					270		
Leu	Glu	Leu	Pro	Pro	Gly	Cys	Val	Arg	Arg	Ala	Gly	Ala	Gly	Asp	Phe
		275					280					285			
Met	Arg	Tyr	His	Tyr	Asn	Gly	Ser	Leu	Met	Asp	Gly	Thr	Leu	Phe	Asp
	290					295					300				
Ser	Ser	Tyr	Ser	Arg	Asn	His	Thr	Tyr	Asn	Thr	Tyr	Ile	Gly	Gln	Gly
	305				310					315				320	
Tyr	Ile	Ile	Pro	Gly	Met	Asp	Gln	Gly	Leu	Gln	Gly	Ala	Cys	Met	Gly
				325					330					335	
Glu	Arg	Arg	Arg	Ile	Thr	Ile	Pro	Pro	His	Leu	Ala	Tyr	Gly	Glu	Asn
			340					345					350		
Gly	Thr	Gly	Asp	Lys	Ile	Pro	Gly	Ser	Ala	Val	Leu	Ile	Phe	Asn	Val
		355					360					365			
His	Val	Ile	Asp	Phe	His	Asn	Pro	Ala	Asp	Val	Val	Glu	Ile	Arg	Thr
	370					375					380				
Leu	Ser	Arg	Pro	Ser	Glu	Thr	C								

THE UNIVERSITY OF CHICAGO PRESS

[illegible]

```
<210> 33
<211> 410
<212> PRT
<213> Homo sapiens
```

<400>	33														
Met	Glu	Leu	Pro	Ser	Gly	Pro	Gly	Pro	Glu	Arg	Leu	Phe	Asp	Ser	His
1				5					10					15	
Arg	Leu	Pro	Gly	Asp	Cys	Phe	Leu	Leu	Leu	Val	Leu	Leu	Leu	Tyr	Ala
			20					25					30		
Pro	Val	Gly	Phe	Cys	Leu	Leu	Val	Leu	Arg	Leu	Phe	Leu	Gly	Ile	His
		35					40					45			
Val	Phe	Leu	Val	Ser	Cys	Ala	Leu	Pro	Asp	Ser	Val	Leu	Arg	Arg	Phe
	50					55					60				
Val	Val	Arg	Thr	Met	Cys	Ala	Val	Leu	Gly	Leu	Val	Ala	Arg	Gln	Glu
65				70					75					80	
Asp	Ser	Gly	Leu	Arg	Asp	His	Ser	Val	Arg	Val	Leu	Ile	Ser	Asn	His
				85				90						95	
Val	Thr	Pro	Phe	Asp	His	Asn	Ile	Val	Asn	Leu	Leu	Thr	Thr	Cys	Ser
			100					105					110		
Thr	Pro	Leu	Leu	Asn	Ser	Pro	Pro	Ser	Phe	Val	Cys	Trp	Ser	Arg	Gly
		115					120					125			
Phe	Met	Glu	Met	Asn	Gly	Arg	Gly	Glu	Leu	Val	Glu	Ser	Leu	Lys	Arg
	130				135						140				
Phe	Cys	Ala	Ser	Thr	Arg	Leu	Pro	Pro	Thr	Pro	Leu	Leu	Phe	Pro	
145					150					155				160	
Glu	Glu	Glu	Ala	Thr	Asn	Gly	Arg	Glu	Gly	Leu	Leu	Arg	Phe	Ser	Ser
			165						170					175	
Trp	Pro	Phe	Ser	Ile	Gln	Asp	Val	Val	Gln	Pro	Leu	Thr	Leu	Gln	Val
			180					185					190		
Gln	Arg	Pro	Leu	Val	Ser	Val	Thr	Val	Ser	Asp	Ala	Ser	Trp	Val	Ser
		195					200					205			
Glu	Leu	Leu	Trp	Ser	Leu	Phe	Val	Pro	Phe	Thr	Val	Tyr	Gln	Val	Arg
	210					215					220				
Trp	Leu	Arg	Pro	Val	His	Arg	Gln	Leu	Gly	Glu	Ala	Asn	Glu	Glu	Phe
225					230					235				240	
Ala	Leu	Arg	Val	Gln	Gln	Leu	Val	Ala	Lys	Glu	Leu	Gly	Gln	Thr	Gly
			245						250					255	
Thr	Arg	Leu	Thr	Pro	Ala	Asp	Lys	Ala	Glu	His	Met	Lys	Arg	Gln	Arg
			260					265					270		
His	Pro	Arg	Leu	Arg	Pro	Gln	Ser	Ala	Gln	Ser	Ser	Phe	Pro	Pro	Ser
		275					280					285			
Pro	Gly	Pro	Ser	Pro	Asp	Val	Gln	Leu	Ala	Thr	Leu	Ala	Gln	Arg	Val
	290					295					300				
Lys	Glu	Val	Leu	Pro	His	Val	Pro	Leu	Gly	Val	Ile	Gln	Arg	Asp	Leu
305					310					315				320	
Ala	Lys	Thr	Gly	Cys	Val	Asp	Leu	Thr	Ile	Thr	Asn	Leu	Leu	Glu	Gly
				325					330					335	
Ala	Val	Ala	Phe	Met	Pro	Glu	Asp	Ile	Thr	Lys	Gly	Thr	Gln	Ser	Leu
			340					34							

```

          355          360          365
Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu
      370          375          380
Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg
385          390          395          400
Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp
          405          410

```

<210> 34
 <211> 483
 <212> PRT
 <213> Homo sapiens

```

<400> 34
Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
  1          5          10          15
Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Arg
      20          25          30
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
      35          40          45
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
      50          55          60
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Cys Ile
      65          70          75          80
Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Lys Asp Tyr Lys
      85          90          95
Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe Lys Gln Ser Ser
      100          105          110
Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu Val Cys His Gly
      115          120          125
Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr Gly Gln Lys Ile
      130          135          140
Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala Lys Asn Leu Leu
      145          150          155          160
Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys Ser Asn Glu Ile
      165          170          175
Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly
      180          185          190
Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser
      195          200          205
Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu
      210          215          220
Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr
      225          230          235          240
Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val
      245          250          255
Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu
      260          265          270
Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe
      275          280          285
Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe
      290          295          300
Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr
      305          310          315          320
Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys
      325          330          335
Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp
      340          345          350
Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp
      355          360          365
Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu

```

370					375					380					
Glu	His	Ile	Glu	Trp	Ala	Lys	Lys	Asn	Thr	Ala	Arg	Ala	Tyr	His	Leu
385					390					395					
Gln	Asp	Asp	Gly	Thr	Gln	Thr	Val	Arg	Met	Val	Ser	His	Phe	Tyr	Gly
405					410					415					
Asn	Gly	Asp	Ile	Cys	Asp	Ile	Thr	Asp	Lys	Pro	Arg	Gln	Val	Thr	Val
420					425					430					
Lys	Leu	Lys	Cys	Lys	Glu	Ser	Asp	Ser	Pro	His	Ala	Val	Thr	Val	Tyr
435					440					445					
Met	Leu	Glu	Pro	His	Ser	Cys	Gln	Tyr	Ile	Leu	Gly	Val	Glu	Ser	Pro
450					455					460					
Val	Ile	Cys	Lys	Ile	Leu	Asp	Thr	Ala	Asp	Glu	Asn	Gly	Leu	Leu	Ser
465					470					475					
Leu	Pro	Asn													480

```
<210> 35
<211> 607
<212> PRT
<213> Homo sapiens
```

<div><400></div>	35														
Met	Gly	Phe	Glu	Glu	Leu	Leu	Glu	Gln	Val	Gly	Gly	Phe	Gly	Pro	Phe
1				5					10					15	
Gln	Leu	Arg	Asn	Val	Ala	Leu	Leu	Ala	Leu	Pro	Arg	Val	Leu	Leu	Pro
			20					25					30		
Leu	His	Phe	Leu	Leu	Pro	Ile	Phe	Leu	Ala	Ala	Val	Pro	Ala	His	Arg
		35					40					45			
Cys	Ala	Leu	Pro	Gly	Ala	Pro	Ala	Asn	Phe	Ser	His	Gln	Asp	Val	Trp
50						55					60				
Leu	Glu	Ala	His	Leu	Pro	Arg	Glu	Pro	Asp	Gly	Thr	Leu	Ser	Ser	Cys
65					70					75					80
Leu	Arg	Phe	Ala	Tyr	Pro	Gln	Ala	Leu	Pro	Asn	Thr	Thr	Leu	Gly	Glu
				85					90					95	
Glu	Arg	Gln	Ser	Arg	Gly	Glu	Leu	Glu	Asp	Glu	Pro	Ala	Thr	Val	Pro
			100					105					110		
Cys	Ser	Gln	Gly	Trp	Glu	Tyr	Asp	His	Ser	Glu	Phe	Ser	Ser	Thr	Ile
		115					120					125			
Ala	Thr	Glu	Ser	Gln	Val	Gly	Ile	Tyr	Ile	Ile	His	Leu	Glu	Val	Glu
130						135					140				
Cys	Arg	Trp	Arg	Gln	Ser	Pro	Trp	Glu	Ala	Ala	Gly	Arg	Gly	Leu	Pro
145					150					155					160
Trp	Glu	Glu	Ala	Glu	Ala	Ala	Gly	Leu	Gly	Arg	Asp	Lys	Val	Ser	Tyr
				165					170					175	
Ser	Pro	Ser	Trp	Arg	Glu	Ser	Leu	Gly	Gly	Leu	Leu	Ser	Gly	Met	Glu
			180					185					190		
Trp	Asp	Leu	Val	Cys	Glu	Gln	Lys	Gly	Leu	Asn	Arg	Ala	Ala	Ser	Thr
		195					200					205			
Phe	Phe	Phe	Ala	Gly	Val	Leu	Val	Gly	Ala	Val	Ala	Phe	Gly	Tyr	Leu
210						215				220					
Ser	Asp	Arg	Phe	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Val	Ala	Tyr	Val	Ser
225					230					235					240
Thr	Leu	Val	Leu	Gly	Leu	Ala	Ser	Ala	Ala	Ser	Val	Ser	Tyr	Val	Met
				245					250					255	
Phe	Ala	Ile	Thr	Arg	Thr	Leu	Thr	Gly	Ser	Ala	Leu	Ala	Gly	Phe	Thr
			260					265					270		
Ile	Ile	Val	Met	Pro	Leu	Glu	Leu	Glu	Trp	Leu	Asp	Val	Glu	His	Arg
275							280					285			
Thr	Val	Ala	Gly	Val	Leu	Ser	Ser	Thr	Phe	Trp	Thr	Gly	Gly	Val	Met
290						295					300				
Leu	Leu	Ala	Leu	Val	Gly	Tyr	Leu	Ile	Arg	Asp	Trp	Arg	Trp	Leu	Leu


```

305          310          315          320
Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile Leu Ser Leu Trp Trp
          325          330          335
Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln Gly His Val Lys Glu
          340          345          350
Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu Asn Gly Arg Pro Val
          355          360          365
Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser Lys Val Ala Ala Gly
          370          375          380
Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp Leu Phe Arg Thr Pro
385          390          395
Arg Leu Arg His Ile Ser Leu Cys Cys Val Val Val Trp Phe Gly Val
          405          410          415
Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val Ser Gly Leu Gly Leu
          420          425          430
Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala Val Glu Leu Pro Ser
          435          440          445
Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala Gly Arg Arg Leu Thr
          450          455          460
Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala Phe Gly Thr Arg Leu
465          470          475
Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr Val Leu Ala Val Met
          485          490          495
Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr Ala Tyr Leu Phe Thr
          500          505          510
Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr Gly Met Gly Leu Thr
          515          520          525
Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala Pro Leu Ala Ala Leu
          530          535          540
Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu Thr Tyr Gly Gly Ile
545          550          555
Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Pro Glu Thr Arg Gln
          565          570          575
Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu Arg Lys Ser Ala Pro
          580          585          590
Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys Gln Val Gln Asn
          595          600          605

```

<210> 36
 <211> 314
 <212> PRT
 <213> Homo sapiens

```

<400> 36
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala
 1          5          10          15
Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
          20          25          30
Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
          35          40          45
Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
          50          55          60
His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
          65          70          75          80
Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
          85          90          95
Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
          100          105          110
Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
          115          120          125
Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser

```

	130						135						140					
Ala 145	Pro	Val	Thr	Tyr	Thr	Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala			
Ser	Thr	Phe	Glu	Phe	Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp			
				165							170							
Gly	Tyr	Ile	Lys	Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln			
			180									185						
Glu	Val	Gln	Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe			
		195										200						
Leu	Lys	Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala			
	210					215					220							
Gly 225	Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly			
				230						235								
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	Val			
			245							250								
Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Thr			
			260					265						270				
Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	Ala	Gln	Ser			
		275					280					285						
Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	Phe	Phe	Pro	Leu			
	290					295					300							
Leu 305	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val									
					310													

```
<210> 37
<211> 94
<212> PRT
<213> Homo sapiens
```

<400> 37															
Met	Glu	Leu	Ser	Asp	Val	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asn	Glu	Val
1				5					10					15	
Met	Val	Val	Ala	Gly	Val	Val	Val	Leu	Ile	Leu	Ala	Leu	Val	Leu	Ala
			20					25					30		
Trp	Leu	Ser	Thr	Tyr	Val	Ala	Asp	Ser	Gly	Ser	Asn	Gln	Leu	Leu	Gly
		35					40					45			
Ala	Ile	Val	Ser	Ala	Gly	Asp	Thr	Ser	Val	Leu	His	Leu	Gly	His	Val
	50					55					60				
Asp	His	Leu	Val	Ala	Gly	Gln	Gly	Asn	Pro	Glu	Pro	Thr	Glu	Leu	Pro
65					70					75					80
His	Pro	Ser	Glu	Ala	Asn	Thr	Ser	Leu	Asp	Lys	Lys	Ala	Arg		
				85					90						

```
<210> 38
<211> 218
<212> PRT
<213> Homo sapiens
```

<400> 38															
Met	Ala	Ser	Lys	Ile	Gly	Ser	Arg	Arg	Trp	Met	Leu	Gln	Leu	Ile	Met
1				5					10					15	
Gln	Leu	Gly	Ser	Val	Leu	Leu	Thr	Arg	Cys	Pro	Phe	Trp	Gly	Cys	Phe
			20					25					30		
Ser	Gln	Leu	Met	Leu	Tyr	Ala	Glu	Arg	Ala	Glu	Ala	Arg	Arg	Lys	Pro
		35					40					45			
Asp	Ile	Pro	Val	Pro	Tyr	Leu	Tyr	Phe	Asp	Met	Gly	Ala	Ala	Val	Leu
	50					55					60				
Cys	Ala	Ser	Phe	Met	Ser	Phe	Gly	Val	Lys	Arg	Arg	Trp	Phe	Ala	Leu
65				70					75					80	
Gly	Ala	Ala	Leu	Gln	Leu	Ala	Ile	Ser	Thr	Tyr	Ala	Ala	Tyr	Ile	Gly
				85					90					95	

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln Arg Cys Trp
 115 120 125
 Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala Val His Arg
 130 135 140
 Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu Leu Thr Ala
 145 150 155 160
 Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser Pro Arg Arg
 165 170 175
 Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His Pro Gly Pro
 180 185 190
 Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro Asp Pro Gly
 195 200 205
 Cys Thr Ala Ala Pro Cys His Ala Ala His
 210 215

<210> 39
 <211> 460
 <212> PRT
 <213> Homo sapiens

<400> 39
 Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser
 1 5 10 15
 Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu
 20 25 30
 Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn
 35 40 45
 Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr
 50 55 60
 Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln
 65 70 75 80
 Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu
 85 90 95
 Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu
 100 105 110
 Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu
 115 120 125
 Glu Glu Lys Ile Leu Leu Gln Lys Val Lys Tyr Leu Glu Glu Gln
 130 135 140
 Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu
 145 150 155 160
 Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys
 165 170 175
 Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln
 180 185 190
 His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile
 195 200 205
 Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg
 210 215 220
 Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp
 225 230 235 240
 Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr
 245 250 255
 Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val
 260 265 270
 Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg
 275 280 285
 Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr
 290 295 300

Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile
 305 310 315 320
 Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu
 325 330 335
 Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly
 340 345 350
 Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
 355 360 365
 Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
 370 375 380
 Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
 385 390 395 400
 Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
 405 410 415
 Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
 420 425 430
 Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
 435 440 445
 Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 450 455 460

<210> 40
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys Pro Leu Leu Leu
 1 5 10 15
 Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu Leu Gly Ile Lys
 20 25 30
 Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu Gly Gly Phe
 35 40 45
 Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu Trp Gly Leu Arg
 50 55 60
 Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly Pro Ser Gly Asn
 65 70 75 80
 Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr Glu Glu Ala Val
 85 90 95
 Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu Asp Gln Pro Pro
 100 105 110
 Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu Glu Glu Gln Pro
 115 120 125
 Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu Gln Arg Arg Met
 130 135 140
 Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro Gly Arg Ala Pro
 145 150 155 160
 Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser Tnr Ala Pro Asp
 165 170 175
 Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro Leu Thr Pro Pro
 180 185 190
 Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp Asp Ser Val Phe
 195 200 205
 Tyr Glu Asp Asn Trp Ala Pro Pro
 210 215

<210> 41
 <211> 4335
 <212> DNA
 <213> Homo sapiens

<400> 41

atgcagggcc	caccgctcct	gaccgcccgc	cacctcctct	gegtgtgcac	cgccgcgctg	60
gccgtggctc	ccgggcccct	gtttctgggt	acagccccag	ggatcatcag	gcccggagga	120
aatgtgacta	ttgggggtgga	gcttctggaa	cactgccctt	cacaggtgac	tgtgaaggcg	180
gagctgctca	agacagcatc	aaacctcact	gtctctgtcc	tggaagcaga	aggagtcttt	240
gaaaaaggct	cttttaagac	acttactctt	ccatcactac	ctctgaacag	tgcagatgag	300
atztatgagc	tacgtgtaac	cggacgtacc	caggatgaga	ttttattctc	taatagtacc	360
cgcttatcat	ttgagaccaa	gagaatatct	gtcttcattc	aaacagacaa	ggccttatac	420
aagccaaagc	aagaagtga	gtttcgcatt	gttacactct	tctcagattt	taagccttac	480
aaaacctctt	taaaccattct	cattaaggac	cccaaataca	at ttgatcca	acagtggttg	540
tcacaacaaa	gtgatcttgg	agtcatttcc	aaaacttttc	agctatcttc	ccatccaata	600
cttggtgact	ggctatttca	agttcaagtg	aatgaccaga	catattatca	atcattttcag	660
gtttcagaat	atgtattacc	aaaatttgaa	gtgactttgc	agacaccatt	atattgttct	720
atgaattcta	agcatttaaa	tggtaccatc	acggcaaagt	atacatatgg	gaagccagtg	780
aaaggagacg	taacgcttac	at ttttacct	ttatcctttt	ggggaaagaa	gaaaaatatt	840
acaaaaacat	ttaagataaa	tggatctgca	aacttctctt	ttaatgatga	agagatgaaa	900
aatgtaatgg	attcttcaaa	tggactttct	gaatacctgg	atctatcttt	ccctggacca	960
gtagaaattt	taaccacagt	gacagaatca	gttacaggta	tttcaagaaa	tgtaagcact	1020
aatgtgttct	tcaagcaaca	tgattacatc	attgagtttt	ttgattatac	tactgtcttg	1080
aagccatctc	tcaacttcac	agccactgtg	aaggtaactc	gtgctgatgg	caaccaactg	1140
actcttgaag	aaagaagaaa	taatgtagtc	ataacagtga	cacagagaaa	ctatactgag	1200
tactggagcg	gatctaacag	tggaaatcag	aaaatggaag	ctgttcagaa	aataaattat	1260
actgtccccc	aaagtggaa	ttttaagatt	gaattcccaa	tcctggagga	ttccagtgag	1320
ctacagttga	aggcctattt	ccttggtagt	aaaagtagca	tggcagttca	tagtctgttt	1380
aagtctccta	gtaagacata	catccaacta	aaaacaagag	atgaaaatat	aaaggtggga	1440
tcgccttttg	agttggtggt	tagtggcaac	aaacgatgga	aggagttaag	ctatatggta	1500
gtatccaggg	gacagtgggt	ggctgtagga	aaacaaaatt	caacaatggt	ctctttaaca	1560
ccagaaaatt	cttggactcc	aaaagcctgt	gtaattgtgt	attatattga	agatgatggg	1620
gaaattataa	gtgatgttct	aaaaattcct	gttcagcttg	tttttaaaaa	taagataaag	1680
ctatattgga	gtaaagtga	agctgaacca	tctgagaaag	tctctcttag	gatctctgtg	1740
acacagcctg	actccatagt	tgggattgta	gctgttgaca	aaagtgtgaa	tctgatgaat	1800
gcctctaatt	atattacaat	ggaaaatgtg	gtccatgagt	tggaaactta	taacacagga	1860
tattatttag	gcattctcat	gaattccttt	gcagtccttc	aggaatgtgg	actctgggta	1920
ttgacagatg	caaacctcac	gaaggattat	attgatgggt	tttatgacaa	tgcagatat	1980
gctgagaggt	ttatggagga	aaatgaagga	catattgtag	atattcatga	cttttctttg	2040
ggtagcagtc	cacatgtccg	aaagcatttt	ccagagactt	ggatttggct	agacaccaac	2100
atgggttcca	ggattttacca	agaatttgaa	gtaactgtac	ctgattctat	cacttctctg	2160
gtggctactg	gtttttgtgat	ctctgaggac	ctgggtcttg	gactaacaac	tactccagtg	2220
gagctccaag	ccttccaacc	at ttttcatt	tttttgaatc	ttccctactc	tgttatcaga	2280
gggtgaagaat	ttgcttttga	aataactata	tcaattattt	tgaagatgc	cactgaggtt	2340
aaggtaatca	ttgagaaaa	tgacaaaatt	gatattctaa	tgacttcaag	tgaataaat	2400
gccacaggcc	accagcagac	ccttctgggt	ccagtgagg	atggggcaac	tgttcttttt	2460
cccatcaggc	caacacatct	gggagaaaat	cctatcacag	tcacagctct	ttcaccact	2520
gcttctgatg	ctatcaccca	gatgatttta	gtaaaggctg	aaggaaataga	aaaatcatat	2580
tcacaatcca	tcttattaga	cttgactgac	aataggctac	agagtaccct	gaaaactttg	2640
agtttctcat	ttcctcctaa	tacagtgact	ggcagtga	gagttcagat	cactgcaatt	2700
ggagatgttc	ttggtccttc	catcaatggc	ttagcctcat	tgattcggat	gccttatggc	2760
tgtggtgaac	agaacatgat	aaattttgct	ccaaatattt	acatttttga	ttatctgact	2820
aaaaagaaac	aactgacaga	taattttgaa	gaaaaagctc	tttcattttat	gaggcaaggt	2880
taccagagag	aacttctcta	tcagagggaa	gatggctctt	tcagtgcctt	tgggaattat	2940
gacccttctg	ggagcacttg	gttgtcagct	tttgttttaa	gatgtttcct	tgaagccgat	3000
ccttacatag	atattgatca	gaatgtgtta	cacagaacat	acacttggct	taaaggacat	3060
cagaaatcca	acggtgaatt	ttgggatcca	ggaagagtga	ttcatagtga	gcttcaaggt	3120
ggcaataaaa	gtccagtaac	acttacagcc	tatatgttaa	cttctctcct	gggatataga	3180
aagtatcagc	ctaaccattga	tgtgcaagag	tctatccatt	ttttggagtc	tgaattcagt	3240
agaggaattt	cagacaatta	tactctagcc	cttataactt	atgcattgtc	atcagtgagg	3300
agtcctaaa	cgaagggaag	tttgaatatg	ctgacttggg	gagcagaaca	agaaggtggc	3360
atgcaattct	gggtgtcatc	agagtccaaa	ctttctgact	cctggcagcc	acgtcctctg	3420
gatattgaag	ttgcagccta	tgactgtctc	tcacacttct	tacaatttca	gacttctgag	3480
ggaatcccaa	ttatgaggtg	gctaagcagg	caaagaaata	gcttgggtgg	ttttgcatct	3540
actcaggata	ccactgtggc	tttaaaggct	ctgtctgaat	ttgcagccct	aatgaataca	3600

gaaaggacaa	atatccaagt	gaccgtgacg	gggcctagct	caccaagtcc	tgtaaagtgt	3660
ctgattgaca	cacacaaccg	cttactcctt	cagacagcag	agcttgctgt	ggtacagcca	3720
acggcagtta	atatttcgcg	aaatggtttt	ggatttgcta	tttgtcagct	caatgttgta	3780
tataatgtga	aggcttctgg	gtcttctaga	agacgaagat	ctatccaaaa	tcaagaagcc	3840
tttgatttag	atgttgctgt	aaaagaaaat	aaagatgata	tcaatcatgt	ggatttgaat	3900
gtgtgtacaa	gcttttcggg	cccgggtagg	agtggcatgg	ctcttatgga	agttaaccta	3960
ttaagtggct	ttatgggtgc	ttcagaagca	atttctctga	gcgagacagt	gaagaaagtg	4020
gaatatgata	atggaaaact	caacctctat	ttagattctg	taaatgaaac	ccagttttgt	4080
gttaatatcc	ctgctgtgag	aaactttaaa	gtttcaaata	cccaagatgc	ttcagtgtcc	4140
atagtggatt	actatgagcc	aaggagacag	gcggtgagaa	gttacaactc	tgaagtgaag	4200
ctgtcctcct	gtgacctttg	cagtgatgtc	cagggtgcgc	gtccttgtga	ggatggagct	4260
tcaggctccc	atcatcactc	ttcagtcatt	tttattttct	gtttcaagct	tctgtacttt	4320
atggaacttt	ggctg					4335

<210> 42
 <211> 1746
 <212> DNA
 <213> Homo sapiens

<400> 42						
atgttccccg	cgggcccccc	cagccacagc	ctcctccggc	tccccctgct	gcagttgctg	60
ctactgggtg	tgcaggccgt	ggggaggggg	ctgggcccgc	ccagcccggc	cgggggcccc	120
ctggaagatg	tggtcatcga	gaggtaccac	atccccaggg	cctgtccccg	ggaagtgcag	180
atgggggatt	ttgtgcgcta	ccactacaac	ggcacttttg	aagatggcaa	gaagtttgat	240
tcaagctatg	atcgcaacac	cttgggtggc	atcgtgggtg	gtgtggggcg	cctcatcact	300
ggcatggacc	gaggcctcat	ggcatgtgt	gtcaacgagc	ggcgacgcct	cattgtgcct	360
ccccacctgg	gctatgggag	catcggcctg	gcggggctca	ttccaccgga	tgccacctc	420
tacttcgatg	tggttctgct	ggatgtgtgg	aacaaggaag	acaccgtgca	ggtgagcaca	480
ttgctgcgcc	cgccccactg	cccccgcatg	gtccaggacg	gcgactttgt	ccgctaccac	540
tacaatggca	ccctgctgga	cggcacctcc	ttcgacacca	gctacagtaa	ggcgggcact	600
tatgacacct	acgtcggctc	tggttggctg	atcaagggca	tggaccaggg	gctgctgggc	660
atgtgtcctg	gagagagaag	gaagattatc	atccctccat	tcttggccta	tggcgagaaa	720
ggctatggga	cgtgatcccc	cccacaggcc	tcgctggtct	ttcacgtcct	cctgattgac	780
gtgcacaacc	cgaaggacgc	tgtccagcta	gagacgtgg	agctccccc	cggctgtgtc	840
cgcagagccg	gggcccggga	cttcatgcgc	taccactaca	atggctcctt	gatggacggc	900
accctcttcg	attccagcta	ctcccgcaac	cacacctaca	atacctatat	cgggcagggg	960
tacatcatcc	ccgggatgga	ccaggggctg	caggggtgct	gcatggggga	acgccggaga	1020
attaccatcc	ccccgcacct	cgctatggg	gagaatggaa	ctggagacaa	gatccctggc	1080
tctgccgtgc	taatcttcaa	cgtccatgtc	attgacttcc	acaacctgc	ggatgtgggtg	1140
gaaatcagga	cactgtcccc	gccatctgag	acctgcaatg	agaccaccaa	gcttggggag	1200
tttgttcgat	accattacaa	ctgttctttg	ctggacggca	cccagctgtt	cacctcgcat	1260
gactacgggg	ccccccagga	ggcgactctc	ggggccaaca	aggtgatcga	aggcctggac	1320
acgggcctgc	agggcatgtg	tgtgggagag	aggcggcagc	tcacgtgtcc	cccgcacctg	1380
gcccacgggg	agagtggagc	ccggggagtc	ccaggcagtg	ctgtgctgct	gtttgaggtg	1440
gagctggtgt	ccggggagga	tgggtgtccc	acaggctacc	tgtttgtgtg	gcacaaggac	1500
cctcctgcc	acctgtttga	agacatggac	ctcaacaag	atggcgaggt	ccctccggag	1560
gagttctcca	ccttcatcaa	ggctcaagt	agtgagggca	aaggacgcct	catgcctggg	1620
caggaccttg	agaaaacat	aggagacatg	ttccagaacc	aggaccgcaa	ccaggacggc	1680
aagatcacag	tcgacgagct	caagctgaag	tcagatgagg	acgaggagcg	ggtccacgag	1740
gagctc						1746

<210> 43
 <211> 1230
 <212> DNA
 <213> Homo sapiens

<400> 43						
atggagcttc	cctcagggcc	ggggccggag	cggtctcttg	actcgcaccg	gcttccgggt	60
gactgcttcc	tactgtcgt	gctgtgtctc	tacgcgccag	tgggttctg	cctcctcgtc	120
ctgcgcctct	ttctcgggat	ccacgtcttc	ctggctagct	gcgcgtgcc	agacagcgtc	180
cttcgcagat	tcgtagtgcg	gacctgtgt	gcggtgctag	ggctcgtggc	ccggcaggag	240

gactccggac	tccgggatca	cagtgtcagg	gtcctcattt	ccaaccatgt	gacacctttc	300
gaccacaaca	tagtcaattt	gcttaccacc	tgtagcacc	ctctactcaa	tagtcccccc	360
agcttttgt	gctggctctg	gggcttcacg	gagatgaatg	ggcgggggga	gttgggtggag	420
tcactcaaga	gattctgtgc	ttccacgagg	cttcccccca	ctcctctgct	gctattccct	480
gaggaagagg	ccaccaatgg	ccgggagggg	ctcctgcgct	tcagttcctg	gccattttct	540
atccaagatg	tggtagaacc	tcttaccctg	caagttcaga	gacccctggg	ctctgtgacg	600
gtgtcagatg	cctcctgggt	ctcagaactg	ctgtggtcac	ttttcgtccc	tttcacgggtg	660
tatcaagtaa	ggtggcttcg	tcctgttcac	cgccaactag	gggaagcgaa	tgaggagtgt	720
gcactccgtg	tacaacagct	ggtggccaag	gaattggggc	agacagggac	acggctcact	780
ccagctgaca	aagcagagca	catgaagcga	caaagacacc	ccagattgag	ccccagtgca	840
gccagctctt	ctttccctcc	ctccccctgt	ccttctcttg	atgtgcaact	ggcaactctg	900
gctcagagag	tcaagggaagt	tttgccccat	gtgcatttgg	gtgtcatcca	gagagacctg	960
gccaaagactg	gctgtgtaga	cttgactatc	actaatctgc	ttgagggggc	cgtagctttc	1020
atgcctgaag	acatcaccaa	gggaactcag	tccttaccga	cagcctctgc	ctccaagtgt	1080
cccagctctg	gcccgggtgac	ccctcagcca	acagccctaa	catttgccaa	gtcttctctg	1140
gcccggcagg	agagcctgca	ggagcgcaag	caagcactat	atgaatacgc	aagaaggaga	1200
ttcacagaga	gacgagccca	ggaggtctgac				1230

<210> 44
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 44						
atggaggaag	gaggcggcgg	cgtacggagt	ctgggtcccg	gcgggcccggt	gttactggtc	60
ctctgcggcc	tcctggaggc	gtccggcggc	ggccgagccc	ttcctcaact	cagcgatgac	120
atccctttcc	gagtcaactg	gcccggcacc	gagttctctc	tgcccacaac	tggagtttta	180
tataaagaag	ataattatgt	catcatgaca	actgcacata	aagaaaaata	taaatgcata	240
cttccccctg	tgacaagtgg	ggatgaggaa	gaagaaaagg	attataaagg	ccctaattcca	300
agagagcttt	tggagccact	atttaaaaca	agcagttgtt	cctacagaat	tgagtcttat	360
tggacttacg	aagtatgtca	tggaaaacac	attcggcagt	accatgaaga	gaaagaaact	420
ggtcagaaaa	taaatattca	cgagtactac	cttggggaata	tgttggccaa	gaaccttcta	480
tttgaaaaag	aacgagaagc	agaagaaaag	gaaaaatcaa	atgagattcc	cactaaaaat	540
atcgaagggt	agatgacacc	atactatcct	gtgggaatgg	gaaatggtac	accttgtagt	600
ttgaaacaga	accggccccag	atcaagtact	gtgatgtaca	tatgtcatec	tgaatctaag	660
catgaaattc	tttcagtagc	tgaagttaca	acttgtgaat	atgaagtgtg	cattttgaca	720
ccactcttgt	gcagtcatec	taaatatagg	ttcagagcat	ctcctgtgaa	tgacatattt	780
tgtcaatcac	tgccaggatc	tccatttaag	ccccacccc	tgaggcagct	ggagcagcag	840
gaagaaatac	taagggtgcc	ttttaggaga	aataaagagg	aagatttgca	atcaactaaa	900
gaagagagat	ttccagcgat	ccacaagtgc	attgctattg	gctctcagcc	agtgtcact	960
gttggggaca	cccacatata	caaatttgaca	gatgaccaac	tcataaaaaga	gtttcttagt	1020
ggttcttact	gctttcgtgg	gggtgtcggt	tgggtgaaat	atgaattctg	ctatggcaaa	1080
catgtacatc	aataccatga	ggacaaggat	agtgggaaaa	cctctgtggt	tgtcgggaca	1140
tggaaaccaag	aagagcatat	tgaatgggct	aagaagaata	ctgctagagc	ttatcatctt	1200
caagacgatg	gtacccagac	agtcaggatg	gtgtcacatt	tttatggaaa	tggagatatt	1260
tgtgatataa	ctgacaaacc	aagacagggt	actgtaaaac	taaagtgcaa	agaatcagat	1320
tcacctcatg	ctgttactgt	atatatgcta	gagcctcact	cctgtcaata	tattcttggg	1380
gttgaaatctc	cagtgtatctg	taaaatctta	gatacagcag	atgaaaaagg	acttctttct	1440
ctccccaac						1449

<210> 45
 <211> 1821
 <212> DNA
 <213> Homo sapiens

<400> 45						
atgggctttg	aggagctgct	ggagcagggt	ggcggctttg	ggcccttcca	actgcggaat	60
gtggcactgc	tggccctgcc	ccgagtgtct	ctaccactgc	acttctctct	gcccatcttc	120
ctggctgccc	tgccctgcca	ccgatgtgcc	ctgccgggtg	cccctgcca	cttcagccat	180
caggatgtgt	ggctggaggc	ccatcttccc	cgggagcctg	atggcacgct	cagctcctgc	240
ctccgctttg	cctatcccca	ggctctcccc	aacaccacgt	tgggggaaga	aaggcagagc	300

cgtgggggagc	tggaggatga	acctgccaca	gtgccctgct	ctcaggggctg	ggagtagcac	360
cactcagaat	tctcctctac	cattgcaact	gagteccagg	tgggtattta	cataatccat	420
ctggagggtgg	aatgtcgggtg	gaggcagttct	ccctggggagg	cagcagggtcg	aggccttctct	480
tgggaagaag	ctgaggctgc	aggactgggg	agggacaaag	tttccctatcc	cccaagctgg	540
cgtgaatcgt	tgggagggttt	attatctggc	atggagtggg	atctgggtgtg	tgagcagaaa	600
ggtctgaaca	gagctgcgtc	cactttcttc	ttcgccgggtg	tgctgggtggg	ggctgtggcc	660
tttgatatac	tgctccgacag	gtttggggcgg	cggcgctctgc	tgctggtagc	ctacgtgagt	720
accctgggtgc	tgggcctggc	atctgcagcc	tccgtcagct	atgtaatgtt	tgccatcacc	780
cgcaccctta	ctggctcagc	cctggctgggt	tttaccatca	tctgtgatgcc	actggagctg	840
gagtggctgg	atgtggagca	ccgcaccgtg	gctggagtcc	tgagcagcac	cttctggaca	900
gggggctgta	tgctgctggc	actggttggg	tacctgatac	gggactggcg	atggcttctg	960
ctagctgtca	ccctgccttg	tgccccaggc	atcctcagcc	tctgggtgggt	gcctgagtct	1020
gcacgctggc	ttctgaccca	aggccatgtg	aaagaggccc	acaggtaactt	gctccactgt	1080
gccaggctca	atgggcggcc	agtgtgtgag	gacagcttca	gccaggaggc	tgtgagcaaa	1140
gtggccgccc	gggaacgggt	ggtccgaaga	ccttcatacc	tagacctgtt	ccgcacacca	1200
cggctccgac	acatctcact	gtgctgcgtg	gtgggtgtgt	tggagtgaa	cttctcctat	1260
tacggcctga	gtctggatgt	gtcggggctg	gggctgaacg	tgtaccagac	acagctgttg	1320
ttcggggctg	tggaaactgcc	ctccaagctg	ctggtctact	tgtcgggtgcg	ctacgcagga	1380
cgcgcctca	cgaagccgg	gacactgctg	ggcagggccc	tggcggttcgg	cactagactg	1440
ctagtgtcct	ctgatatgaa	gtcctggagc	actgtcctgg	cagtgatggg	gaaagctttt	1500
tctgaagctg	ccttcaccac	tgcttacctg	ttcacttcag	agttgtaccc	tacggtgctc	1560
agacagacag	ggatggggct	gactgcactg	gtggggccggc	tggggggctc	tttggcccca	1620
ctggcggcct	tgctggatgg	agtgtggctg	tactgcccc	agcttactta	tggggggatc	1680
gccctgctgg	ctgccggcac	cgccctcctg	ctgccagaga	cgaggcaggc	acagctgcc	1740
gagaccatcc	aggacgtgga	gagaaagagt	gccccaacca	gtcttcagga	ggaagagatg	1800
cccatgaagc	aggtccagaa	c				1821

<210> 46
 <211> 942
 <212> DNA
 <213> Homo sapiens

atggggcgcg	gcgggggcgct	gctgctggcg	ctgctgctgg	ctcgggctgg	actcaggaag	60
ccggagtcgc	aggaggcggc	gccgttatca	ggaccatgcg	gccgacgggt	catcacgtcg	120
cgcacgtgg	gtggagagga	cgcgaactc	ggcggttggc	cgtggcaggg	gagcctgcgc	180
ctgtgggatt	cccacgtatg	cggagtggc	ctgctcagcc	accgctgggc	actcacggcg	240
gcgcactgct	ttgaaacctta	tagtgacctt	agtgatecct	ccgggtggat	ggtccagttt	300
ggccagctga	cttccatgcc	atccttcttg	agcctgcagg	cctactacac	ccgttacttc	360
gtatogaata	tctatctgag	ccctcgctac	ctgggggaatt	caccctatga	cattgccttg	420
gtgaagctgt	ctgcacctgt	cacctacact	aaacacatcc	agcccatctg	tctccaggcc	480
tccacatttg	agtttgagaa	ccggacagac	tgctgggtga	ctggctgggg	gtacatcaaa	540
gaggatgagg	cactgccatc	tccccacacc	ctccaggaag	ttcaggtcgc	catcataaac	600
aactctatgt	gcaaccacct	cttccctcaag	tacagtttcc	gcaaggacat	ctttggagac	660
atggttttgtg	ctggcaatgc	ccaaggcggg	aaggatgcct	gcttcgggtga	ctcaggtgga	720
cccttggcct	gtaacaagaa	tggactgtgg	tatcagattg	gagtcgtgag	ctggggagtg	780
ggctgtgggt	ggcccaatcg	gcccggtgtc	tacaccaata	tcagccacca	ctttgagtg	840
atccagaagc	tgatggccca	gagtggcatg	tccagccag	accctcctg	gccgctactc	900
tttttccctc	ttctctgggc	tctccactc	ctggggccgg	tc		942

<210> 47
 <211> 282
 <212> DNA
 <213> Homo sapiens

atggagctct	ctgatgtcac	cctcattgag	ggtgtgggta	atgaggtgat	ggtgggtggca	60
ggtgtgggtg	tgctgattct	agccttgggtc	ctagcttggc	tctctaccta	cgtagcagac	120
agcggtagca	accagctcct	ggcgctatt	gtgtcagcag	gcgacacatc	cgtcctccac	180
ctggggcatg	tggaccacct	ggtggcaggc	caaggcaacc	ccgagccaac	tgaactcccc	240
catccatcag	aggcaaatac	ttccctggac	aagaaagcca	ga		282

<210> 48
 <211> 654
 <212> DNA
 <213> Homo sapiens

<400> 48
 atggcgtcga agataggttc gagacgggtg atgttgccgc tgatcatgca gttgggttcg 60
 gtgctgctca cacgctgccc cttttggggc tgcttcagcc agctcatgct gtacgctgag 120
 agggctgagg cacgccggaa gcccgacatc ccagtgcctt acctgtattt cgacatgggg 180
 gcagccgtgc tgtgcgctag tttcatgtcc tttggcgtga agcggcgctg gttcgcgctg 240
 ggggccgcac tccaattggc cattagcacc tacgccgcct acatcggggg ctacgtccac 300
 tacggggact ggctgaaggt ccgtatgtac tcgcgcacag ttgccatcat cggcggactt 360
 tcttgtgttg gccagcgggt ctggggagct gtaccgcggg aaacctcgca gccgctccct 420
 gcagtccacc ggccaggtgt tcctgggtat ctacctcacc tgtgtggcct actcactgca 480
 gcacagcaag gaggaccggc tggcgtatct gaacctatct ccaggagggg agctgatgat 540
 ccagctgttc ttcgtgctgt atggcaccct ggccctggcc tttctgtcag gctactacgt 600
 gaccctcgct gccagatcc tggctgtact gctgccccct gtcattgctgc tcat 654

<210> 49
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<400> 49
 atgttcacaa ttaagctcct tcttttttatt gttcctctag ttatttcctc cagaattgat 60
 caagacaatt catcatttga ttctctatct ccagagccaa aatcaagatt tgctatgtta 120
 gacgatgtaa aaatttttagc caatggcctc cttcagttgg gacatggctt taaagacttt 180
 gtccataaga cgaagggcc aattaatgac atattttcaa aactcaacat atttgatcag 240
 tcttttttatg atctatcgct gcaaacccagt gaaatcaaag aagaagaaaa ggaactgaga 300
 agaactacat ataaactaca agtcaaaaat gaagaggtaa agaatatgtc acttgaactc 360
 aactcaaaac ttgaaagcct cctagaagaa aaaattctac ttcaacaaaa agtgaaatat 420
 ttagaagagc aactaactaa cttaattcaa aatcaacctg aaactccaga acaccagaa 480
 gtaacttcac ttaaaacttt tgtagaaaaa caagataata gcatcaaaga ctttctccag 540
 accgtggaag accaatataa acaattaaac caacagcata gtcaaataaa agaaatagaa 600
 aatcagctca gaaggactag tattcaagaa cccacagaaa tttctctatc ttccaagcca 660
 agagcaccac gaactactcc ctttcttcag ttgaatgaaa taagaaatgt aaaacatgat 720
 ggcattcctg ctgaatgtac caccatttat aacagagggt aacatacaag tggcatgtat 780
 gccatcagac ccagcaactc tcaagttttt catgtctact gtgatgttat atcaggtagt 840
 ccattgacat taattcaaca tcgaatagat ggatcacaaa acttcaatga aacgtgggag 900
 aactacaaat atgggttttg gaggcttgat ggagaaattt ggttgggcct agagaagata 960
 tactccatag tgaagcaatc taattatgtt ttacgaattg agctggaaga ctggaaagac 1020
 aacaaacatt atattgaata ttctttttac ttgggaaatc acgaaaccaa ctatacgcta 1080
 catctagttg cgattactgg caatgtcccc aatgcaatcc cggaaaacaa agattttggtg 1140
 ttttctactt gggatcacaa agcaaaaagga cacttcaact gtccagaggg ttattcagga 1200
 ggctggtggt ggcatgatga gtgtggagaa aacaacctaa atggtaaata taacaaacca 1260
 agagcaaaat ctaagccaga gaggagaaga ggattatctt ggaagtctca aaatggaagg 1320
 ttatactcta taaaatcaac caaaatgttg atccatccaa cagattcaga aagctttgaa 1380

<210> 50
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 50
 atgggtgccaa tgcacttact ggggagactg gagaagccgc ttctcctcct gtgctgcgcc 60
 tccttcctac tggggctggc tttgctgggc ataaagacgg acatcacccc cgttgcttat 120
 ttctttctca cattgggttg cttcttcttg tttgcctatc tcctggctcg gtttctggaa 180
 tgggggcttc ggtcccagct ccaatcaatg cagactgaga gccaggggcc ctacaggcaat 240
 gcacgggaca atgaagcctt tgaagtgcc agtctatga aggccgtggg gggactagaa 300
 tcccagtgcc gcccccaga gttggaccac ccacccccct acagcactgt tgtgataccc 360

ccagcacctg	aggaggaaca	acctagccat	ccagaggggt	ccaggagagc	caaactggaa	420
cagaggcgaa	tggcctcaga	ggggtcctatg	gcccaggaag	gaagccctgg	aagagctcca	480
atcaaccttc	ggctctgggg	accacgggt	gtgtccactg	ctctgatct	gcagagcttg	540
gcggcagtc	ccacattaga	gctctgact	ccacctccctg	cctatgatgt	ctgctttggt	600
caccctgatg	atgatagtgt	tttttatgaq	gacaactqqq	cacccct		64

```
<210> 51
<211> 4473
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (45) ... (4382)
```

<400> 51																
aacttccccg gcagcggact gtagcccagg cagacgccgt cgag atg cag ggc cca																56
Met Gln Gly Pro																
1																
ccg ctc ctg acc gcc gcc cac ctc ctc tgc gtg tgc acc gcc gcg ctg	104															
Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys Thr Ala Ala Leu																
5 10 15 20																
gcc gtg gct ccc ggg cct cgg ttt ctg gtg aca gcc cca ggg atc atc	152															
Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala Pro Gly Ile Ile																
25 30 35																
agg ccc gga gga aat gtg act att ggg gtg gag ctt ctg gaa cac tgc	200															
Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu Leu Glu His Cys																
40 45 50																
cct tca cag gtg act gtg aag gcg gag ctg ctc aag aca gca tca aac	248															
Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys Thr Ala Ser Asn																
55 60 65																
ctc act gtc tct gtc ctg gaa gca gaa gga gtc ttt gaa aaa ggc tct	296															
Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe Glu Lys Gly Ser																
70 75 80																
ttt aag aca ctt act ctt cca tca cta cct ctg aac agt gca gat gag	344															
Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn Ser Ala Asp Glu																
85 90 95 100																
att tat gag cta cgt gta acc gga cgt acc cag gat gag att tta ttc	392															
Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp Glu Ile Leu Phe																
105 110 115																
tct aat agt acc cgc tta tca ttt gag acc aag aga ata tct gtc ttc	440															
Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg Ile Ser Val Phe																
120 125 130																
att caa aca gac aag gcc tta tac aag cca aag caa gaa gtg aag ttt	488															
Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln Glu Val Lys Phe																
135 140 145																
cgc att gtt aca ctc ttc tca gat ttt aag cct tac aaa acc tct tta	536															
Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr Lys Thr Ser Leu																
150 155 160																
aac att ctc att aag gac ccc aaa tca aat ttg atc caa cag tgg ttg	584															
Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile Gln Gln Trp Leu																
165 170 175 180																
tca caa caa agt gat ctt gga gtc att tcc aaa act ttt cag cta tct	632															
Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr Phe Gln Leu Ser																
185 190 195																
tcc cat cca ata ctt ggt gac tgg tct att caa gtt caa gtg aat gac	680															
Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val Gln Val Asn Asp																
200 205 210																
cag aca tat tat caa tca ttt cag gtt tca gaa tat gta tta cca aaa	728															
Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr Val Leu Pro Lys																
215 220 225																

870					875					880						
cct	cct	aat	aca	gtg	act	ggc	agt	gaa	aga	gtt	cag	atc	act	gca	att	2744
Pro	Pro	Asn	Thr	Val	Thr	Gly	Ser	Glu	Arg	Val	Gln	Ile	Thr	Ala	Ile	
885					890					895					900	
gga	gat	gtt	ctt	ggg	cct	tcc	atc	aat	ggc	tta	gcc	tca	ttg	att	cgg	2792
Gly	Asp	Val	Leu	Gly	Pro	Ser	Ile	Asn	Gly	Leu	Ala	Ser	Leu	Ile	Arg	
				905					910						915	
atg	cct	tat	ggc	tgt	ggg	gaa	cag	aac	atg	ata	aat	ttt	gct	cca	aat	2840
Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	Asn	Phe	Ala	Pro	Asn	
			920					925					930			
att	tac	att	ttg	gat	tat	ctg	act	aaa	aag	aaa	caa	ctg	aca	gat	aat	2888
Ile	Tyr	Ile	Leu	Asp	Tyr	Leu	Thr	Lys	Lys	Lys	Gln	Leu	Thr	Asp	Asn	
		935					940					945				
ttg	aaa	gaa	aaa	gct	ctt	tca	ttt	atg	agg	caa	ggg	tac	cag	aga	gaa	2936
Leu	Lys	Glu	Lys	Ala	Leu	Ser	Phe	Met	Arg	Gln	Gly	Tyr	Gln	Arg	Glu	
	950					955				960						
ctt	ctc	tat	cag	agg	gaa	gat	ggc	tct	ttc	agt	gct	ttt	ggg	aat	tat	2984
Leu	Leu	Tyr	Gln	Arg	Glu	Asp	Gly	Ser	Phe	Ser	Ala	Phe	Gly	Asn	Tyr	
965				970					975						980	
gac	cct	tct	ggg	agc	act	tgg	ttg	tca	gct	ttt	gtt	tta	aga	tgt	ttc	3032
Asp	Pro	Ser	Gly	Ser	Thr	Trp	Leu	Ser	Ala	Phe	Val	Leu	Arg	Cys	Phe	
			985					990						995		
ctt	gaa	gcc	gat	cct	tac	ata	gat	att	gat	cag	aat	gtg	tta	cac	aga	3080
Leu	Glu	Ala	Asp	Pro	Tyr	Ile	Asp	Ile	Asp	Gln	Asn	Val	Leu	His	Arg	
		1000					1005					1010				
aca	tac	act	tgg	ctt	aaa	gga	cat	cag	aaa	tcc	aac	ggg	gaa	ttt	tgg	3128
Thr	Tyr	Thr	Trp	Leu	Lys	Gly	His	Gln	Lys	Ser	Asn	Gly	Glu	Phe	Trp	
		1015					1020					1025				
gat	cca	gga	aga	gtg	att	cat	agt	gag	ctt	caa	ggg	ggc	aat	aaa	agt	3176
Asp	Pro	Gly	Arg	Val	Ile	His	Ser	Glu	Leu	Gln	Gly	Gly	Asn	Lys	Ser	
	1030					1035				1040						
cca	gta	aca	ctt	aca	gcc	tat	att	gta	act	tct	ctc	ctg	gga	tat	aga	3224
Pro	Val	Thr	Leu	Thr	Ala	Tyr	Ile	Val	Thr	Ser	Leu	Leu	Gly	Tyr	Arg	
1045					1050					1055					1060	
aag	tat	cag	cct	aac	att	gat	gtg	caa	gag	tct	atc	cat	ttt	ttg	gag	3272
Lys	Tyr	Gln	Pro	Asn	Ile	Asp	Val	Gln	Glu	Ser	Ile	His	Phe	Leu	Glu	
			1065					1070					1075			
tct	gaa	ttc	agt	aga	gga	att	tca	gac	aat	tat	act	cta	gcc	ctt	ata	3320
Ser	Glu	Phe	Ser	Arg	Gly	Ile	Ser	Asp	Asn	Tyr	Thr	Leu	Ala	Leu	Ile	
			1080					1085				1090				
act	tat	gca	ttg	tca	tca	gtg	ggg	agt	cct	aaa	gcg	aag	gaa	gct	ttg	3363
Thr	Tyr	Ala	Leu	Ser	Ser	Val	Gly	Ser	Pro	Lys	Ala	Lys	Glu	Ala	Leu	
		1095				1100					1105					
aat	atg	ctg	act	tgg	aga	gca	gaa	caa	gaa	ggg	ggc	atg	caa	ttc	tgg	3416
Asn	Met	Leu	Thr	Trp	Arg	Ala	Glu	Gln	Glu	Gly	Gly	Met	Gln	Phe	Trp	
		1110			1115					1120						
gtg	tca	tca	gag	tcc	aaa	ctt	tct	gac	tcc	tgg	cag	cca	cgc	tcc	ctg	3464
Val	Ser	Ser	Glu	Ser	Lys	Leu	Ser	Asp	Ser	Trp	Gln	Pro	Arg	Ser	Leu	
1125				1130					1135						1140	
gat	att	gaa	gtt	gca	gcc	tat	gca	ctg	ctc	tca	cac	ttc	tta	caa	ttt	3512
Asp	Ile	Glu	Val	Ala	Ala	Tyr	Ala	Leu	Leu	Ser	His	Phe	Leu	Gln	Phe	
			1145					1150				1155				
cag	act	tct	gag	gga	atc	cca	att	atg	agg	tgg	cta	agc	agg	caa	aga	3560
Gln	Thr	Ser	Glu	Gly	Ile	Pro	Ile	Met	Arg	Trp	Leu	Ser	Arg	Gln	Arg	
			1160				1165				1170					
aat	agc	ttg	ggg	ggg	ttt	gca	tct	act	cag	gat	acc	act	gtg	gct	tta	3608
Asn	Ser	Leu	Gly	Gly	Phe	Ala	Ser	Thr	Gln	Asp	Thr	Thr	Val	Ala	Leu	
		1175			1180						1185					
aag	gct	ctg	tct	gaa	ttt	gca	gcc	cta	atg	aat	aca	gaa	agg	aca	aat	3656
Lys	Ala	Leu	Ser	Glu	Phe	Ala	Ala	Leu	Met	Asn	Thr	Glu	Arg	Thr	Asn	
	1190				1195						1200					

atc	caa	gtg	acc	gtg	acg	ggg	cct	agc	tca	cca	agt	cct	gta	aag	ttt	3704
Ile	Gln	Val	Thr	Val	Thr	Gly	Pro	Ser	Ser	Pro	Ser	Pro	Val	Lys	Phe	
1205					1210					1215					1220	
ctg	att	gac	aca	cac	aac	cgc	tta	ctc	ctt	cag	aca	gca	gag	ctt	gct	3752
Leu	Ile	Asp	Thr	His	Asn	Arg	Leu	Leu	Leu	Gln	Thr	Ala	Glu	Leu	Ala	
				1225					1230					1235		
gtg	gta	cag	cca	acg	gca	gtt	aat	att	tcc	gca	aat	ggg	ttt	gga	ttt	3800
Val	Val	Gln	Pro	Thr	Ala	Val	Asn	Ile	Ser	Ala	Asn	Gly	Phe	Gly	Phe	
			1240					1245					1250			
gct	att	tgt	cag	ctc	aat	gtt	gta	tat	aat	gtg	aag	gct	tct	ggg	tct	3848
Ala	Ile	Cys	Gln	Leu	Asn	Val	Val	Tyr	Asn	Val	Lys	Ala	Ser	Gly	Ser	
		1255				1260						1265				
tct	aga	aga	cga	aga	tct	atc	caa	aat	caa	gaa	gcc	ttt	gat	tta	gat	3896
Ser	Arg	Arg	Arg	Arg	Ser	Ile	Gln	Asn	Gln	Glu	Ala	Phe	Asp	Leu	Asp	
	1270					1275					1280					
gtt	gct	gta	aaa	gaa	aat	aaa	gat	gat	ctc	aat	cat	gtg	gat	ttg	aat	3944
Val	Ala	Val	Lys	Glu	Asn	Lys	Asp	Asp	Leu	Asn	His	Val	Asp	Leu	Asn	
1285					1290					1295					1300	
gtg	tgt	aca	agc	ttt	tcg	ggc	ccg	ggg	agg	agt	ggc	atg	gct	ctt	atg	3992
Val	Cys	Thr	Ser	Phe	Ser	Gly	Pro	Gly	Arg	Ser	Gly	Met	Ala	Leu	Met	
				1305					1310				1315			
gaa	gtt	aac	cta	tta	agt	ggc	ttt	atg	gtg	cct	tca	gaa	gca	att	tct	4040
Glu	Val	Asn	Leu	Leu	Ser	Gly	Phe	Met	Val	Pro	Ser	Glu	Ala	Ile	Ser	
			1320					1325				1330				
ctg	agc	gag	aca	gtg	aag	aaa	gtg	gaa	tat	gat	cat	gga	aaa	ctc	aac	4088
Leu	Ser	Glu	Thr	Val	Lys	Lys	Val	Glu	Tyr	Asp	His	Gly	Lys	Leu	Asn	
		1335				1340						1345				
ctc	tat	tta	gat	tct	gta	aat	gaa	acc	cag	ttt	tgt	gtt	aat	att	cct	4136
Leu	Tyr	Leu	Asp	Ser	Val	Asn	Glu	Thr	Gln	Phe	Cys	Val	Asn	Ile	Pro	
	1350					1355					1360					
gct	gtg	aga	aac	ttt	aaa	gtt	tca	aat	acc	caa	gat	gct	tca	gtg	tcc	4184
Ala	Val	Arg	Asn	Phe	Lys	Val	Ser	Asn	Thr	Gln	Asp	Ala	Ser	Val	Ser	
1365					1370					1375					1380	
ata	gtg	gat	tac	tat	gag	cca	agg	aga	cag	gcg	gtg	aga	agt	tac	aac	4232
Ile	Val	Asp	Tyr	Tyr	Glu	Pro	Arg	Arg	Gln	Ala	Val	Arg	Ser	Tyr	Asn	
				1385					1390					1395		
tct	gaa	gtg	aag	ctg	tcc	tcc	tgt	gac	ctt	tgc	agt	gat	gtc	cag	ggc	4280
Ser	Glu	Val	Lys	Leu	Ser	Ser	Cys	Asp	Leu							

```
<210> 52
<211> 2630
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (82) ... (1830)
```

<400> 52
agttctggga ggcgggggga aggaggttgg tggcgactcc ctgcctgcc ctactgcc 60

gcggtcccaa	ctccaggcac	c	atg	ttc	ccc	gcg	ggc	ccc	ccc	agc	cac	agc	111
	Met	Phe	Pro	Ala	Gly	Pro	Pro	Ser	His	Ser			
	1				5								
ctc	ctc	cgg	ctc	ccc	ctg	ctg	cag	ttg	ctg	cta	ctg	gtg	159
Leu	Leu	Arg	Leu	Pro	Leu	Leu	Gln	Leu	Leu	Leu	Val	Val	
				15				20				25	
gtg	ggg	agg	ggg	ctg	ggc	cgc	gcc	agc	ccg	gcc	ggg	ggc	207
Val	Gly	Arg	Gly	Leu	Gly	Arg	Ala	Ser	Pro	Ala	Gly	Gly	
			30					35				40	
gat	gtg	gtc	atc	gag	agg	tac	cac	atc	ccc	agg	gcc	tgt	255
Asp	Val	Val	Ile	Glu	Arg	Tyr	His	Ile	Pro	Arg	Ala	Cys	
		45					50					55	
gtg	cag	atg	ggg	gat	ttt	gtg	cgc	tac	cac	tac	aac	ggc	303
Val	Gln	Met	Gly	Asp	Phe	Val	Arg	Tyr	His	Tyr	Asn	Gly	
	60					65					70		
gat	ggc	aag	aag	ttt	gat	tca	agc	tat	gat	cgc	aac	acc	351
Asp	Gly	Lys	Lys	Phe	Asp	Ser	Ser	Tyr	Asp	Arg	Asn	Thr	
	75				80					85		90	
atc	gtg	gtg	ggg	gtg	ggg	cgc	ctc	atc	act	ggc	atg	gac	399
Ile	Val	Val	Gly	Val	Gly	Arg	Leu	Ile	Thr	Gly	Met	Asp	
			95						100				105
atg	ggc	atg	tgt	gtc	aac	gag	cgg	cga	cgc	ctc	att	gtg	447
Met	Gly	Met	Cys	Val	Asn	Glu	Arg	Arg	Arg	Leu	Ile	Val	
			110					115				120	
ctg	ggc	tat	ggg	agc	atc	ggc	ctg	gcg	ggg	ctc	att	cca	495
Leu	Gly	Tyr	Gly	Ser	Ile	Gly	Leu	Ala	Gly	Leu	Ile	Pro	
		125					130					135	
acc	ctc	tac	ttc	gat	gtg	gtt	ctg	ctg	gat	gtg	tgg	aac	543
Thr	Leu	Tyr	Phe	Asp	Val	Val	Leu	Leu	Asp	Val	Trp	Asn	
		140				145					150		
acc	gtg	cag	gtg	agc	aca	ttg	ctg	cgc	ccg	ccc	cac	tgc	591
Thr	Val	Gln	Val	Ser	Thr	Leu	Leu	Arg	Pro	Pro	His	Cys	
		155			160				165			170	
gtc	cag	gac	ggc	gac	ttt	gtc	cgc	tac	cac	tac	aac	ggc	639
Val	Gln	Asp	Gly	Asp	Phe	Val	Arg	Tyr	His	Tyr	Asn	Gly	
			175					180				185	
gac	ggc	acc	tcc	ttc	gac	acc	agc	tac	agt	aag	ggc	ggc	687
Asp	Gly	Thr	Ser	Phe	Asp	Thr	Ser	Tyr	Ser	Lys	Gly	Gly	
		190						195				200	
acc	tac	gtc	ggc	tct	ggg	tgg	ctg	atc	aag	ggc	atg	gac	735
Thr	Tyr	Val	Gly	Ser	Gly	Trp	Leu	Ile	Lys	Gly	Met	Asp	
		205					210					215	
ctg	ggc	atg	tgt	cct	gga	gag	aga	agg	aag	att	atc	atc	783
Leu	Gly	Met	Cys	Pro	Gly	Glu	Arg	Arg	Lys	Ile	Ile	Ile	
		220				225						230	
ctg	ggc	tat	ggc	gag	aaa	ggc	tat	ggg	acg	gtg	atc	ccc	831
Leu	Ala	Tyr	Gly	Glu	Lys	Gly	Tyr	Gly	Thr	Val	Ile	Pro	
		235			240					245		250	
tcg	ctg	gtc	ttt	cac	gtc	ctc	ctg	att	gac	gtg	cac	aac	879
Ser	Leu	Val	Phe	His	Val	Leu	Leu	Ile	Asp	Val	His	Asn	
			255						260			265	
gct	gtc	cag	cta	gag	acg	ctg	gag	ctc	ccc	ccc	ggc	tgt	927
Ala	Val	Gln	Leu	Glu	Thr	Leu	Glu	Leu	Pro	Pro	Gly	Cys	
		270						275				280	
gcc	ggg	gcc	ggg	gac	ttc	atg	cgc	tac	cac	tac	aac	ggc	975
Ala	Gly	Ala	Gly	Asp	Phe	Met	Arg	Tyr	His	Tyr	Asn	Gly	
		285					290					295	
gac	ggc	acc	ctc	ttc	gat	tcc	agc	tac	tcc	cgc	aac	cac	1023
Asp	Gly	Thr	Leu	Phe	Asp	Ser	Ser	Tyr	Ser	Arg	Asn	His	
		300				305					310		
acc	tat	atc	ggg	cag	ggg	tac	atc	atc	ccc	ggg	atg	gac	1071

Thr	Tyr	Ile	Gly	Gln	Gly	Tyr	Ile	Ile	Pro	Gly	Met	Asp	Gln	Gly	Leu	
315					320					325					330	
cag	ggt	gcc	tgc	atg	ggg	gaa	cgc	cgg	aga	att	acc	atc	ccc	ccg	cac	1119
Gln	Gly	Ala	Cys	Met	Gly	Glu	Arg	Arg	Arg	Ile	Thr	Ile	Pro	Pro	His	
				335					340						345	
ctc	gcc	tat	ggg	gag	aat	gga	act	gga	gac	aag	atc	cct	ggc	tct	gcc	1167
Leu	Ala	Tyr	Gly	Glu	Asn	Gly	Thr	Gly	Asp	Lys	Ile	Pro	Gly	Ser	Ala	
			350					355					360			
gtg	cta	atc	ttc	aac	gtc	cat	gtc	att	gac	ttc	cac	aac	cct	gcg	gat	1215
Val	Leu	Ile	Phe	Asn	Val	His	Val	Ile	Asp	Phe	His	Asn	Pro	Ala	Asp	
		365					370					375				
gtg	gtg	gaa	atc	agg	aca	ctg	tcc	cgg	cca	tct	gag	acc	tgc	aat	gag	1263
Val	Val	Glu	Ile	Arg	Thr	Leu	Ser	Arg	Pro	Ser	Glu	Thr	Cys	Asn	Glu	
		380				385				390						
acc	acc	aag	ctt	ggg	gac	ttt	gtt	cga	tac	cat	tac	aac	tgt	tct	ttg	1311
Thr	Thr	Lys	Leu	Gly	Asp	Phe	Val	Arg	Tyr	His	Tyr	Asn	Cys	Ser	Leu	
395				400					405						410	
ctg	gac	ggc	acc	cag	ctg	ttc	acc	tcg	cat	gac	tac	ggg	gcc	ccc	cag	1359
Leu	Asp	Gly	Thr	Gln	Leu	Phe	Thr	Ser	His	Asp	Tyr	Gly	Ala	Pro	Gln	
				415				420						425		
gag	gcg	act	ctc	ggg	gcc	aac	aag	gtg	atc	gaa	ggc	ctg	gac	acg	ggc	1407
Glu	Ala	Thr	Leu	Gly	Ala	Asn	Lys	Val	Ile	Glu	Gly	Leu	Asp	Thr	Gly	
			430					435					440			
ctg	cag	ggc	atg	tgt	gtg	gga	gag	agg	cgg	cag	ctc	atc	gtg	ccc	ccg	1455
Leu	Gln	Gly	Met	Cys	Val	Gly	Glu	Arg	Arg	Gln	Leu	Ile	Val	Pro	Pro	
		445				450					455					
cac	ctg	gcc	cac	ggg	gag	agt	gga	gcc	cgg	gga	gtc	cca	ggc	agt	gct	1503
His	Leu	Ala	His	Gly	Glu	Ser	Gly	Ala	Arg	Gly	Val	Pro	Gly	Ser	Ala	
		460				465					470					
gtg	ctg	ctg	ttt	gag	gtg	gag	ctg	gtg	tcc	cgg	gag	gat	ggg	ctg	ccc	1551
Val	Leu	Leu	Phe	Glu	Val	Glu	Leu	Val	Ser	Arg	Glu	Asp	Gly	Leu	Pro	
475				480					485					490		
aca	ggc	tac	ctg	ttt	gtg	tgg	cac	aag	gac	cct	cct	gcc	aac	ctg	ttt	1599
Thr	Gly	Tyr	Leu	Phe	Val	Trp	His	Lys	Asp	Pro	Pro	Ala	Asn	Leu	Phe	
				495				500						505		
gaa	gac	atg	gac	ctc	aac	aag	gat	ggc	gag	gtc	cct	ccg	gag	gag	ttc	1647
Glu	Asp	Met	Asp	Leu	Asn	Lys	Asp	Gly	Glu	Val	Pro	Pro	Glu	Glu	Phe	
		510						515					520			
tcc	acc	ttc	atc	aag	gct	caa	gtg	agt	gag	ggc	aaa	gga	cgc	ctc	atg	1695
Ser	Thr	Phe	Ile	Lys	Ala	Gln	Val	Ser	Glu	Gly	Lys	Gly	Arg	Leu	Met	
		525				530						535				
cct	ggg	cag	gac	cct	gag	aaa	acc	ata	gga	gac	atg	ttc	cag	aac	cag	1743
Pro	Gly	Gln	Asp	Pro	Glu	Lys	Thr	Ile	Gly	Asp	Met	Phe	Gln	Asn	Gln	
		540				545					550					
gac	cgc	aac	cag	gac	ggc	aag	atc	aca	gtc	gac	gag	ctc	aag	ctg	aag	1791
Asp	Arg	Asn	Gln	Asp	Gly	Lys	Ile	Thr	Val	Asp	Glu	Leu	Lys	Leu	Lys	
555				560					565					570		
tca	gat	gag	gac	gag	gag	cgg	gtc	cac	gag	gag	ctc	tga	ggggcagggg			1840
Ser	Asp	Glu	Asp	Glu	Glu	Arg	Val	His	Glu	Glu	Leu					
				575					580							
gcttgccag	gctgagaca	cagaggcca	ctgcgagggg	gacagtggcg	gtgggactga											1900
cctgctgaca	gtcaccctcc	ctctgctggg	atgaggtcca	ggagccaact	aaaacaatgg											1960
cagaggagac	atctctgggtg	ttcccaccac	cctagatgaa	aatccacagc	acagacctct											2020
accgtgtttc	tcttccatcc	ctaaaccact	tccttaaaat	gtttggattt	gcaaagccaa											2080
tttggggcct	gtggagcctg	gggttgata	gggccatggc	tgggtcccca	ccatacctcc											2140
cctccacatc	actgacacag	ctgagcttgt	tatccatctc	cccaaacttt	ctctttcttt											2200
gtacttcttg	tcatcccccac	tcccagcccc	tattctctta	tgtgacagct	ggctaggacc											2260
cctctgcctt	cctccccaat	cctgactggc	tcctagggaa	ggggaaggct	cctggagggc											2320
agccctacct	ctcccattgcc	ctttgccttc	ctccctcgcc	tccagtggag	gctgagctga											2380
ccctgggctg	ctggaggcca	gactgggctg	tagttaagctt	ttcatcccta	aagaaggctt											2440
tccctaagga	accatagaag	agaggaagaa	aacaaagggc	atgtgtgagg	gaagctgctt											2500

gggtgggtgt tagggctatg aaatcttggg tttggggctg aggggtggga gggagggcag 2560
agctctgcac actcaaaggc taaactgggtg tcagtccttt tttcctttgt tccaaataaa 2620
agattaaacc 2630

<210> 53
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (89)...(1321)

<400> 53
aaaaagactc cgccttccca agagccctg cggccgggcg cgaaaatggc ggcggcggcg 60
acggccgggc gctcctgaag cagcagtt atg gag ctt ccc tca ggg ccg ggg 112
Met Glu Leu Pro Ser Gly Pro Gly
1 5
ccg gag cgg ctc ttt gac tgc cac cgg ctt ccg ggt gac tgc ttc cta 160
Pro Glu Arg Leu Phe Asp Ser His Arg Leu Pro Gly Asp Cys Phe Leu
10 15 20
ctg ctc gtg ctg ctg ctc tac gcg cca gtc ggg ttc tgc ctc ctc gtc 208
Leu Leu Val Leu Leu Leu Tyr Ala Pro Val Gly Phe Cys Leu Leu Val
25 30 35 40
ctg cgc ctc ttt ctc ggg atc cac gtc ttc ctg gtc agc tgc gcg ctg 256
Leu Arg Leu Phe Leu Gly Ile His Val Phe Leu Val Ser Cys Ala Leu
45 50 55
cca gac agc gtc ctt cgc aga ttc gta gtg cgg acc atg tgt gcg gtg 304
Pro Asp Ser Val Leu Arg Arg Phe Val Val Arg Thr Met Cys Ala Val
60 65 70
cta ggg ctc gtg gcc cgg cag gag gac tcc gga ctc cgg gat cac agt 352
Leu Gly Leu Val Ala Arg Gln Glu Asp Ser Gly Leu Arg Asp His Ser
75 80 85
gtc agg gtc ctc att tcc aac cat gtg aca cct ttc gac cac aac ata 400
Val Arg Val Leu Ile Ser Asn His Val Thr Pro Phe Asp His Asn Ile
90 95 100
gtc aat ttg ctt acc acc tgt agc acc cct cta ctc aat agt ccc ccc 448
Val Asn Leu Leu Thr Cys Ser Thr Pro Leu Leu Asn Ser Pro Pro
105 110 115 120
agc ttt gtg tgc tgg tct cgg ggc ttc atg gag atg aat ggg cgg ggg 496
Ser Phe Val Cys Trp Ser Arg Gly Phe Met Glu Met Asn Gly Arg Gly
125 130 135
gag ttg gtg gag tca ctc aag aga ttc tgt gct tcc acg agg ctt ccc 544
Glu Leu Val Glu Ser Leu Lys Arg Phe Cys Ala Ser Thr Arg Leu Pro
140 145 150
ccc act cct ctg ctg cta ttc cct gag gaa gag gcc acc aat ggc cgg 592
Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu Glu Ala Thr Asn Gly Arg
155 160 165
gag ggg ctc ctg cgc ttc agt tcc tgg cca ttt tct atc caa gat gtg 640
Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro Phe Ser Ile Gln Asp Val
170 175 180
gta caa cct ctt acc ctg caa gtt cag aga ccc ctg gtc tct gtg acg 688
Val Gln Pro Leu Thr Leu Gln Val Gln Arg Pro Leu Val Ser Val Thr
185 190 195 200
gtg tca gat gcc tcc tgg gtc tca gaa ctg ctg tgg tca ctt ttc gtc 736
Val Ser Asp Ala Ser Trp Val Ser Glu Leu Leu Trp Ser Leu Phe Val
205 210 215
cct ttc acg gtg tat caa gta agg tgg ctt cgt cct gtt cat cgc caa 784
Pro Phe Thr Val Tyr Gln Val Arg Trp Leu Arg Pro Val His Arg Gln
220 225 230
cta ggg gaa gcg aat gag gag ttt gca ctc cgt gta caa cag ctg gtg 832

```

Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val
      235                240                245
gcc aag gaa ttg ggc cag aca ggg aca cgg ctc act cca gct gac aaa      880
Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys
      250                255                260
gca gag cac atg aag cga caa aga cac ccc aga ttg cgc ccc cag tca      928
Ala Glu His Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser
      265                270                275                280
gcc cag tct tct ttc cct ccc tcc cct ggt cct tct cct gat gtg caa      976
Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln
      285                290                295
ctg gca act ctg gct cag aga gtc aag gaa gtt ttg ccc cat gtg cca      1024
Leu Ala Thr Leu Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro
      300                305                310
ttg ggt gtc atc cag aga gac ctg gcc aag act ggc tgt gta gac ttg      1072
Leu Gly Val Ile Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu
      315                320                325
act atc act aat ctg ctt gag ggg gcc gta gct ttc atg cct gaa gac      1120
Thr Ile Thr Asn Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp
      330                335                340
atc acc aag gga act cag tcc cta ccc aca gcc tct gcc tcc aag ttt      1168
Ile Thr Lys Gly Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe
      345                350                355                360
ccc agc tct ggc ccg gtg acc cct cag cca aca gcc cta aca ttt gcc      1216
Pro Ser Ser Gly Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala
      365                370                375
aag tct tcc tgg gcc cgg cag gag agc ctg cag gag cgc aag caa gca      1264
Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala
      380                385                390
cta tat gaa tac gca aga agg aga ttc aca gag aga cga gcc cag gag      1312
Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu
      395                400                405
gct gac tgagctcaaa ggaacaggat ggcacccaga gccgcaggac ggagactggg gg      1370
Ala Asp
      410
cagccctcac ccaactcaca acaggctgga tgggtgggtg gtaaaaaggg aaggatgagg      1430
ctcccccaat gtcacattaa attcatggtt ttcattcaag gc      1472

```

<210> 54
 <211> 1652
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (17)...(1468)

```

<400> 54
aaagcggcgg cggagg atg gag gaa gga ggc ggc ggc gta cgg agt ctg gtc      52
      Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val
      1          5          10
ccg ggc ggc ccg gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc      100
Pro Gly Gly Pro Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser
      15          20          25
ggc ggc ggc cga gcc ctt cct caa ctc agc gat gac atc cct ttc cga      148
Gly Gly Gly Arg Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg
      30          35          40
gtc aac tgg ccc ggc acc gag ttc tct ctg ccc aca act gga gtt tta      196
Val Asn Trp Pro Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu
      45          50          55          60
tat aaa gaa gat aat tat gtc atc atg aca act gca cat aaa gaa aaa      244

```



```

      385      390      395
gct tat cat ctt caa gac gat ggt acc cag aca gtc agg atg gtg tca 1252
Ala Tyr His Leu Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser
      400      405      410
cat ttt tat gga aat gga gat att tgt gat ata act gac aaa cca aga 1300
His Phe Tyr Gly Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg
      415      420      425
cag gtg act gta aaa cta aag tgc aaa gaa tca gat tca cct cat gct 1348
Gln Val Thr Val Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala
      430      435      440
gtt act gta tat atg cta gag cct cac tcc tgt caa tat att ctt ggg 1396
Val Thr Val Tyr Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly
      445      450      455      460
gtt gaa tct cca gtg atc tgt aaa atc tta gat aca gca gat gaa aat 1444
Val Glu Ser Pro Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn
      465      470      475
gga ctt ctt tct ctc ccc aac taaaggatat taaagttagg ggaaa 1490
Gly Leu Leu Ser Leu Pro Asn
      480
gaaaagatca ttgaaagtca tgataatttc tgtccactg tgtctcatta tagagttctc 1550
agccattgga cctcttctaa aggatggtat aaaatgactc tcaaccactt tgtgaataca 1610
tatgtgtata taagagggtta ttgataaact tctgaggcag ac 1652

<210> 55
<211> 2112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (20)...(1843)

<400> 55
attttggtgg gtgagcagc atg ggc ttt gag gag ctg ctg gag cag gtg ggc 52
Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly
      1      5      10
ggc ttt ggg ccc ttc caa ctg cgg aat gtg gca ctg ctg gcc ctg ccc 100
Gly Phe Gly Pro Phe Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro
      15      20      25
cga gtg ctg cta cca ctg cac ttc ctc ctg ccc atc ttc ctg gct gcc 148
Arg Val Leu Leu Pro Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala
      30      35      40
gtg cct gcc cac cga tgt gcc ctg ccg ggt gcc cct gcc aac ttc agc 196
Val Pro Ala His Arg Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser
      45      50      55
cat cag gat gtg tgg ctg gag gcc cat ctt ccc cgg gag cct gat ggc 244
His Gln Asp Val Trp Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly
      60      65      70      75
acg ctc agc tcc tgc ctc cgc ttt gcc tat ccc cag gct ctc ccc aac 292
Thr Leu Ser Ser Cys Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn
      80      85      90
acc acg ttg ggg gaa gaa agg cag agc cgt ggg gag ctg gag gat gaa 340
Thr Thr Leu Gly Glu Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu
      95      100      105
cct gcc aca gtg ccc tgc tct cag ggc tgg gag tac gac cac tca gaa 388
Pro Ala Thr Val Pro Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu
      110      115      120
ttc tcc tct acc att gca act gag tcc cag gtc ggt att tac ata atc 436
Phe Ser Ser Thr Ile Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile
      125      130      135
cat ctg gag gtg gaa tgt cgg tgg agg cag tct ccc tgg gag gca gca 484

```

His 140	Leu	Glu	Val	Glu	Cys 145	Arg	Trp	Arg	Gln	Ser 150	Pro	Trp	Glu	Ala	Ala 155	
ggt	cga	ggc	ctt	cct	tgg	gaa	gaa	gct	gag	gct	gca	gga	ctg	ggg	agg	532
Gly	Arg	Gly	Leu	Pro	Trp	Glu	Glu	Ala	Glu	Ala	Ala	Gly	Leu	Gly	Arg	
				160					165					170		
gac	aaa	gtt	tcc	tat	tcc	cca	agc	tgg	cgt	gaa	tcg	ttg	gga	ggg	tta	580
Asp	Lys	Val	Ser	Tyr	Ser	Pro	Ser	Trp	Arg	Glu	Ser	Leu	Gly	Gly	Leu	
				175					180					185		
tta	tct	ggc	atg	gag	tgg	gat	ctg	gtg	tgt	gag	cag	aaa	ggg	ctg	aac	628
Leu	Ser	Gly	Met	Glu	Trp	Asp	Leu	Val	Cys	Glu	Gln	Lys	Gly	Leu	Asn	
				190					195					200		
aga	gct	gcg	tcc	act	ttc	ttc	ttc	gcc	ggg	gtg	ctg	gtg	ggg	gct	gtg	676
Arg	Ala	Ala	Ser	Thr	Phe	Phe	Phe	Ala	Gly	Val	Leu	Val	Gly	Ala	Val	
				205										215		
gcc	ttt	gga	tat	ctg	tcc	gac	agg	ttt	ggg	cgg	cgg	cgt	ctg	ctg	ctg	724
Ala	Phe	Gly	Tyr	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Arg	Arg	Leu	Leu	Leu	
220				225										235		
gta	gcc	tac	gtg	agt	acc	ctg	gtg	ctg	ggc	ctg	gca	tct	gca	gcc	tcc	772
Val	Ala	Tyr	Val	Ser	Thr	Leu	Val	Leu	Gly	Leu	Ala	Ser	Ala	Ala	Ser	
				240										250		
gtc	agc	tat	gta	atg	ttt	gcc	atc	acc	cgc	acc	ctt	act	ggc	tca	gcc	820
Val	Ser	Tyr	Val	Met	Phe	Ala	Ile	Thr	Arg	Thr	Leu	Thr	Gly	Ser	Ala	
				255										265		
ctg	gct	ggg	ttt	acc	atc	atc	gtg	atg	cca	ctg	gag	ctg	gag	tgg	ctg	868
Leu	Ala	Gly	Phe	Thr	Ile	Ile	Val	Met	Pro	Leu	Glu	Leu	Glu	Trp	Leu	
				270										280		
gat	gtg	gag	cac	cgc	acc	gtg	gct	gga	gtc	ctg	agc	acc	acc	ttc	tgg	916
Asp	Val	Glu	His	Arg	Thr	Val	Ala	Gly	Val	Leu	Ser	Ser	Thr	Phe	Trp	
				285										295		
aca	ggg	ggc	gtg	atg	ctg	ctg	gca	ctg	gtt	ggg	tac	ctg	ata	cgg	gac	964
Thr	Gly	Gly	Val	Met	Leu	Leu	Ala	Leu	Val	Gly	Tyr	Leu	Ile	Arg	Asp	
300				305										315		
tgg	cga	tgg	ctt	ctg	cta	gct	gtc	acc	ctg	cct	tgt	gcc	cca	ggc	atc	1012
Trp	Arg	Trp	Leu	Leu	Leu	Ala	Val	Thr	Leu	Pro	Cys	Ala	Pro	Gly	Ile	
				320										330		
ctc	agc	ctc	tgg	tgg	gtg	cct	gag	tct	gca	cgc	tgg	ctt	ctg	acc	caa	1060
Leu	Ser	Leu	Trp	Trp	Val	Pro	Glu	Ser	Ala	Arg	Trp	Leu	Leu	Thr	Gln	
				335										345		
ggc	cat	gtg	aaa	gag	gcc	cac	agg	tac	ttg	ctc	cac	tgt	gcc	agg	ctc	1108
Gly	His	Val	Lys	Glu	Ala	His	Arg	Tyr	Leu	Leu	His	Cys	Ala	Arg	Leu	
				350										360		
aat	ggg	cgg	cca	gtg	tgt	gag	gac	agc	ttc	agc	cag	gag	gct	gtg	agc	1156
Asn	Gly	Arg	Pro	Val	Cys	Glu	Asp	Ser	Phe	Ser	Gln	Glu	Ala	Val	Ser	
				365										375		
aaa	gtg	gcc	gcc	ggg	gaa	cgg	gtg	gtc	cga	aga	cct	tca	tac	cta	gac	1204
Lys	Val	Ala	Ala	Gly	Glu	Arg	Val	Val	Arg	Arg	Pro	Ser	Tyr	Leu	Asp	
380				385										395		
ctg	ttc	cgc	aca	cca	cgg	ctc	cga	cac	atc	tca	ctg	tgc	tgc	gtg	gtg	1252
Leu	Phe	Arg	Thr	Pro	Arg	Leu	Arg	His	Ile	Ser	Leu	Cys	Cys	Val	Val	
				400										410		
gtg	tgg	ttc	gga	gtg	aac	ttc	tcc	tat	tac	ggc	ctg	agt	ctg	gat	gtg	1300
Val	Trp	Phe	Gly	Val	Asn	Phe	Ser	Tyr	Tyr	Gly	Leu	Ser	Leu	Asp	Val	
				415										425		
tcg	ggg	ctg	ggg	ctg	aac	gtg	tac	cag	aca	cag	ctg	ttg	ttc	ggg	gct	1348
Ser	Gly	Leu	Gly	Leu	Asn	Val	Tyr	Gln	Thr	Gln	Leu	Leu	Phe	Gly	Ala	
				430										440		
gtg	gaa	ctg	ccc	tcc	aag	ctg	ctg	gtc	tac	ttg	tcg	gtg	cgc	tac	gca	1396
Val	Glu	Leu	Pro	Ser	Lys	Leu	Leu	Val	Tyr	Leu	Ser	Val	Arg	Tyr	Ala	
				445										455		
gga	cgc	cgc	ctc	acg	caa	gcc	ggg	aca	ctg	ctg	ggc	acg	gcc	ctg	gcg	1444
Gly	Arg	Arg	Leu	Thr	Gln	Ala	Gly	Thr	Leu	Leu	Gly	Thr	Ala	Leu	Ala	

```

460          465          470          475
ttc ggc act aga ctg cta gtg tcc tct gat atg aag tcc tgg agc act 1492
Phe Gly Thr Arg Leu Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr
          480          485          490
gtc ctg gca gtg atg ggg aaa gct ttt tct gaa gct gcc ttc acc act 1540
Val Leu Ala Val Met Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr
          495          500          505
gcc tac ctg ttc act tca gag ttg tac cct acg gtg ctc aga cag aca 1588
Ala Tyr Leu Phe Thr Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr
          510          515          520
ggg atg ggg ctg act gca ctg gtg ggc cgg ctg ggg ggc tct ttg gcc 1636
Gly Met Gly Leu Thr Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala
          525          530          535
cca ctg gcg gcc ttg ctg gat gga gtg tgg ctg tca ctg ccc aag ctt 1684
Pro Leu Ala Ala Leu Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu
          540          545          550          555
act tat ggg ggg atc gcc ctg ctg gct gcc ggc acc gcc ctc ctg ctg 1732
Thr Tyr Gly Gly Ile Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu
          560          565          570
cca gag acg agg cag gca cag ctg cca gag acc atc cag gac gtg gag 1780
Pro Glu Thr Arg Gln Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu
          575          580          585
aga aag agt gcc cca acc agt ctt cag gag gaa gag atg ccc atg aag 1828
Arg Lys Ser Ala Pro Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys
          590          595          600
cag gtc cag aac taagtgggag tggaggcagg ccctccacag aagctctgca 1880
Gln Val Gln Asn
          605
gcaggggctg ggagagcaga agggcaggcc ctgcaactca ggctgggagt atcgaaccct 1940
ctgcctaggg ccggagttgc tgccagtacc cgctccctct gctcatccat ccttgattat 2000
ttggcttcta ggaacagttg acttcccaga atgcagtggg ctgctgggca cccctctcac 2060
ggttggggag gattctgtaa ataaaggtgc cccttgggtt ggggcagtgg tg 2112

```

<210> 56
 <211> 1087
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (33) ... (977)

```

<400> 56
agagggggcg tcaggccgcg ggagaggagg cc atg ggc gcg cgc ggg gcg ctg 53
          Met Gly Ala Arg Gly Ala Leu
          1          5
ctg ctg gcg ctg ctg ctg gct cgg gct gga ctc agg aag ccg gag tgc 101
Leu Leu Ala Leu Leu Leu Ala Arg Ala Gly Leu Arg Lys Pro Glu Ser
          10          15          20
cag gag gcg gcg ccg tta tca gga cca tgc ggc cga cgg gtc atc acg 149
Gln Glu Ala Ala Pro Leu Ser Gly Pro Cys Gly Arg Arg Val Ile Thr
          25          30          35
tcg cgc atc gtg ggt gga gag gac gcc gaa ctc ggg cgt tgg ccg tgg 197
Ser Arg Ile Val Gly Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp
          40          45          50          55
cag ggg agc ctg cgc ctg tgg gat tcc cac gta tgc gga gtg agc ctg 245
Gln Gly Ser Leu Arg Leu Trp Asp Ser His Val Cys Gly Val Ser Leu
          60          65          70
ctc agc cac cgc tgg gca ctc acg gcg gcg cac tgc ttt gaa acc tat 293
Leu Ser His Arg Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr
          75          80          85

```

```

agt gac ctt agt gat ccc tcc ggg tgg atg gtc cag ttt ggc cag ctg      341
Ser Asp Leu Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu
      90                      95                      100
act tcc atg cca tcc ttc tgg agc ctg cag gcc tac tac acc cgt tac      389
Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr
      105                      110                      115
ttc gta tcg aat atc tat ctg agc cct cgc tac ctg ggg aat tca ccc      437
Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
      120                      125                      130                      135
tat gac att gcc ttg gtg aag ctg tct gca cct gtc acc tac act aaa      485
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr Lys
      140                      145                      150
cac atc cag ccc atc tgt ctc cag gcc tcc aca ttt gag ttt gag aac      533
His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe Glu Asn
      155                      160                      165
cgg aca gac tgc tgg gtg act ggc tgg ggg tac atc aaa gag gat gag      581
Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys Glu Asp Glu
      170                      175                      180
gca ctg cca tct ccc cac acc ctc cag gaa gtt cag gtc gcc atc ata      629
Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln Val Ala Ile Ile
      185                      190                      195
aac aac tct atg tgc aac cac ctc ttc ctc aag tac agt ttc cgc aag      677
Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys Tyr Ser Phe Arg Lys
      200                      205                      210                      215
gac atc ttt gga gac atg gtt tgt gct ggc aat gcc caa ggc ggg aag      725
Asp Ile Phe Gly Asp Met Val Cys Ala Gly Asn Ala Gln Gly Gly Lys
      220                      225                      230
gat gcc tgc ttc ggt gac tca ggt gga ccc ttg gcc tgt aac aag aat      773
Asp Ala Cys Phe Gly Asp Ser Gly Gly Pro Leu Ala Cys Asn Lys Asn
      235                      240                      245
gga ctg tgg tat cag att gga gtc gtg agc tgg gga gtg gcc tgt ggt      821
Gly Leu Trp Tyr Gln Ile Gly Val Ser Trp Gly Val Gly Cys Gly
      250                      255                      260
cgg ccc aat cgg ccc ggt gtc tac acc aat atc agc cac cac ttt gag      869
Arg Pro Asn Arg Pro Gly Val Tyr Thr Asn Ile Ser His His Phe Glu
      265                      270                      275
tgg atc cag aag ctg atg gcc cag agt ggc atg tcc cag cca gac ccc      917
Trp Ile Gln Lys Leu Met Ala Gln Ser Gly Met Ser Gln Pro Asp Pro
      280                      285                      290                      295
tcc tgg ccg sta ctc ttt ttc cct ctt ctc tgg gct ctc cca ctc ctg      963
Ser Trp Pro Leu Leu Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu
      300                      305                      310
ggg ccg gtc tgagcctacc tgagcccatg cagcctgggg ccactgccaa gtcagg      1020
Gly Pro Val

ccctggttct cttctgtctt gtttgtaaat aaacacattc cagttgatgc cttgcagggc      1080
attcttc      1087

```

<210> 57
 <211> 1694
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (216) ... (500)

```

<400> 57
cccgaagttt gaggggtgtg gacggtttgt gacccccctta gccgacccta ctectcactg      60
gccgggacaa ctggtcttat cacggaggct ggggccaggc agcccttcgg ttcgggtggg      120
cccatggacc ccagtcacac gccgagggaa taggaccatc caaaagcgga accttcgcct      180

```



```

cgg aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca      194
Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
                    50                    55                    60
gcc gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg      242
Ala Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp
                    65                    70                    75
ttc gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc      290
Phe Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala
                    80                    85                    90
tac atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg      338
Tyr Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met
                    95                    100                    105
tac tcg cgc aca gtt gcc atc atc ggc gga ctt tct tgt gtt ggc cag      386
Tyr Ser Arg Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln
110                    115                    120                    125
cgg tgc tgg gga gct gta ccg ccg gaa acc tcg cag ccg ctc cct gca      434
Arg Cys Trp Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala
                    130                    135                    140
gtc cac cgg cca ggt gtt cct ggg tat cta cct cat ctg tgt ggc cta      482
Val His Arg Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu
                    145                    150                    155
ctc act gca gca cag caa gga gga ccg gct ggc gta tct gaa cca tct      530
Leu Thr Ala Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser
                    160                    165                    170
ccc agg agg gga gct gat gat cca gct gtt ctt cgt gct gta tgg cat      578
Pro Arg Arg Gly Ala Asp Pro Ala Val Leu Arg Ala Val Trp His
175                    180                    185
cct ggc cct ggc ctt tct gtc agg cta cta cgt gac cct cgc tgc cca      626
Pro Gly Pro Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro
190                    195                    200                    205
gat cct ggc tgt act gct gcc ccc tgt cat gct gct cat tgatg      670
Asp Pro Gly Cys Thr Ala Ala Pro Cys His Ala Ala His
                    210                    215
gcaatgttgc ttactggcac aacacgcggc gtgttgagtt ctggaaccag atgaagctcc      730
ttggagagag tgtgggcac ttcggaactg ctgtcatctg gccactgatg gctgagtttt      790
atggcaagag gctgagatgg gcacagggag ccactgaggg tcaccctgcc ttctctcttg      850
ctggcccagc tgcgtgtttat ttatgctttt tggctctgtt gtttgatctt ttgctttttt      910
aaaattgttt tttgcagtta agaggcagct catttgctcca aatttctggg ctgagcgctt      970
gggagggcag gagccctggc actaatgctg tacaggtttt ttctctgtta ggagagctga      1030
ggccagctgc ccactgagtc tcctgtccct gagaaggag tatggcaggg ctgggatgcg      1090
gctactgaga gtgggagagt gggagacaga ggaaggaa tggagattgg aagtgaacaa      1150
atgtgaaaaa ttctctcttg aacctggcag atgcagctag gctctgcagt gctgtttgga      1210
gactgtgaga gggagtgcgt gtgttgacac atgtggatca ggcccaggaa gggcacaggg      1270
gctgagcact acagaagtca catgggttct cagggtatgc caggggcaga aacagtaccg      1330
gctctctgtc actcaccttg agagtagagc agaccctgtt ctgctctggg ctgtgaaggg      1390
gtggagcagg cagtggccag ctttgccctt cctgctgtct ctgtttctag ctccatggtt      1450
ggcctggtgg ggtgtgagtt cctcccaaaa caccagacca cacagtcctc caaaaataaa      1510
cattttatat ag
                    1522

```

<210> 59
 <211> 1591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (44)...(1426)

```

<400> 59
gaaaacagtt ccacgttgct tgaaattgaa aatcaagata aaa atg ttc aca att      55
Met Phe Thr Ile

```

1																
aag	ctc	ctt	ctt	ttt	att	gtt	cct	cta	gtt	att	tcc	tcc	aga	att	gat	103
Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile	Ser	Ser	Arg	Ile	Asp	
5					10					15					20	
caa	gac	aat	tca	tca	ttt	gat	tct	cta	tct	cca	gag	cca	aaa	tca	aga	151
Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser	Pro	Glu	Pro	Lys	Ser	Arg	
				25					30					35		
ttt	gct	atg	tta	gac	gat	gta	aaa	att	tta	gcc	aat	ggc	ctc	ctt	cag	199
Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile	Leu	Ala	Asn	Gly	Leu	Leu	Gln	
			40					45					50			
ttg	gga	cat	ggt	ctt	aaa	gac	ttt	gtc	cat	aag	acg	aag	ggc	caa	att	247
Leu	Gly	His	Gly	Leu	Lys	Asp	Phe	Val	His	Lys	Thr	Lys	Gly	Gln	Ile	
		55					60					65				
aat	gac	ata	ttt	caa	aaa	ctc	aac	ata	ttt	gat	cag	tct	ttt	tat	gat	295
Asn	Asp	Ile	Phe	Gln	Lys	Leu	Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	
		70				75					80					
cta	tcg	ctg	caa	acc	agt	gaa	atc	aaa	gaa	gaa	gaa	aag	gaa	ctg	aga	343
Leu	Ser	Leu	Gln	Thr	Ser	Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	
85					90					95					100	
aga	act	aca	tat	aaa	cta	caa	gtc	aaa	aat	gaa	gag	gta	aag	aat	atg	391
Arg	Thr	Thr	Tyr	Lys	Leu	Gln	Val	Lys	Asn	Glu	Glu	Val	Lys	Asn	Met	
				105					110					115		
tca	ctt	gaa	ctc	aac	tca	aaa	ctt	gaa	agc	ctc	cta	gaa	gaa	aaa	att	439
Ser	Leu	Glu	Leu	Asn	Ser	Lys	Leu	Glu	Ser	Leu	Leu	Glu	Glu	Lys	Ile	
			120					125					130			
cta	ctt	caa	caa	aaa	gtg	aaa	tat	tta	gaa	gag	caa	cta	act	aac	tta	487
Leu	Leu	Gln	Gln	Lys	Val	Lys	Tyr	Leu	Glu	Glu	Gln	Leu	Thr	Asn	Leu	
		135					140					145				
att	caa	aat	caa	cct	gaa	act	cca	gaa	cac	cca	gaa	gta	act	tca	ctt	535
Ile	Gln	Asn	Gln	Pro	Glu	Thr	Pro	Glu	His	Pro	Glu	Val	Thr	Ser	Leu	
		150				155					160					
aaa	act	ttt	gta	gaa	aaa	caa	gat	aat	agc	atc	aaa	gac	ctt	ctc	cag	583
Lys	Thr	Phe	Val	Glu	Lys	Gln	Asp	Asn	Ser	Ile	Lys	Asp	Leu	Leu	Gln	
165					170					175					180	
acc	gtg	gaa	gac	caa	tat	aaa	caa	tta	aac	caa	cag	cat	agt	caa	ata	631
Thr	Val	Glu	Asp	Gln	Tyr	Lys	Gln	Leu	Asn	Gln	Gln	His	Ser	Gln	Ile	
			185						190					195		
aaa	gaa	ata	gaa	aat	cag	ctc	aga	agg	act	agt	att	caa	gaa	ccc	aca	679
Lys	Glu	Ile	Glu	Asn	Gln	Leu	Arg	Arg	Thr	Ser	Ile	Gln	Glu	Pro	Thr	
			200					205					210			
gaa	att	tct	cta	tct	tcc	aag	cca	aga	gca	cca	aga	act	act	ccc	ttt	727
Glu	Ile	Ser	Leu	Ser	Ser	Lys	Pro	Arg	Ala	Pro	Arg	Thr	Thr	Pro	Phe	
			215				220					225				
ctt	cag	ttg	aat	gaa	ata	aga	aat	gta	aaa	cat	gat	ggc	att	cct	gct	775
Leu	Gln	Leu	Asn	Glu	Ile	Arg	Asn	Val	Lys	His	Asp	Gly	Ile	Pro	Ala	
		230				235					240					
gaa	tgt	acc	acc	att	tat	aac	aga	ggt	gaa	cat	aca	agt	ggc	atg	tat	823
Glu	Cys	Thr	Thr	Ile	Tyr	Asn	Arg	Gly	Glu	His	Thr	Ser	Gly	Met	Tyr	
245					250					255					260	
gcc	atc	aga	ccc	agc	aac	tct	caa	gtt	ttt	cat	gtc	tac	tgt	gat	gtt	871
Ala	Ile	Arg	Pro	Ser	Asn	Ser	Gln	Val	Phe	His	Val	Tyr	Cys	Asp	Val	
			265					270						275		
ata	tca	ggt	agt	cca	tgg	aca	tta	att	caa	cat	cga	ata	gat	gga	tca	919
Ile	Ser	Gly	Ser	Pro	Trp	Thr	Leu	Ile	Gln	His	Arg	Ile	Asp	Gly	Ser	
			280					285					290			
caa	aac	ttc	aat	gaa	acg	tgg	gag	aac	tac	aaa	tat	ggt	ttt	ggg	agg	967
Gln	Asn	Phe	Asn	Glu	Thr	Trp	Glu	Asn	Tyr	Lys	Tyr	Gly	Phe	Gly	Arg	
		295					300					305				
ctt	gat	gga	gaa	ttt	tgg	ttg	ggc	cta	gag	aag	ata	tac	tcc	ata	gtg	1015
Leu	Asp	Gly	Glu	Phe	Trp	Leu	Gly	Leu	Glu	Lys	Ile	Tyr	Ser	Ile	Val	
		310				315					320					

```

aag caa tct aat tat gtt tta cga att gag ctg gaa gac tgg aaa gac      1063
Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp
325                               330                               335                               340
aac aaa cat tat att gaa tat tct ttt tac ttg gga aat cac gaa acc      1111
Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr
                               345                               350                               355
aac tat acg cta cat cta gtt gcg att act ggc aat gtc ccc aat gca      1159
Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala
                               360                               365                               370
atc ccg gaa aac aaa gat ttg gtg ttt tct act tgg gat cac aaa gca      1207
Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala
                               375                               380                               385
aaa gga cac ttc aac tgt cca gag ggt tat tca gga ggc tgg tgg tgg      1255
Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp
390                               395                               400
cat gat gag tgt gga gaa aac aac cta aat ggt aaa tat aac aaa cca      1303
His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
405                               410                               415                               420
aga gca aaa tct aag cca gag agg aga aga gga tta tct tgg aag tct      1351
Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys Ser
                               425                               430                               435
caa aat gga agg tta tac tct ata aaa tca acc aaa atg ttg atc cat      1399
Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu Ile His
440                               445                               450
cca aca gat tca gaa agc ttt gaa tgaactgagg caaatttaaa aggcaat      1450
Pro Thr Asp Ser Glu Ser Phe Glu
455                               460
aatttaaacaa ttaacctcat tccaagttaa tgtggtctaa taatctggta ttaaatecctt      1510
aagagaaagc ttgagaaata gatttttttt tatcttaag tcactgtcta tttaagatta      1570
aacatacaat cacataacct t      1591

```

<210> 60
 <211> 1249
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (134)...(784)

```

<400> 60
aacagtctgt ggagacagtt gtgtccctgt ggcttttggtg cgccctgtgtg cactttctcc      60
ctccacctgg agcatgggct aacaccggag gaaaggaaaa gacagagtca gacagggagc      120
ctgggggaggg gcc atg gtg cca atg cac tta ctg ggg aga ctg gag aag      169
                Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys
                1                5                10
ccg ctt ctc ctc ctg tgc tgc gcc tcc ttc cta ctg ggg ctg gct ttg      217
Pro Leu Leu Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu
                15                20                25
ctg ggc ata aag acg gac atc acc ccc gtt gct tat ttc ttt ctc aca      265
Leu Gly Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr
                30                35                40
ttg ggt ggc ttc ttc ttg ttt gcc tat ctc ctg gtc cgg ttt ctg gaa      313
Leu Gly Gly Phe Phe Leu Phe Ala Tyr Leu Val Arg Phe Leu Glu
                45                50                55                60
tgg ggg ctt cgg tcc cag ctc caa tca atg cag act gag agc cca ggg      361
Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly
                65                70                75
ccc tca ggc aat gca cgg gac aat gaa gcc ttt gaa gtg cca gtc tat      409
Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr
                80                85                90

```

```

gaa gag gcc gtg gtg gga cta gaa tcc cag tgc cgc ccc caa gag ttg      457
Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu
      95      100      105
gac caa cca ccc ccc tac agc act gtt gtg ata ccc cca gca cct gag      505
Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu
      110      115      120
gag gaa caa cct agc cat cca gag ggg tcc agg aga gcc aaa ctg gaa      553
Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu
      125      130      135      140
cag agg cga atg gcc tca gag ggg tcc atg gcc cag gaa gga agc cct      601
Gln Arg Arg Met Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro
      145      150      155
gga aga gct cca atc aac ctt cgg ctt cgg gga cca cgg gct gtg tcc      649
Gly Arg Ala Pro Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser
      160      165      170
act gct cct gat ctg cag agc ttg gcg gca gtc ccc aca tta gag cct      697
Thr Ala Pro Asp Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro
      175      180      185
ctg act cca ccc cct gcc tat gat gtc tgc ttt ggt cac cct gat gat      745
Leu Thr Pro Pro Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp
      190      195      200
gat agt gtt ttt tat gag gac aac tgg gca ccc cct taaatgact      790
Asp Ser Val Phe Tyr Glu Asp Asn Trp Ala Pro Pro
      205      210      215
ctcccaagat ttctcttctc tccacaccag acctcggtca tttgactaac attttccagc      850
gcctactatg tgtcagaaac aagtgtttct gcctggacat cataaatggg gacttggacc      910
ctgaggagag tcaggccacg gtaagccctt cccagctgag atatgggtgg cataatttga      970
gtcttctggc aacattttgt gacctacccc atatccaata tttccagcgt tagattgagg      1030
atgaggtagg gaggtgatcc agagaaggcg gagaaggaag aagtaacctc tgagtggcgg      1090
ctattgcttc tgttccaggt gctgttcgag ctgttagaac ccttaggctt gacagctttg      1150
tgagttatta ttgaaaaatg aggattccaa gagtcagagg agtttgataa tgtgcacgag      1210
ggcacactgc tagtaaaataa cattaataa actggaatg      1249

```

<210> 61
 <211> 392
 <212> PRT
 <213> Homo sapiens

```

<400> 61
Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu
  1      5      10      15
Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
      20      25      30
Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
      35      40      45
Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
      50      55      60
Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
      65      70      75      80
Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His
      85      90      95
Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln
      100      105      110
Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln
      115      120      125
Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly
      130      135      140
Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met
      145      150      155      160
Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys
      165      170      175

```

His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys
 180 185 190
 Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val
 195 200 205
 Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala
 210 215 220
 Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe
 225 230 235 240
 Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly
 245 250 255
 Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg
 260 265 270
 Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu
 275 280 285
 Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly
 290 295 300
 Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu
 305 310 315 320
 Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335
 Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350
 Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365
 Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380
 Pro Arg Arg Ser Glu Lys Gln Pro
 385 390

<210> 62
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 62
 Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
 1 5 10 15
 Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
 20 25 30
 Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
 35 40 45
 Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
 50 55 60
 Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
 65 70 75 80
 Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
 85 90 95
 Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
 100 105 110
 Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Trp Lys Gly Ala Ala
 115 120 125
 Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
 130 135 140
 Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala
 145 150 155 160
 Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
 165 170 175
 Leu Cys Gly Pro Val Gly Pro Arg Leu His Glu Leu Leu Asp Asp Asn
 180 185 190
 Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
 195 200 205

```

Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
210                215                220
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
225                230                235                240
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
                245                250                255
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu
                260                265                270
Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile
275                280                285
Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg
290                295                300
Glu Leu Met Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr
305                310                315                320
Ser Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala
                325                330                335
Ser Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val
340                345                350
Gly Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg
355                360                365
Ser Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu
370                375                380
Val Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu
385                390                395                400
Ala Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala
                405                410                415
Thr Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu
420                425                430
Phe Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro
435                440                445
Asn Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe
450                455                460
Thr Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly
465                470                475                480
Asp Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His
                485                490                495
Tyr

```

```

<210> 63
<211> 417
<212> PRT
<213> Homo sapiens

```

```

<400> 63
Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro Phe Pro
1                5                10                15
Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala Val Arg
                20                25                30
Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val Ala His
35                40                45
Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu Ala Pro
50                55                60
Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu Leu Gly
65                70                75                80
Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala Leu Cys
                85                90                95
Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val Val Gly
100               105               110
Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro His Leu
115               120               125
Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala Leu Val

```

130	135	140
Asn Val Gln Ile Pro Leu	Leu Leu Gly Gln Leu	Val Glu Val Val Ala
145	150	155
Lys Tyr Thr Arg Asp	His Val Gly Ser Phe	Met Thr Glu Ser Gln Asn
165	170	175
Leu Ser Thr His Leu	Leu Ile Leu Tyr Gly	Val Gln Gly Leu Leu Thr
180	185	190
Phe Gly Tyr Leu Val	Leu Leu Ser His Val	Gly Glu Arg Met Ala Val
195	200	205
Asp Met Arg Arg Ala	Leu Phe Ser Ser Leu	Leu Arg Tyr Cys Gln Pro
210	215	220
Gln Gly Ala Glu Leu	Gly Gln Asp Ile Thr	Phe Phe Asp Ala Asn Lys
225	230	235
Thr Gly Gln Leu Val	Ser Arg Leu Thr Thr	Asp Val Gln Glu Phe Lys
245	250	255
Ser Ser Phe Lys Leu	Val Ile Ser Gln Gly	Leu Arg Ser Cys Thr Gln
260	265	270
Val Ala Gly Cys Leu	Val Ser Leu Ser Met	Leu Ser Thr Arg Leu Thr
275	280	285
Leu Leu Leu Met Val	Ala Thr Pro Ala Leu	Met Gly Val Gly Thr Leu
290	295	300
Met Gly Ser Gly Leu	Arg Lys Leu Ser Cys	Gln Cys Gln Glu Gln Ile
305	310	315
Ala Arg Ala Met Gly	Val Ala Asp Glu Ala	Leu Gly Asn Val Arg Thr
325	330	335
Val Arg Ala Phe Ala	Met Glu Gln Arg Glu	Glu Glu Arg Tyr Gly Ala
340	345	350
Glu Leu Glu Ala Cys	Arg Cys Arg Ala Glu	Glu Glu Leu Gly Arg Gly Ile
355	360	365
Ala Leu Phe Gln Gly	Leu Ser Asn Ile Ala	Phe Asn Cys Met Val Leu
370	375	380
Gly Thr Leu Phe Ile	Gly Gly Ser Leu Val	Ala Gly Gln Gln Leu Thr
385	390	395
Gly Gly Asp Leu Met	Ser Phe Leu Val Ala	Ser Gln Thr Val Gln Arg
405	410	415
Leu		

<210> 64
 <211> 649
 <212> PRT
 <213> Homo sapiens

<400> 64
Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly Ser His Gln Pro Ala
1 5 10 15
Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu Asp His Ile Leu Pro
20 25 30
Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu Val Val Gly Ser Val
35 40 45
Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly Asp Phe Val Phe Asp
50 55 60
Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala Gly Val Val Gly Arg
65 70 75 80
Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Ser Phe Leu Gly Tyr
85 90 95
Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly Ala His Ser Ser Thr
100 105 110
Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala Val Ala Met Leu Cys
115 120 125
Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn Ala Val Phe Asp Ile
130 135 140

Leu	Val	Ile	Gly	Lys	Phe	Asn	Val	Leu	Glu	Ile	Val	Gln	Lys	Val	Leu
145					150					155					160
His	Lys	Asp	Lys	Ser	Leu	Glu	Asn	Leu	Gly	Met	Leu	Arg	Asn	Gly	Gly
				165					170					175	
Leu	Leu	Phe	Arg	Met	Thr	Leu	Leu	Thr	Ser	Gly	Gly	Ala	Gly	Met	Leu
			180					185					190		
Tyr	Val	Arg	Trp	Arg	Ile	Met	Gly	Thr	Gly	Pro	Pro	Ala	Phe	Thr	Glu
		195					200					205			
Val	Asp	Asn	Pro	Ala	Ser	Phe	Ala	Asp	Ser	Met	Leu	Val	Arg	Ala	Val
	210					215					220				
Asn	Tyr	Asn	Tyr	Tyr	Tyr	Ser	Leu	Asn	Ala	Trp	Leu	Leu	Leu	Cys	Pro
225					230					235					240
Trp	Trp	Leu	Cys	Phe	Asp	Trp	Ser	Met	Gly	Cys	Ile	Pro	Leu	Ile	Lys
			245						250					255	
Ser	Ile	Ser	Asp	Trp	Arg	Val	Ile	Ala	Leu	Ala	Ala	Leu	Trp	Phe	Cys
			260					265					270		
Leu	Ile	Gly	Leu	Ile	Cys	Gln	Ala	Leu	Cys	Ser	Glu	Asp	Gly	His	Lys
		275					280					285			
Arg	Arg	Ile	Leu	Thr	Leu	Gly	Leu	Gly	Phe	Leu	Val	Ile	Pro	Phe	Leu
	290					295					300				
Pro	Ala	Ser	Asn	Leu	Phe	Phe	Arg	Val	Gly	Phe	Val	Val	Ala	Glu	Arg
305					310					315					320
Val	Leu	Tyr	Leu	Pro	Ser	Ile	Gly	Tyr	Cys	Val	Leu	Leu	Thr	Phe	Gly
			325						330					335	
Phe	Gly	Ala	Leu	Ser	Lys	His	Thr	Lys	Lys	Lys	Lys	Leu	Ile	Ala	Ala
		340					345						350		
Val	Val	Leu	Gly	Ile	Leu	Phe	Ile	Asn	Thr	Leu	Arg	Cys	Val	Leu	Arg
		355				360						365			
Ser	Gly	Glu	Trp	Arg	Ser	Glu	Glu	Gln	Leu	Phe	Arg	Ser	Ala	Leu	Ser
	370					375					380				
Val	Cys	Pro	Leu	Asn	Ala	Lys	Val	His	Tyr	Asn	Ile	Gly	Lys	Asn	Leu
385					390					395					400
Ala	Asp	Lys	Gly	Asn	Gln	Thr	Ala	Ala	Ile	Arg	Tyr	Tyr	Arg	Glu	Ala
			405						410					415	
Val	Arg	Leu	Asn	Pro	Lys	Tyr	Val	His	Ala	Met	Asn	Asn	Leu	Gly	Asn
			420					425					430		
Ile	Leu	Lys	Glu	Arg	Asn	Glu	Leu	Gln	Glu	Ala	Glu	Glu	Leu	Leu	Ser
	435					440						445			
Leu	Ala	Val	Gln	Ile	Gln	Pro	Asp	Phe	Ala	Ala	Ala	Trp	Met	Asn	Leu
	450					455					460				
Gly	Ile	Val	Gln	Asn	Ser	Leu	Lys	Arg	Phe	Glu	Ala	Ala	Glu	Gln	Ser
465					470					475					480
Tyr	Arg	Thr	Ala	Ile	Lys	His	Arg	Arg	Lys	Tyr	Pro	Asp	Cys	Tyr	Tyr
			485						490					495	
Asn	Leu	Gly	Arg	Leu	Tyr	Ala	Asp	Leu	Asn	Arg	His	Val	Asp	Ala	Leu
		500					505						510		
Asn	Ala	Trp	Arg	Asn	Ala	Thr	Val	Leu	Lys	Pro	Glu	His	Ser	Leu	Ala
	515						520					525			
Trp	Asn	Asn	Met	Ile	Ile	Leu	Leu	Asp	Asn	Thr	Gly	Asn	Leu	Ala	Gln
	530					535					540				
Ala	Glu	Ala	Val	Gly	Arg	Glu	Ala	Leu	Glu	Leu	Ile	Pro	Asn	Asp	His
545					550					555					560
Ser	Leu	Met	Phe	Ser	Leu	Ala	Asn	Val	Leu	Gly	Lys	Ser	Gln	Lys	Tyr
			565						570					575	
Lys	Glu	Ser	Glu	Ala	Leu	Phe	Leu	Lys	Ala	Ile	Lys	Ala	Asn	Pro	Asn
		580					585						590		
Ala	Ala	Ser	Tyr	His	Gly	Asn	Leu	Ala	Val	Leu	Tyr	His	Arg	Trp	Gly
	595					600						605			
His	Leu	Asp	Leu	Ala	Lys	Lys	His	Tyr	Glu	Ile	Ser	Leu	Gln	Leu	Asp
	610				615						620				
Pro	Thr	Ala	Ser	Gly	Thr	Lys	Glu	Asn	Tyr	Gly	Leu	Leu	Arg	Arg	Lys

625 630 635 640
 Leu Glu Leu Met Gln Lys Lys Ala Val
 645

<210> 65
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 65
 Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
 1 5 10 15
 Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 20 25 30
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 35 40 45
 Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 50 55 60
 Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 65 70 75 80
 Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 85 90

<210> 66
 <211> 425
 <212> PRT
 <213> Homo sapiens

<400> 66
 Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
 1 5 10 15
 Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
 20 25 30
 Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
 35 40 45
 Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
 50 55 60
 Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
 65 70 75 80
 His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
 85 90 95
 Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
 100 105 110
 Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
 115 120 125
 Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
 130 135 140
 Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
 145 150 155 160
 Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
 165 170 175
 Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
 180 185 190
 Gly Leu Leu Leu Leu Leu Pro Pro Pro Ser Val Pro Thr Gly Glu
 195 200 205
 Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
 210 215 220
 Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
 225 230 235 240
 Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
 245 250 255

Ala	Cys	Leu	Leu	Gly	Leu	Leu	Ala	Ala	Thr	Asn	Ala	Leu	Thr	Asn	Gly
			260					265					270		
Val	Leu	Pro	Ala	Val	Gln	Ser	Phe	Ser	Cys	Leu	Pro	Tyr	Gly	Arg	Leu
		275					280					285			
Ala	Tyr	His	Leu	Ala	Val	Val	Leu	Gly	Ser	Ala	Ala	Asn	Pro	Leu	Ala
		290				295					300				
Cys	Phe	Leu	Ala	Met	Gly	Val	Leu	Cys	Arg	Ser	Leu	Ala	Gly	Leu	Gly
305					310					315					320
Gly	Leu	Ser	Leu	Leu	Gly	Val	Phe	Cys	Gly	Gly	Tyr	Leu	Met	Ala	Leu
				325					330					335	
Ala	Val	Leu	Ser	Pro	Cys	Pro	Pro	Leu	Val	Gly	Thr	Ser	Ala	Gly	Val
			340					345					350		
Val	Leu	Val	Val	Leu	Ser	Trp	Val	Leu	Cys	Leu	Gly	Val	Phe	Ser	Tyr
		355					360					365			
Val	Lys	Val	Ala	Ala	Ser	Ser	Leu	Leu	His	Gly	Gly	Gly	Arg	Pro	Ala
		370				375					380				
Leu	Leu	Ala	Ala	Gly	Val	Ala	Ile	Gln	Val	Gly	Ser	Leu	Leu	Gly	Ala
385					390					395					400
Val	Ala	Met	Phe	Pro	Pro	Thr	Ser	Ile	Tyr	His	Val	Phe	His	Ser	Arg
				405					410					415	
Lys	Asp	Cys	Ala	Asp	Pro	Cys	Asp	Ser							
			420					425							

```
<210> 67
<211> 149
<212> PRT
<213> Homo sapiens
```

[illegible]

```
<210> 68
<211> 396
<212> PRT
<213> Homo sapiens
```

<400> 68															
Met	Ala	Met	Ile	Glu	Leu	Gly	Phe	Gly	Arg	Gln	Asn	Phe	His	Pro	Leu
1				5					10					15	
Lys	Arg	Lys	Ser	Ser	Leu	Leu	Leu	Lys	Leu	Ile	Ala	Val	Val	Phe	Ala
			20					25					30		
Val	Leu	Leu	Phe	Cys	Glu	Phe	Leu	Ile	Tyr	Tyr	Leu	Ala	Ile	Phe	Gln

Ukuzibiza kwakhe kwakwazi ukuba akhona umsebenzi wakhe, akhona umsebenzi wakhe, akhona umsebenzi wakhe.

	35						40						45					
Cys 50	Asn	Trp	Pro	Glu	Val	Lys 55	Thr	Thr	Ala	Ser	Asp 60	Gly	Glu	Gln	Thr			
Thr 65	Arg	Glu	Pro	Val	Leu 70	Lys	Ala	Met	Phe	Leu 75	Ala	Asp	Thr	His	Leu 80			
Leu	Gly	Glu	Phe	Leu 85	Gly	His	Trp	Leu	Asp 90	Lys	Leu	Arg	Arg	Glu 95	Trp			
Gln	Met	Glu	Arg	Ala 100	Phe	Gln	Thr	Ala 105	Leu	Trp	Leu	Leu	Gln 110	Pro	Glu			
Val	Val	Phe 115	Ile	Leu	Gly	Asp 120	Ile	Phe 120	Asp	Glu	Gly	Lys 125	Trp	Ser	Thr			
Pro	Glu 130	Ala	Trp	Ala	Asp	Asp 135	Val	Glu	Arg	Phe	Gln 140	Lys	Met	Phe	Arg			
His 145	Pro	Ser	His	Val 150	Gln	Leu	Lys	Val	Val 155	Ala	Gly	Asn	His	Asp	Ile 160			
Gly	Phe	His	Tyr	Glu 165	Met	Asn	Thr	Tyr 170	Lys	Val	Glu	Arg	Phe	Glu 175	Lys			
Val	Phe	Ser	Ser 180	Glu	Arg	Leu	Phe	Ser 185	Trp	Lys	Gly	Ile	Asn 190	Phe	Val			
Met	Val	Asn 195	Ser	Val	Ala	Leu	Asn 200	Gly	Asp	Gly	Cys	Gly 205	Ile	Cys	Ser			
Glu 210	Thr	Glu	Ala	Glu	Leu	Ile 215	Glu	Val	Ser	His	Arg 220	Leu	Asn	Cys	Ser			
Arg 225	Glu	Ala	Arg	Gly	Ser 230	Ser	Arg	Cys	Gly	Pro 235	Gly	Pro	Leu	Leu	Pro 240			
Thr	Ser	Ala	Pro	Val 245	Leu	Leu	Gln	His	Tyr 250	Pro	Leu	Tyr	Arg	Arg 255	Ser			
Asp	Ala	Asn 260	Cys	Ser	Gly	Glu	Asp 265	Ala	Ala	Pro	Ala	Glu	Glu	Arg	Asp			
Ile	Pro	Phe 275	Lys	Glu	Asn	Tyr	Asp 280	Val	Leu	Ser	Arg	Glu	Ala	Ser	Gln			
Lys	Leu 290	Leu	Trp	Trp	Leu	Gln 295	Pro	Arg	Leu	Val	Leu 300	Ser	Gly	His	Thr			
His 305	Ser	Ala	Cys	Glu	Val 310	His	His	Gly	Gly	Arg 315	Val	Pro	Glu	Leu	Ser 320			
Val	Pro	Ser	Phe	Ser 325	Trp	Arg	Asn	Arg	Asn 330	Asn	Pro	Ser	Phe	Ile 335	Met			
Gly	Ser	Ile 340	Thr	Pro	Thr	Asp	Tyr	Thr 345	Leu	Ser	Lys	Cys	Tyr	Leu	Pro			
Arg	Glu	Asp 355	Val	Val	Leu	Ile	Ile 360	Tyr	Cys	Gly	Val	Val 365	Gly	Phe	Leu			
Val	Val 370	Leu	Thr	Leu	Thr	His 375	Phe	Gly	Leu	Leu	Ala 380	Ser	Pro	Phe	Leu			
Ser 385	Gly	Leu	Asn	Leu 390	Leu	Gly	Lys	Arg	Lys	Thr 395	Arg							

```
<210> 69
<211> 350
<212> PRT
<213> Homo sapiens
```

<400> 69
Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu Ser Glu Glu
1 5 10 15
Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu Gln Asp Lys
20 25 30
Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly Leu Asp Ser
35 40 45
Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys Leu Lys Asn
50 55 60
Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu Met Ala Val

65					70					75					80
Ala	Val	Phe	Leu	Val	Tyr	Arg	Thr	Ile	Thr	Asp	Phe	Arg	Glu	Lys	Leu
				85					90					95	
Lys	His	Pro	Val	Met	Ser	Val	Ser	Tyr	Lys	Glu	Val	Asp	Arg	Tyr	Asp
			100					105					110		
Ala	Pro	Gly	Ile	Ala	Leu	Tyr	Pro	Gly	Gln	Ala	Gln	Leu	Leu	Ser	Cys
		115					120					125			
Lys	His	His	Tyr	Glu	Val	Ile	Pro	Pro	Leu	Thr	Ser	Pro	Gly	Gln	Pro
	130					135					140				
Gly	Asp	Met	Asn	Cys	Thr	Thr	Gln	Arg	Ile	Asn	Tyr	Thr	Asp	Pro	Phe
145					150					155					160
Ser	Asn	Gln	Thr	Val	Lys	Ser	Ala	Leu	Ile	Val	Gln	Gly	Pro	Arg	Glu
				165					170					175	
Val	Lys	Lys	Arg	Glu	Leu	Val	Phe	Leu	Gln	Phe	Arg	Leu	Asn	Lys	Ser
			180					185					190		
Ser	Glu	Asp	Phe	Ser	Ala	Ile	Asp	Tyr	Leu	Leu	Phe	Ser	Ser	Phe	Gln
		195					200					205			
Glu	Phe	Leu	Gln	Ser	Pro	Asn	Arg	Val	Gly	Phe	Met	Gln	Ala	Cys	Glu
	210					215					220				
Ser	Ala	Tyr	Ser	Ser	Trp	Lys	Phe	Ser	Gly	Gly	Phe	Arg	Thr	Trp	Val
225					230					235					240
Lys	Met	Ser	Leu	Val	Lys	Thr	Lys	Glu	Glu	Asp	Gly	Arg	Glu	Ala	Val
				245					250					255	
Glu	Phe	Arg	Gln	Glu	Thr	Ser	Val	Val	Asn	Tyr	Ile	Asp	Gln	Arg	Pro
			260					265					270		
Ala	Ala	Lys	Lys	Ser	Ala	Gln	Leu	Phe	Phe	Val	Val	Phe	Glu	Trp	Lys
		275					280					285			
Asp	Pro	Phe	Ile	Gln	Lys	Val	Gln	Asp	Ile	Val	Thr	Ala	Asn	Pro	Trp
	290					295					300				
Asn	Thr	Ile	Ala	Leu	Leu	Cys	Gly	Ala	Phe	Leu	Ala	Leu	Phe	Lys	Ala
305					310					315					320
Ala	Glu	Phe	Ala	Lys	Leu	Ser	Ile	Lys	Trp	Met	Ile	Lys	Ile	Arg	Lys
				325					330					335	
Arg	Tyr	Leu	Lys	Arg	Arg	Gly	Gln	Ala	Thr	Ser	His	Ile	Ser		
			340					345					350		

```
<210> 70
<211> 153
<212> PRT
<213> Homo sapiens
```

<400> 70															
Met	Thr	Ile	His	Ile	Leu	Ile	Leu	Leu	Leu	Leu	Leu	Ala	Phe	Ser	Ala
1				5					10					15	
Gln	Gly	Asp	Leu	Asp	Thr	Ala	Ala	Arg	Arg	Gly	Gln	His	Gln	Val	Pro
			20					25					30		
Gln	His	Arg	Gly	His	Val	Cys	Tyr	Leu	Gly	Val	Cys	Arg	Thr	His	Arg
		35				40					45				
Leu	Ala	Glu	Ile	Ile	Tyr	Trp	Ile	Arg	Cys	Leu	His	Gln	Gly	Ala	Leu
	50					55					60				
Gly	Glu	Gly	Gln	Pro	Arg	Ala	Pro	Gly	Pro	Leu	Gln	Leu	Trp	Ala	Pro
	65				70					75					80
Pro	Val	Ala	Arg	Gly	Gly	Ser	Pro	Ala	Arg	Phe	Pro	Gly	Phe	Arg	Pro
				85					90					95	
Ala	Ala	Arg	Gly	Leu	Ala	Gln	Cys	Pro	Ala	Arg	Trp	Val	Thr	Ser	Gly
			100					105					110		
Thr	Ala	Arg	Pro	Leu	Leu	Gly	Phe	Ser	Leu	Pro	Ile	Cys	Met	Leu	Glu
		115					120					125			
Leu	Leu	Leu	His	Ile	Ser	Ser	Pro	Leu	Thr	Pro	Ala	Pro	Glu	Thr	Val
	130					135					140				
Phe	Pro	Ser	Pro	Ser	Pro	Gly	Cys	Asp							

145

150

```
<210> 71
<211> 1176
<212> DNA
<213> Homo sapiens
```

<400> 71						
atggaggggag	tgagcgcgct	gctgggccgc	tgccccacgg	ccggcctggc	cggcggcctg	60
ggggtcacgg	cgtgcgccgc	ggccggcggtg	ttgctctacc	ggatcgcgcg	gaggatgaag	120
ccaacgcaca	cgatggtcaa	ctgctggttc	tgcaaccagg	atacgtgtgt	gccctatggg	180
aaccgcaact	gctgggactg	tccccactgc	gagcagtaga	acggcttcca	ggagaacggc	240
gactacaaca	agccgactcc	cgcccagtag	ttggagcacc	tgaaccacgt	ggtgagcagc	300
gcgcccagcc	tgcgcgaccc	ttcgcagccg	cagcagtggt	tgagcagcca	agtcctgtctg	360
tgcaagaggt	gcaaccacca	ccagaccacc	aagatcaagc	agctggccgc	cttcgctccc	420
cgcgaggagg	gcaggtatga	cgaggaggtc	gaggtgtacc	ggcatcacct	ggagcagatg	480
tacaagctgt	gccggccgtg	ccaagcggct	gtggagtact	acatcaagca	ccagaaccgc	540
cagctgcgcg	ccctgttgtc	cagccaccag	ttcaagcgcc	gggaggccga	ccagaccacc	600
gcacagaact	tctctcctgc	cgtgaagtc	ccggtccagg	tcatectgct	ccgtgccttc	660
gccttcctgg	cctgcgcctt	ccctactgac	accgcgtgtg	atggggccag	ggcaccttc	720
gccccaggca	ccactgtgcc	cctggccctg	ccacctgggtg	gcaatggctc	agccacacct	780
gacaatggca	ccacccctgg	ggccgagggc	tggcggcagt	tgctgggcct	actccccgag	840
cacatggcgg	agaagctgtg	tgaggcctgg	gcctttgggc	agagccacca	gacgggcgtc	900
gtggcactgg	gcctactcac	ctgcctgctg	gcaatgtctc	tggttggecg	catcaggctc	960
cggaggatcg	atgcctttctg	cacctgcctg	tgggccctgc	tgctggggct	gcacctggct	1020
gagcagcacc	tgcaggccgc	ctcgctagc	tggctagaca	cgtcaagtt	cagcaccaca	1080
tctttgtgct	gcctggttgg	cttcacggcg	gctgtggcca	caaggaaggc	aacgggccca	1140
cggagggttcc	ggccccgaag	gtcagagaag	cagcca			1176

```
<210> 72
<211> 1491
<212> DNA
<213> Homo sapiens
```

[illegible]

```
<210> 73
<211> 1251
<212> DNA
<213> Homo sapiens
```

<400>	73						
atgctggtgc	atattatttcg	ggtcgggatt	cgggggtggcc	cattcccagg	caggetgcta		60
ccgcccctcc	gcttcagac	attctcagct	gtcaggtact	ctgatggcta	ccgcagctcc		120
tcctcctcc	gggccgtggc	ccacctgcgg	tcccagctct	gggccacct	ccctcgagcc		180
cccctagctc	ccagatggag	ccccctctgc	tgggtgctggg	ttggggggagc	cctgctaggc		240
cccattggtac	tgagtaagca	tccccacctc	tgccttgtg	ccctgtgtga	ggcagaagag		300
gccccctctg	ccagctccac	accccatgtc	gtgggggtctc	gctttaactg	gaagctcttc		360
tggcagtttc	tgcaccccca	cctgctggtc	ctgggggtag	ccgtcgtagt	ggccttgggt		420
gcggcactcg	tgaatgtaca	gatccccctg	ctcctgggcc	agctggtaga	ggtcgtggcc		480
aagtacacaa	gggaccacgt	agggagtttc	atgactgagt	cccagaatct	cagcaccac		540
ctgcttatcc	tctatggtgt	ccagggaactg	ctgaccttcg	ggtacctggt	gctgctgtcc		600
cacggttggcg	agcgcagtggc	tgtggacatg	cggaggggccc	tcttcagctc	cctgctccgg		660
tactgccagc	cgcagggtgc	agagttggga	caagacatca	ccttctttga	cgccaataag		720
acagggcagc	tggtgagcgg	cttgacaact	gacgtgcagg	agtttaagtc	atccttcaag		780
cttgtcatct	cccaggggct	gcgaagctgc	accagggtgg	caggctgcct	ggtgtccctg		840
tccatgctgt	cgacacgcct	cacgtgctg	ctgatggtgg	ccacaccagc	cctgatggga		900
gtgggcaccc	tgatgggctc	aggcctccga	aaattgtctt	gccagtgtca	ggagcagatc		960
gccagggcaa	tgggcgtagc	agacgaggcc	ctgggcaatg	tgcggactgt	gcgtgccttc		1020
gccattggagc	aacgggaaga	ggagcgctat	ggggcagagc	tggaagcctg	ccgctgccgg		1080
gcagaggagc	tgggcgcggg	catcgcttg	ttccaagggc	tttccaacat	cgcttcaac		1140
tgcattggtct	tgggtaccct	atttattggg	ggctcccttg	tggccggaca	gcagctgaca		1200
ggggggagacc	tcatgtcctt	cctggtggcc	tcccagacag	tgcaaaagct	g		1251

```
<210> 74
<211> 1947
<212> DNA
<213> Homo sapiens
```

[illegible]

aatttagccc	aagctgaage	agttggaaga	gaggcactgg	aattaatacc	taatgatcac	1680
tctctcatgt	tctcgttggc	aaacgtgctg	gggaaatccc	agaaatacaa	ggaatctgaa	1740
gctttattcc	tcaaggcaat	taaagcaaat	ccaaatgctg	caagttacca	tggtaatattg	1800
gctgtgcttt	atcatcgttg	gggacatcta	gacttggcca	agaaacacta	tgaaatctcc	1860
ttgcagcttg	accccacggc	atcaggaact	aaggagaatt	acggtctgct	gagaagaaag	1920
ctagaactaa	tgcaaaagaa	agctgtc				1947

<210> 75
 <211> 279
 <212> DNA
 <213> Homo sapiens

<400> 75						
atgatccatc	tggtgcacat	cctcttctctg	cttttgcctc	cagtggctgc	agctcagacg	60
actccaggag	agagatcatc	actccctgcc	ttttaccctg	gcacttcagg	ctcttggttc	120
ggatgtgggt	ccctctctct	gccgctcctg	gcaggcctcg	tggtgtctga	tgcggtggca	180
tcgtgtctca	tcgtgggggc	ggtgttctctg	tgcgcacgcc	cacgcgcgag	ccccgcccaa	240
gaagatggca	aagtctacat	caacatgcca	ggcaggggc			279

<210> 76
 <211> 1275
 <212> DNA
 <213> Homo sapiens

<400> 76						
atgggctcct	gggctgcggt	caatgggata	tggttgagac	tacctgtggt	ggtcaaagag	60
cttccagagg	gttgagacct	ccctctttac	gtctctgtgc	ttgtggctct	ggggaacctg	120
ggtctgctgg	tggtgacctt	ctggaggagg	ctggccccag	gaaaggacga	gcagggtccc	180
atccgggttg	tgaggtgct	gggcatggtg	ggcacagccc	tgttggtctc	tctgtggcac	240
catgtggccc	cagtggcagg	acagttgcat	tctgtggcct	tcttagcact	ggcctttgtg	300
ctggcactgg	catgctgtgc	ctcgaatgtc	actttctctg	ccttcttgag	ccacctgcca	360
cctcgcttct	tacgggtcatt	cttctctggg	caaggcctga	gtgcccctgt	gccttgctgt	420
ctggccctag	tgcagggtgt	gggcgcctc	gagtgcctgc	cagcccccat	caacggcacc	480
cctggccccc	cgtcgacctt	ccttgagcgt	tttcccgcca	gcaccttctt	ctgggcaact	540
actgcccttc	tggtcgcttc	agctgctgcc	ttccagggtc	ttctgctgct	gttgccgcca	600
ccaccatctg	taccacacag	ggagttagga	tcaggcctcc	aggtgggagc	cccaggagca	660
gaggaagagg	tgaagagtc	ctcaccactg	caagagccac	caagccaggc	agcaggcacc	720
acccctggtc	cagaccctaa	ggcctatcag	cttctatcag	cccgcagtgc	ctgcctgctg	780
ggcctgttgg	ccgccaccaa	cgcgctgacc	aatggcgtgc	tgccctgcct	gcagagcttt	840
tctgtcttac	cttacggggc	tctggcctac	cacctggctg	tggtgctggg	cagtgtctgc	900
aatccccctg	cctgcttctt	ggcctatggg	gtgctgtgca	ggctcctggc	agggctgggc	960
ggcctctctc	tgtgtggcgt	gttctgtggg	ggctacctga	tggtgctggc	agtcctgagc	1020
ccctgcccgc	ccctgtgtgg	cacctcgccg	gggtgtgtcc	tcgtgtgtgt	gtcgtgggtg	1080
ctgtgtcttg	gcgtgtttct	ctacgtgaag	gtggcagcca	gtccctctgt	gcattggcgg	1140
ggcggccgg	cattgtgtgc	agcggcgtg	gccatccagg	tgggtctctt	gtcggcgct	1200
gttgcctatg	cccccccgac	cagcatctat	cacgtgttcc	acagcagaaa	ggactgtgca	1260
gacctctgtg	actcc					1275

<210> 77
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 77						
atggagactt	tgtaccgtgt	cccgttctta	gtgctcgaat	gtcccaacct	gaagctgaag	60
aagccgccct	ggttgacat	gccgtcggcc	atgactgtgt	atgctctggg	ggtgggtgtc	120
tacttctctc	tcaccggagg	aataatttat	gatgttattg	ttgaacctcc	aagtgtcggt	180
tctatgactg	atgaacatgg	gcacagagg	ccagtagctt	tcttggccta	cagagtaaat	240
ggacaatata	ttatggaagg	acttgcatcc	agcttcttat	ttacaatggg	aggttttaggt	300
ttcataatcc	tggaccgatc	gaatgcacca	aatatcccaa	aactcaatag	attccttctt	360
ctgttcattg	gattcgtctg	tgtcctattg	agttttttca	tggttagagt	attcatgaga	420

atgaaactgc cgggctatct gatgggt

447

<210> 78

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 78

atggcgatga	tcgaattggg	gtttggaaga	cagaattttc	atccattaaa	gaggaagagt	60
tcattgctgt	tgaaactcat	agctgttgct	tttgctgtgc	ttctattttg	tgaattttta	120
atctattact	tagcgatctt	tcagtgtaat	tggcctgaag	tgaaaaccac	agcctctgat	180
ggtgaacaga	ccacacgtga	gcctgtgctc	aaagccatgt	ttttggctga	caccattttg	240
cttggggaat	tcctaggcca	ctggctggac	aaattacgaa	gggaatggca	gatggagaga	300
gcgttcacga	cagctctgtg	gttgctgcag	ccggaagtgc	tcttcatact	gggggatata	360
tttgatgaag	ggaagtggag	cacccctgag	gcctgggcgg	atgatgtgga	gcggtttcag	420
aaaatgttca	gacacccaag	tcatgtacag	ctgaaggtag	ttgctggaaa	ccatgacatt	480
ggcttcacat	atgagatgaa	cacatacaaa	gtagaacgct	ttgagaaagt	gttcagctct	540
gaaagactgt	tttcttggaa	aggcattaac	tttgtgatgg	tcaacagcgt	ggcgttgaac	600
gggatgggtg	gtggcatctg	ctctgaaaca	gaagcagagc	tcattgaagt	ttctcacaga	660
ctgaactgct	cccgagaggc	acgtggctcc	agccggtgtg	gacctgggcc	tctgtgccc	720
acgtctgccc	ctgtctctct	gcagcattat	cctctgtatc	ggagaagtga	tgctaactgt	780
tctggggaag	acgtctgctc	tgcagaggaa	agggacatcc	catttaagga	gaactatgac	840
gtgctttcac	gggaggcatc	acaaaagctg	ctgtgggtgg	tccagccgcg	cctgggtctc	900
agtggccaca	cgcacagcgc	ctgcgaggtg	caccacgggg	gccgagtcgc	cgagctcagc	960
gtcccatctt	tcagttggag	gaacagaaac	aaccccagtt	tcatactggg	tagcatcacg	1020
cccacagact	acaccctctc	caagtgtctc	ctcccacgtg	aggatgtggg	tttgatcacc	1080
tactgtggag	tgggtggctt	ccttgtggtc	ctcacactca	ctcactttgg	gcttctagcc	1140
tcaccttttc	tttctggttt	gaacttgctc	ggaaagcgta	agacaaga		1188

<210> 79

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 79

atgatccggc	aggagcgtc	cacatcctac	caggagctga	gtgaggagt	gggccagggtg	60
gttgagaact	cagagctggc	agacgagcag	gacaaggaga	cggtcagagt	ccaaggctccg	120
ggtatcttac	caggcctgga	cagcgagtcc	gcctccagca	gcatacgcct	cagcaaggcc	180
tgcctgaaga	acgtctcttc	ggtcctactc	atcttcatct	acctgctgct	catggctgtg	240
gccgtcttcc	tggctctacc	gaccatcaca	gactttcgtg	agaaactcaa	gcacctgtgc	300
atgtctgtgt	cttacaagga	agtggatcgc	tatgatgccc	caggtattgc	cttgatcccc	360
ggtcaggccc	agttgctcag	ctgtaagcac	cattacgagg	tcattcctcc	tctgacaagc	420
cctggccagc	cgggtgacat	gaattgcacc	acccagagga	tcaactacac	ggaccccttc	480
tccaatcaga	ctgtgaaatc	tgccttgatt	gtccaggggc	cccgggaagt	gaaaaagcgg	540
gagctgggtc	tcctccagtt	ccgcctgaac	aagagttagt	aggacttcag	cgccattgat	600
tacctcctct	tctcttcttt	ccaggagttc	ctgcaaagcc	caaacagggt	aggcttcatg	660
caggcctgtg	agagtgccta	ttccagctgg	aagtctctct	ggggcttccg	cacctgggtc	720
aagatgtcac	tggtaaagac	caaggaggag	gatgggcggg	aagcagtggg	gttcgggcag	780
gagacaagtg	tggtttaacta	cattgaccag	aggccagctg	ccaaaaaaag	tgctcaattg	840
ttttttgtgg	tctttgaatg	gaaagatcct	ttcatccaga	aagtccaaga	tatagtcact	900
gccaatcctt	ggaacacaat	tgctcttctc	tgtgggcgct	tcttggcatt	atttaaagca	960
gcagagtttg	ccaaactgag	tataaaatgg	atgatcaaaa	ttagaaaagag	ataccttaaa	1020
agaagagggtc	aggcaacgag	ccacataagc				1050

<210> 80

<211> 459

<212> DNA

<213> Homo sapiens

<400> 80

atgactatcc	acatcctcat	cctgctgttg	ctcctcgcc	tctccgccc	aggggacctg	60
------------	------------	------------	-----------	-----------	------------	----


```

gacactgcag ccaggcgagg ccagcaccag gtccccagc accgcgggca cgtctgctac 120
ctgggcgtat gccggaccca ccgcctggcg gagatcatat actggattcg ctgtctccac 180
caaggagccc tcggggaagg ccagccacga gccccaggac ccctacagct atgggcgccc 240
ccggtggcgc gaggcggaag ccggctcgg ttcccaggat tccggcctgc agcgaggggg 300
ctagcgcagt gccagctcg ctgggtgacc tcgggcacgg ctcgccccct cctcggttc 360
agtttgcta tctgtatgtt ggagcttcta ctccacatctt cttctccccct aactccagcc 420
cctgaaaccg tcttccccag tccctccccg ggctgcgac 459

```

<210> 81
 <211> 4027
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (192)...(1370)

```

<400> 81
gccgctaca aagcggcgaa ggtcacggcg cgaggaggcg cgcgtgcgcg ccccgcgtec 60
cgctgcggc ccgcgcccc ggctcacgc ctcctgccg gcctgcccgc ctgcccgcc 120
gccgcctac ccgctaccc gccctaccgc ctacccccct gccggcctgc cgtccttcca 180
cgcgagagc c atg gag gga gtg agc gcg ctg ctg gcc cgc tgc ccc acg 230
          Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr
                1          5          10
gcc ggc ctg gcc ggc ggc ctg ggg gtc acg gcg tgc gcc gcg gcc ggc 273
Ala Gly Leu Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly
          15          20          25
gtg ttg ctc tac cgg atc gcg cgg agg atg aag cca acg cac acg atg 326
Val Leu Leu Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met
          30          35          40          45
gtc aac tgc tgg ttc tgc aac cag gat acg ctg gtg ccc tat ggg aac 374
Val Asn Cys Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn
          50          55          60
cgc aac tgc tgg gac tgt ccc cac tgc gag cag tac aac ggc ttc cag 422
Arg Asn Cys Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln
          65          70          75
gag aac ggc gac tac aac aag ccg atc ccc gcc cag tac ttg gag cac 470
Glu Asn Gly Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His
          80          85          90
ctg aac cac gtg gtg agc agc gcg ccc agc ctg cgc gac cct tgg cag 518
Leu Asn His Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln
          95          100          105
ccg cag cag tgg gtg agc agc caa gtc ctg ctg tgc aag agg tgc aac 566
Pro Gln Gln Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn
          110          115          120          125
cac cac cag acc acc aag atc aag cag ctg gcc gcc ttc gct ccc cgc 614
His His Gln Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg
          130          135          140
gag gag ggc agg tat gac gag gag gtc gag gtg tac cgg cat cac ctg 662
Glu Glu Gly Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu
          145          150          155
gag cag atg tac aag ctg tgc cgg ccg tgc caa gcg gct gtg gag tac 710
Glu Gln Met Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr
          160          165          170
tac atc aag cac cag aac cgc cag ctg cgc gcc ctg ttg ctc agc cac 758
Tyr Ile Lys His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His
          175          180          185
cag ttc aag cgc cgg gag gcc gac cag acc cac gca cag aac ttc tcc 806
Gln Phe Lys Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser
          190          195          200          205
tcc gcc gtg aag tcc ccg gtc cag gtc atc ctg ctc cgt gcc ctc gcc 854

```



```

ttactgggct cagcttgttg ttctgtgtgg agcgtgaggt gagaaaaccc ctctgaaaag 3000
atgtggtcgg ggccacgctt cccactgggt ctgcagttag gagttggggc gggtagagcca 3060
aagcggcccc ccattgtgtc tacctgaggg gcagggaacc gcctgcctgt gcactcacgc 3120
cacccccag cccacaaaga gcccatctga gagaaggacg tggtaggagcc aggacgggaa 3180
agcgtcctgt cggctggcca tgcgtgttgc tgcgtctcga atcttcgggt ctcgaggaag 3240
tgttgacagt gtgatgctaa tgtctgcttt tcttggcggt gggtagaagc aggacatctg 3300
tgtgtatgtg cgtattttaa ttagattatt tataataacc agagccagcc ctgcgcctgg 3360
ccaggatcct cctgccgagc tgatgtcgct cctgccctct gccgggggtcc ggaagcgaca 3420
tctcaggagg tagctctcag cagagttagg attcctgcct ttcgtagagt tttgtgtgac 3480
tttttaaatt attcatgtgt cccttaaaag ttctactacg tggagaaaat tccagcacca 3540
agtgtttgtg caacagctga gagagtgcag gcaccactgt gttgtggctt gttgaccggg 3600
aatgtgtcac ccctgccagg gaactcttct cctgcggggg gacttgggat ggccatcaga 3660
ccttctaggg tctggctggg gtaatcctag gtatgggtga ccgtccctga gacataagcg 3720
aggtagattc agccatcctc accctcagac ttgaggtccc caccagggcc aagccggccc 3780
cccgtacccc ttgcctggga gcaaaccgcc aggacgcagc ctccacgcgc cactgccac 3840
accagccct gccaggaag gaacacatga cccttctgtc tgtgactgtt gctgagtctc 3900
tgtctcatgt cgtagaattg tgataattg tctagttagc ctctcatcac tgtaaccatc 3960
gcgcctggcc tagatgtcgt gttttggatg ctgtgttttc aataaatgcc tctggggccc 4020
tgctttt 4027

```

<210> 82
 <211> 2495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (30)...(1523)

```

<400> 82
gttcgcgcag gtggggcgcc tgggtcccc atg gcg ctg tgg cgc ggc tcc gcg 53
Met Ala Leu Trp Arg Gly Ser Ala
1 5
tac gcg ggc ttc ctg gcg ctg gcc gtg ggc tgc gtc ttc ctg ctg gag 101
Tyr Ala Gly Phe Leu Ala Leu Ala Val Gly Cys Val Phe Leu Leu Glu
10 15 20
cca gag ctg cca ggc tcg gcg ctg cgc tct ctc tgg agc tcg ctg tgt 149
Pro Glu Leu Pro Gly Ser Ala Leu Arg Ser Leu Trp Ser Ser Leu Cys
25 30 35 40
ctg ggg ccc gcg cct gcg ccc ccg gga ccc gtc tcc ccc gag ggc cgg 197
Leu Gly Pro Ala Pro Ala Pro Pro Gly Pro Val Ser Pro Glu Gly Arg
45 50 55
ttg gcg gca gcc tgg gac gcg ctt atc gtg cgg cca gtc cgg cgc tgg 245
Leu Ala Ala Ala Trp Asp Ala Leu Ile Val Arg Pro Val Arg Arg Trp
60 65 70
cgc cgc gtg gca gtg gga gtc aat gca tgt gtt gat gtg gtg ctc tca 293
Arg Arg Val Ala Val Gly Val Asn Ala Cys Val Asp Val Val Leu Ser
75 80 85
ggg gtg aag ctc ttg cag gca ctt ggc ctt agt cct ggg aat ggg aaa 341
Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser Pro Gly Asn Gly Lys
90 95 100
gat cac agc att ctg cat tca agg aat gat ctg gaa gaa gcc ttc att 389
Asp His Ser Ile Leu His Ser Arg Asn Asp Leu Glu Glu Ala Phe Ile
105 110 115 120
cac ttc atg tgg aag gga gca gct gct gag cgc ttc ttc agt gat aag 437
His Phe Met Trp Lys Gly Ala Ala Ala Glu Arg Phe Phe Ser Asp Lys
125 130 135
gaa act ttt cac gac att gcc cag gtt gcg tca gag ttc cca gga gcc 485
Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser Glu Phe Pro Gly Ala
140 145 150
cag cac tat gta gga gga aat gca gct tta att gga cag aaa ttt gca 533

```

Gln	His	Tyr	Val	Gly	Gly	Asn	Ala	Ala	Leu	Ile	Gly	Gln	Lys	Phe	Ala	
		155					160					165				
gcc	aac	tca	gat	tta	aag	gtt	ctt	ctt	tgc	ggt	cca	gtt	ggc	cca	agg	581
Ala	Asn	Ser	Asp	Leu	Lys	Val	Leu	Leu	Cys	Gly	Pro	Val	Gly	Pro	Arg	
		170				175					180					
cta	cat	gag	ctt	ctt	gat	gac	aat	gtc	ttt	gtt	cca	cca	gag	tca	ttg	629
Leu	His	Glu	Leu	Leu	Asp	Asn	Asn	Val	Phe	Val	Pro	Pro	Glu	Ser	Leu	
185					190					195					200	
cag	gaa	gtg	gat	gag	ttc	cac	ctc	att	tta	gag	tat	caa	gca	ggg	gag	677
Gln	Glu	Val	Asp	Glu	Phe	His	Leu	Ile	Leu	Glu	Tyr	Gln	Ala	Gly	Glu	
				205				210				215				
gag	tgg	ggc	cag	tta	aaa	gct	ccc	cat	gcc	aac	cga	ttc	atc	ttc	tct	725
Glu	Trp	Gly	Gln	Leu	Lys	Ala	Pro	His	Ala	Asn	Arg	Phe	Ile	Phe	Ser	
			220				225					230				
cac	gac	ctc	tcc	aac	ggg	gcc	atg	aat	atg	ctg	gag	gtg	ttt	gtg	tct	773
His	Asp	Leu	Ser	Asn	Gly	Ala	Met	Asn	Met	Leu	Glu	Val	Phe	Val	Ser	
			235				240					245				
agc	ctg	gag	gag	ttt	cag	cca	gac	ctg	gtg	gtc	ctc	tct	gga	ttg	cac	821
Ser	Leu	Glu	Glu	Phe	Gln	Pro	Asp	Leu	Val	Val	Leu	Ser	Gly	Leu	His	
					255						260					
atg	atg	gag	gga	caa	agc	aag	gag	ctc	cag	agg	aag	aga	ctc	ttg	gag	869
Met	Met	Glu	Gly	Gln	Ser	Lys	Glu	Leu	Gln	Arg	Lys	Arg	Leu	Leu	Glu	
265					270				275						280	
gtt	gta	acc	tcc	att	tct	gac	atc	ccc	act	ggt	att	cca	gtt	cac	cta	917
Val	Val	Thr	Ser	Ile	Ser	Asp	Ile	Pro	Thr	Gly	Ile	Pro	Val	His	Leu	
				285					290					295		
gag	ctg	gcc	agt	atg	act	aac	agg	gag	ctc	atg	agc	agc	att	gtc	cat	965
Glu	Leu	Ala	Ser	Met	Thr	Asn	Arg	Glu	Leu	Met	Ser	Ser	Ile	Val	His	
			300					305					310			
cag	cag	gtc	ttt	ccc	gcg	gtg	act	tcc	ctt	ggg	ctg	aat	gaa	cag	gag	1013
Gln	Gln	Val	Phe	Pro	Ala	Val	Thr	Ser	Leu	Gly	Leu	Asn	Glu	Gln	Glu	
			315				320					325				
ctg	tta	ttt	ctc	acc	cag	tca	gcc	tct	gga	cct	cac	tct	tct	ctc	tct	1061
Leu	Leu	Phe	Leu	Thr	Gln	Ser	Ala	Ser	Gly	Pro	His	Ser	Ser	Leu	Ser	
						335					340					
tcc	tgg	aac	ggt	gtt	cct	gat	gtg	ggc	atg	gtc	agt	gac	atc	ctc	ttc	1109
Ser	Trp	Asn	Gly	Val	Pro	Asp	Val	Gly	Met	Val	Ser	Asp	Ile	Leu	Phe	
345					350				355						360	
tgg	atc	ttg	aaa	gaa	cat	ggg	agg	agt	aaa	agc	aga	gcc	tcg	gat	ctc	1157
Trp	Ile	Leu	Lys	Glu	His	Gly	Arg	Ser	Lys	Ser	Arg	Ala	Ser	Asp	Leu	
				365					370					375		
acc	agg	atc	cat	ttc	cac	acg	ctg	gtc	tac	cac	atc	ctg	gca	act	gtg	1205
Thr	Arg	Ile	His	Phe	His	Thr	Leu	Val	Tyr	His	Ile	Leu	Ala	Thr	Val	
			380					385					390			
gat	gga	cac	tgg	gcc	aac	cag	ctg	gca	gcc	gtg	gct	gca	gga	gct	cgt	1253
Asp	Gly	His	Trp	Ala	Asn	Gln	Leu	Ala	Ala	Val	Ala	Ala	Gly	Ala	Arg	
			395				400					405				
gtg	gct	ggg	aca	cag	gcc	tgc	gcc	aca	gaa	acc	ata	gac	acc	agc	cga	1301
Val	Ala	Gly	Thr	Gln	Ala	Cys	Ala	Thr	Glu	Thr	Ile	Asp	Thr	Ser	Arg	
					415						420					
gtg	tct	ctg	agg	gca	ccc	caa	gag	ttc	atg	act	tcc	cat	tcg	gag	gca	1349
Val	Ser	Leu	Arg	Ala	Pro	Gln	Glu	Phe	Met	Thr	Ser	His	Ser	Glu	Ala	
425					430					435					440	
ggc	tcc	agg	att	gta	tta	aac	cca	aac	aag	cca	gta	gta	gaa	tgg	cac	1397
Gly	Ser	Arg	Ile	Val	Leu	Asn	Pro	Asn	Lys	Pro	Val	Val	Glu	Trp	His	
				445					450						455	
aga	gag	gga	ata	tcc	ttc	cac	ttc	aca	cca	gta	ttg	gtg	tgt	aaa	gac	1445
Arg	Glu	Gly	Ile	Ser	Phe	His	Phe	Thr	Pro	Val	Leu	Val	Cys	Lys	Asp	
			460					465					470			
ccc	att	cga	act	gta	ggc	ctt	gga	gat	gcc	att	tca	gcc	gaa	gga	ctc	1493
Pro	Ile	Arg	Thr	Val	Gly	Leu	Gly	Asp	Ala	Ile	Ser	Ala	Glu	Gly	Leu	

```

475          480          485
ttc tat tcg gaa gta cac cct cac tat taggaagatt cttaggggta 1540
Phe Tyr Ser Glu Val His Pro His Tyr
490          495
atttttctga ggaaggagaa ctagccaact taagaattac aggaagaaag tggtttgga 1600
gacagccaaa gaaataaaaag cagattaaaac tgtatcaggt acattccagc ctgtttggcaa 1660
ctccataaaa acatttcaga ttttaattccg aatttagcta atgagactgg atttttgttt 1720
tttatgttgt gtgtcacaga gctaaaaaact cagttcccaa atccccagtt tatgcagcgc 1780
catcaggtat ttttaagctaa acttcttcac ccctgagagc atgtcagctg gagaaaagca 1840
gttcttcctt gccacttga gaagtgcacg cccactcacc caacatcctg gtctctagga 1900
aagcctcatg tgaggttctt ctttctttca gctcagtgcc catgggcaag gatcatgatt 1960
tccattccgt gttacaatga caatatTTaa tgagcataac cttctcagtc tctgtctctc 2020
aaatttagga cagagccgct aaggacaaaa caatccctcc cgtgctttat gatggcagca 2080
ggggctgggg agcctctgag ggactctttc attctgcagt tgtctggaag cctgggtggc 2140
gtcatgagct gaaggatcat gctttcctgt cctggctcca taggttatag gctggctggt 2200
gaaaggttca cgtggcccag gctgaacttc attgcctagc tttggatgtg ctttctgcca 2260
taaagactga tttttgttcg ttctgagcct tcaaggaatt tgttttttac aactggaata 2320
tgctcctgtg tgtgttaaca gatcatggat gttttatggt ttcactgata atttaaagag 2380
tttgacctca gagctccagg atcatcagta aatttgtcat gttatatatt tattttttta 2440
taaatcaaga ctctgtgtg ctcttaataa tattaaaaac aatttacatt tcagg 2495

```

<210> 83
 <211> 1617
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (67)...(1320)

```

<400> 83
atagagccct cagtgggatg aggggtgaaac tgctattgcc ggcggtcct gttttaccgc 60
gtcagc atg ctg gtg cat tta ttt cgg gtc ggg att cgg ggt ggc cca 108
      Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro
      1          5          10
ttc cca ggc agg ctg cta ccg ccc ctc cgc ttc cag aca ttc tca gct 156
Phe Pro Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala
      15          20          25          30
gtc agg tac tct gat ggc tac cgc agc tcc tcc ctc ctc cgg gcc gtg 204
Val Arg Tyr Ser Asp Gly Tyr Arg Ser Ser Leu Leu Arg Ala Val
      35          40          45
gcc cac ctg cgg tcc cag ctc tgg gcc cac ctc cct cga gcc ccc cta 252
Ala His Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu
      50          55          60
gct ccc aga tgg agc ccc tct gcc tgg tgc tgg gtt ggg gga gcc ctg 300
Ala Pro Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu
      65          70          75
cta ggc ccc atg gta ctg agt aag cat ccc cac ctc tgc ctt gtg gcc 343
Leu Gly Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala
      80          85          90
ctg tgt gag gca gaa gag gcc cct cct gcc agc tcc aca ccc cat gtc 396
Leu Cys Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val
      95          100          105          110
gtg ggg tct cgc ttt aac tgg aag ctc ttc tgg cag ttt ctg cac ccc 444
Val Gly Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro
      115          120          125
cac ctg ctg gtc ctg ggg gta gcc gtc gtg ctg gcc ttg ggt gcg gca 492
His Leu Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala
      130          135          140
ctc gtg aat gta cag atc ccc ctg ctc ctg gcc cag ctg gta gag gtc 540
Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val

```

```

145      150      155
gtg gcc aag tac aca agg gac cac gta ggg agt ttc atg act gag tcc      588
Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser
160      165      170
cag aat ctg agc acc cac ctg ctt atc ctg tat ggt gtc cag gga ctg      636
Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu
175      180      185      190
ctg acc ttc ggg tac ctg gtg ctg ctg tcc cac gtt ggc gag cgc atg      684
Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met
195      200      205
gct gtg gac atg cgg agg gcc ctg ttc agc tcc ctg ctg cgg tac tgc      732
Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys
210      215      220
cag ccg cag ggt gca gag ttg gga caa gac atc acc ttc ttt gac gcc      780
Gln Pro Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala
225      230      235
aat aag aca ggg cag ctg gtg agc cgc ttg aca act gac gtg cag gag      828
Asn Lys Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu
240      245      250
ttt aag tca tcc ttc aag ctt gtc atc tcc cag ggg ctg cga agc tgc      876
Phe Lys Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys
255      260      265      270
acc cag gtg gca ggc tgc ctg gtg tcc ctg tcc atg ctg tgc aca cgc      924
Thr Gln Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg
275      280      285
ctc acg ctg ctg ctg atg gtg gcc aca cca gcc ctg atg gga gtg gcc      972
Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly
290      295      300
acc ctg atg ggc tca ggc ctc cga aaa ttg tct tgc cag tgt cag gag      1020
Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu
305      310      315
cag atc gcc agg gca atg ggc gta gca gac gag gcc ctg ggc aat gtg      1068
Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val
320      325      330
cgg act gtg cgt gcc ttc gcc atg gag caa cgg gaa gag gag cgc tat      1116
Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr
335      340      345      350
ggg gca gag ctg gaa gcc tgc cgc tgc cgg gca gag gag ctg ggc cgc      1164
Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg
355      360      365
ggc atc gcc ttg ttc caa ggg ctt tcc aac atc gcc ttc aac tgc atg      1212
Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met
370      375      380
gtc ttg ggt acc cta ttt att ggg ggc tcc ctt gtg gcc gga cag cag      1260
Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln
385      390      395
ctg aca ggg gga gac ctc atg tcc ttc ctg gtg gcc tcc cag aca gtg      1308
Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val
400      405      410
caa agg ctg tgacattcca tgcatggaag gaccatcctt gacaggctgt gtg      1360
Gln Arg Leu
415
agctgccctt ccccatgcct gccacttcca gggatgacaa gctgaccctt gtccccacac      1420
acccacccct tatagcttat tgctttgcgt tgggtccaaaa ccaccgctc agctgagcct      1480
ctgggatgac cagagctgat caccagacag ctcaaggcgg gcctcccccc tectatctct      1540
ttccaagcta aacacaagca gttctacata aatatgttat ggtaaataat gagatagtaa      1600
atatgctgta acagatc      1617

```

<210> 84
 <211> 3269
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (260)...(2209)

<400> 84

```

agagttttccg caccgaggag ggagatgagg ccgggggtca ggctccttgc agttgtaatt      60
tagattcgag aagtggttta tcctttgact ggaaaagaaa agtagctgca gtattccccc      120
agcacttgct gagagcatgc cgtatgccag gctgtgaggc tcgagagaca agcagtggaa      180
gagttgcggc ctgtttcacc tctggattgt aaatctgagc ctccttctgg cccctggaag      240
gggacagcat cacgatgga atg att cct aac cag cat aat gct gga gcc ggg      292
                Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly
                1           5           10
agc cac caa cct gca gtt ttc aga atg gcc gtg ttg gac act gat ttg      340
Ser His Gln Pro Ala Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu
                15           20           25
gat cac att ctt cca tct tct gtt ctt cct cca ttc tgg gct aag tta      388
Asp His Ile Leu Pro Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu
                30           35           40
gta gtg gga tgc gtt gcc att gtg tgt ttt gca cgc agc tat gat gga      436
Val Val Gly Ser Val Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly
                45           50           55
gac ttt gtc ttt gat gac tca gaa gct att gtt aac aat aag gtt gct      484
Asp Phe Val Phe Asp Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala
                60           65           70           75
ggg gtt gtc ggc cgt gca gac ctc ctg tgt gcc ctg ttc ttc ttg tta      532
Gly Val Val Gly Arg Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu
                80           85           90
tct ttc ctt ggc tac tgt aaa gca ttt aga gaa agt aac aag gag gga      580
Ser Phe Leu Gly Tyr Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly
                95           100           105
gcg cat tct tcc acc ttc tgg gtg ctg ctg agt atc ttt ctg gga gca      628
Ala His Ser Ser Thr Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala
                110           115           120
gtg gcc atg ctg tgc aaa gag caa ggg atc act gtg ctg ggt tta aat      676
Val Ala Met Leu Cys Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn
                125           130           135
gcg gta ttt gac atc ttg gtg ata ggc aaa ttc aat gtt ctg gaa att      724
Ala Val Phe Asp Ile Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile
                140           145           150           155
gtc cag aag gta cta cat aag gac aag tca tta gag aat ctc ggc atg      772
Val Gln Lys Val Leu His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met
                160           165           170
ctc agg aac ggg ggc ctc ctc ttc aga atg acc ctg ctc acc tct gga      820
Leu Arg Asn Gly Gly Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly
                175           180           185
ggg gct ggg atg ctc tac gtg cgc tgg agg atc atg ggc acg ggc ccg      868
Gly Ala Gly Met Leu Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro
                190           195           200
ccg gcc ttc acc gag gtg gac aac ccg gcc tcc ttt gct gac agc atg      916
Pro Ala Phe Thr Glu Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met
                205           210           215
ctg gtg agg gcc gta aac tac aat tac tac tat tca ttg aat gcc tgg      964
Leu Val Arg Ala Val Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp
                220           225           230           235
ctg ctg ctg tgt ccc tgg tgg ctg tgt ttt gat tgg tca atg ggc tgc      1012
Leu Leu Leu Cys Pro Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys
                240           245           250
atc ccc ctc att aag tcc atc agc gac tgg agg gta att gca ctt gca      1060
Ile Pro Leu Ile Lys Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala

```

																1108
																1156
																1204
																1252
																1300
																1348
																1396
																1444
																1492
																1540
																1588
																1636
																1684
																1732
																1780
																1828
																1876
																1924
																1972
																2020


```

aaa gca aat cca aat gct gca agt tac cat ggt aat ttg gct gtg ctt      2068
Lys Ala Asn Pro Asn Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu
      590      595      600
tat cat cgt tgg gga cat cta gac ttg gcc aag aaa cac tat gaa atc      2116
Tyr His Arg Trp Gly His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile
      605      610      615
tcc ttg cag ctt gac ccc acg gca tca gga act aag gag aat tac ggt      2164
Ser Leu Gln Leu Asp Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly
      620      625      630      635
ctg ctg aga aga aag cta gaa cta atg caa aag aaa gct gtc tgat      2210
Leu Leu Arg Arg Lys Leu Glu Leu Met Gln Lys Lys Ala Val
      640      645
cctgtttcct tcatgttttg agtttgagtg tgtgtgtgca tgaggcatat cattaatagt      2270
atgtggttac atttaacccat ttaaaagtct tagacatggt attttactga tttttttcta      2330
tgaaaacaaa gacatgcaaa aagattatag caccagcaat atactcttga atgcgtgata      2390
tgatttttca ttgaaattgt attttttcag acaactcaaa tgtaattcta aaattccaaa      2450
aatgtctttt ttaattaaac agaaaaagag aaaaaattat cttgagcaac ttttagtaga      2510
attgagctta catttgggat ctgagccttg tcgtgtatgg actagcacta ttaaacttca      2570
attatgacca agaaaggata cactggcccc tacaatttgt ataaatattg aacatgtcta      2630
tatattagca tttttattta atgacaaagc aaattaagtt tttttatctc ttttttttaa      2690
aacaacatac tgtgaacttt gtaaggaaat atttatttgt atttttatgt tttgaatagg      2750
gcaataatc gaatgaggaa tggaaagttt aacatagtat atctatatgc ttttccccat      2810
aggaagaaat tgactcttgc agtttttgga tgctctgact tgtgcaattt caatacacag      2870
gagattatgt aatgtaatat ttttcataag cggttactat caattgaaag ttcaagccat      2930
gctttaggca agagcaggca gcctcacatc tttatttttg ttacatccaa ggtgaagagg      2990
gcaacacatc tgtgtaagct gcttttttag gtgtttatct gaaggccgtt ttccattttg      3050
cttaatgtaa ctacagacat tatccagaaa atgcaaaatt ttctatcaaa tggagccaca      3110
ttcggggaat tcgtggtatt tttaagaatt gagttgttcc tgctgttttt tatttgatcc      3170
aaacaatggt ttgttttggt cttctctgta tgctgttgac ctaatgattt atgcaatctc      3230
tgtaatttct tatgcagtaa aattactaca caaactagc      3269

```

<210> 85
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (66)...(347)

```

<400> 85
acagttcctc tggacttctc tggaccacag tcctctgcc aacccctgcc agaccccaagt      60
ccacc atg atc cat ctg ggt cac atc ctc ttc ctg ctt ttg ctc cca gtg      110
      Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val
      1      5      10      15
gct gca gct cag acg act cca gga gag aga tca tca ctc cct gcc ttt      153
Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe
      20      25      30
tac cct ggc act tca ggc tct tgt tcc gga tgt ggg tcc ctc tct ctg      206
Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu
      35      40      45
ccg ctc ctg gca ggc ctc gtg gct gct gat gcg gtg gca tgc ctg ctc      254
Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu
      50      55      60
atc gtg ggg gcg gtg ttc ctg tgc gca cgc cca cgc cgc agc ccc gcc      302
Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala
      65      70      75
caa gaa gat ggc aaa gtc tac atc aac atg cca ggc agg ggc tgaccc      350
Gln Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
      80      85      90
tcctgcagct tggacctttg acttctgacc ctctcatcct ggatggtgtg tgggtggcaca      410

```

ggaacccccg cccaacttt tggattgtaa taaaacaatt gaaacacc

458

<210> 86

<211> 1712

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (180)...(1457)

<400> 86

tcccgc	ctggc	tagaaga	aagt	cttcact	tcc	caggag	agacc	aaagc	gtgtc	tggcc	ctagg	60
tgggaaa	aga	actgg	ctgtg	acctttg	ccc	tgacct	ggaa	gggcc	cagcc	ttggg	ctgaa	120
tggcag	cacc	cacgcc	cgcc	cgccggt	gc	tgacct	cacct	gctgg	tggt	ctcttc	ggc	179
atg	ggc	tcc	tgg	gct	gcg	gtc	aat	ggg	atc	tgg	gtg	227
Met	Gly	Ser	Trp	Ala	Ala	Val	Asn	Gly	Ile	Trp	Val	
1				5				10			15	
gtg	gtc	aaa	gag	ctt	cca	gag	ggg	tgg	agc	ctc	ccc	275
Val	Val	Lys	Glu	Leu	Pro	Glu	Gly	Trp	Ser	Leu	Pro	
			20					25			30	
gtg	ctt	gtg	gct	ctg	ggg	aac	ctg	ggg	ctg	ctg	gtg	323
Val	Leu	Val	Ala	Leu	Gly	Asn	Leu	Gly	Leu	Leu	Val	
			35				40				45	
agg	agg	ctg	gcc	cca	gga	aag	gac	gag	cag	gtc	ccc	371
Arg	Arg	Leu	Ala	Pro	Gly	Lys	Asp	Glu	Gln	Val	Pro	
		50				55				60		
cag	gtg	ctg	ggc	atg	gtg	ggc	aca	gcc	ctg	ctg	gcc	419
Gln	Val	Leu	Gly	Met	Val	Gly	Thr	Ala	Leu	Leu	Ala	
			65			70				75		
cat	gtg	gcc	cca	gtg	gca	gga	cag	tgg	cat	tct	gtg	467
His	Val	Ala	Pro	Val	Ala	Gly	Gln	Leu	His	Ser	Val	
			85					90			95	
ctg	gcc	ttt	gtg	ctg	gca	ctg	gca	tgc	tgt	gcc	tgc	515
Leu	Ala	Phe	Val	Leu	Ala	Leu	Ala	Cys	Cys	Ala	Ser	
			100					105			110	
ctg	ccc	ttc	ttg	agc	cac	ctg	cca	cct	cgc	ttc	tta	563
Leu	Pro	Phe	Leu	Ser	His	Leu	Pro	Pro	Arg	Phe	Leu	
		115					120				125	
ctg	ggg	caa	ggc	ctg	agt	gcc	ctg	ctg	ccc	tgc	gtg	611
Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Leu	Pro	Cys	Val	
		130				135				140		
cag	ggg	gtg	ggc	cgc	ctc	gag	tgc	ccg	cca	gcc	ccc	659
Gln	Gly	Val	Gly	Arg	Leu	Glu	Cys	Pro	Pro	Ala	Pro	
		145			150					155		
cct	ggc	ccc	ccg	ctc	gac	ttc	ctt	gag	cgt	ttt	ccc	707
Pro	Gly	Pro	Pro	Leu	Asp	Phe	Leu	Glu	Arg	Phe	Pro	
			165					170			175	
ttc	tgg	gca	ctg	act	gcc	ctt	ctg	gtc	gct	tca	gct	755
Phe	Trp	Ala	Leu	Thr	Ala	Leu	Leu	Val	Ala	Ser	Ala	
			180					185			190	
ggg	ctt	ctg	ctg	ctg	ttg	ccg	cca	cca	cca	tct	gta	803
Gly	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Ser	Val	
		195				200					205	
tta	gga	tca	ggc	ctc	cag	gtg	gga	gcc	cca	gga	gca	851
Leu	Gly	Ser	Gly	Leu	Gln	Val	Gly	Ala	Pro	Gly	Ala	
		210				215				220		
gaa	gag	tcc	tca	cca	ctg	caa	gag	cca	cca	agc	cag	899
Glu	Glu	Ser	Ser	Pro	Leu	Gln	Glu	Pro	Pro	Ser	Gln	
		225			230					235		
acc	cct	ggg	cca	gac	cct	aag	gcc	tat	cag	ctt	cta	947
											tca	
											gcc	
											cgc	
											agt	

```

Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
          245          250          255
gcc tgc ctg ctg ggc ctg ttg gcc gcc acc aac gcg ctg acc aat ggc      995
Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
          260          265          270
gtg ctg cct gcc gtg cag agc ttt tcc tgc tta ccc tac ggg cgt ctg      1043
Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
          275          280          285
gcc tac cac ctg gct gtg gtg ctg ggc agt gct gcc aat ccc ctg gcc      1091
Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
          290          295          300
tgc ttc ctg gcc atg ggt gtg ctg tgc agg tcc ttg gca ggg ctg ggc      1139
Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
          305          310          315          320
ggc ctc tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg gcg ctg      1187
Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
          325          330          335
gca gtc ctg agc ccc tgc ccg ccc ctg gtg ggc acc tcg gcg ggg gtg      1235
Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
          340          345          350
gtc ctc gtg gtg ctg tcg tgg gtg ctg tgt ctt ggc gtg ttc tcc tac      1283
Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
          355          360          365
gtg aag gtg gca gcc agc tcc ctg ctg cat ggc ggg ggc cgg ccg gca      1331
Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
          370          375          380
ttg ctg gca gcc ggc gtg gcc atc cag gtg ggc tct ctg ctc ggc gct      1379
Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
          385          390          395          400
gtt gct atg ttc ccc ccg acc agc atc tat cac gtg ttc cac agc aga      1427
Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
          405          410          415
aag gac tgt gca gac ccc tgt gac tcc tgagcctggg caggtgggga ccccgc      1480
Lys Asp Cys Ala Asp Pro Cys Asp Ser
          420          425
tccccaacac ctgtctttcc ctcaatgctg ccaccatgcc tgagtgcctg cagcccagga      1540
ggcccgacaca ccgtacact cgtggacacc tacacactcc ataggagatc ctggctttcc      1600
agggtgggca agggcaagga gcaggcttg agccaggac cagtgggggc tgtagggtaa      1660
gccctgagc ctgggaccta catgtggttt gcgtaataaa acatttgtat tt      1712

```

<210> 87
 <211> 1055
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)...(502)

```

<400> 87
accgggaggc gcgtggggct tgaggccgag aacggccctt gctgccacca ac atg      55
                                     Met
                                     1
gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg      103
Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu
          5          10          15
aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg      151
Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val
          20          25          30
tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att      199
Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile

```

35	40	45	
tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa			247
Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu			
50	55	60	65
cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga			295
His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly			
	70	75	80
caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga			343
Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly			
	85	90	95
ggg tta ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca			391
Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro			
	100	105	110
aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta			439
Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu			
	115	120	125
ttg agt ttt ttc atg gct aga gta ttc atg aga atg aaa ctg ccg ggc			487
Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly			
	130	135	140
tat ctg atg ggt tagagtgcct ttgagaagaa atcagtgat actggatttg c			540
Tyr Leu Met Gly			

tctgtcaat gaagtttttaa aggctgtacc aatcctctaa tatgaaatgt ggaaaagaat	600
gaagagcagc agtaaaagaa atatctagtg aaaaaacagg aagcgtattg aagcttggac	660
tagaattttct tcttggtatt aaagagacaa gtttatcaca gaattttttt tctgtctggc	720
ctattgctat accaatgatg ttgagtggca ttttcttttt agtttttcat taaaatatat	780
tccatatcta caactataat atcaaataaa gtgattattt ttacaaccc tcttaacatt	840
ttttggagat gacatttctg attttcagaa attaacataa aatccagaag caagattccg	900
taagctgaga actctggaca gttgatcagc tttacctatg gtgctttgcc tttactaga	960
gtgtgtgatg gtagattatt tcagatatgt atgtaaaact gtttcttgaa caataagatg	1020
tatgaacgga gcagaaataa atactttttc taatt	1055

<210> 88
 <211> 1616
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (222)...(1412)

<400> 88	
gagctctcac ggttttctct ttcctgacaa aaagaatatt aatgaaactt tatcatcttg	60
gtgagaaaag cattctaata gctttattct gacatacggg ggtatggaga gcttgaagga	120
gtcagagagg tgcccagcta agacctgaat gccatcacc tccccagggc tctgcagttt	180
tctcgtggtg aacccttgat ggatttggtg ttgcttgaga a atg gcg atg atc	233
	Met Ala Met Ile
	1
gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag agt	231
Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys Ser	
5	10
tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta ttt	329
Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu Phe	
	25
tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg cct	377
Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp Pro	
	40
gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag cct	425
Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu Pro	
	55
gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa ttc	473

Val	Leu	Lys	Ala	Met	Phe	Leu	Ala	Asp	Thr	His	Leu	Leu	Gly	Glu	Phe	
70						75					80					
cta	ggc	cac	tgg	ctg	gac	aaa	tta	cga	agg	gaa	tgg	cag	atg	gag	aga	521
Leu	Gly	His	Trp	Leu	Asp	Lys	Leu	Arg	Arg	Glu	Trp	Gln	Met	Glu	Arg	
85					90					95					100	
gcg	ttc	cag	aca	gct	ctg	tgg	ttg	ctg	cag	ccg	gaa	gtc	gtc	ttc	atc	569
Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val	Val	Phe	Ile	
				105					110						115	
ctg	ggg	gat	atc	ttt	gat	gaa	ggg	aag	tgg	agc	acc	cct	gag	gcc	tgg	617
Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro	Glu	Ala	Trp	
				120				125					130			
gcg	gat	gat	gtg	gag	cgg	ttt	cag	aaa	atg	ttc	aga	cac	cca	agt	cat	665
Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His	Pro	Ser	His	
				135			140					145				
gta	cag	ctg	aag	gta	gtt	gct	gga	aac	cat	gac	att	ggc	ttc	cat	tat	713
Val	Gln	Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly	Phe	His	Tyr	
				150		155					160					
gag	atg	aac	aca	tac	aaa	gta	gaa	cgc	ttt	gag	aaa	gtg	ttc	agc	tct	761
Glu	Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val	Phe	Ser	Ser	
165					170					175					180	
gaa	aga	ctg	ttt	tct	tgg	aaa	ggc	att	aac	ttt	gtg	atg	gtc	aac	agc	809
Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met	Val	Asn	Ser	
				185					190						195	
gtg	gcg	ctg	aac	ggg	gat	ggc	tgt	ggc	atc	tgc	tct	gaa	aca	gaa	gca	857
Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu	Thr	Glu	Ala	
				200			205					210				
gag	ctc	att	gaa	gtt	tct	cac	aga	ctg	aac	tgc	tcc	cga	gag	gca	cgt	905
Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg	Glu	Ala	Arg	
				215			220					225				
ggc	tcc	agc	cgg	tgt	gga	cct	ggg	cct	ctg	ctg	ccc	acg	tct	gcc	cct	953
Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu	Pro	Thr	Ser	Ala	Pro	
				230		235					240					
gtc	ctc	ctg	cag	cat	tat	cct	ctg	tat	cgg	aga	agt	gat	gct	aac	tgt	1001
Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg	Arg	Ser	Asp	Ala	Asn	Cys	
245					250					255					260	
tct	ggg	gaa	gac	gct	gct	cct	gca	gag	gaa	agg	gac	atc	cca	ttt	aag	1049
Ser	Gly	Glu	Asp	Ala	Ala	Pro	Ala	Glu	Glu	Arg	Asp	Ile	Pro	Phe	Lys	
				265					270						275	
gag	aac	tat	gac	gtg	ctt	tca	cgg	gag	gca	tca	caa	aag	ctg	ctg	tgg	1097
Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg	Glu	Ala	Ser	Gln	Lys	Leu	Leu	Trp	
				280			285					290				
tgg	ctc	cag	ccg	cgc	ctg	gtt	ctc	agt	ggc	cac	acg	cac	agc	gcc	tgc	1145
Trp	Leu	Gln	Pro	Arg	Leu	Val	Leu	Ser	Gly	His	Thr	His	Ser	Ala	Cys	
				295			300					305				
gag	gtg	cac	cac	ggg	ggc	cga	gtc	ccc	gag	ctc	agc	gtc	cca	tct	ttc	1193
Glu	Val	His	His	Gly	Gly	Arg	Val	Pro	Glu	Leu	Ser	Val	Pro	Ser	Phe	
				310		315					320					
agt	tgg	agg	aac	aga	aac	aac	ccc	agt	ttc	atc	atg	ggg	agc	atc	acg	1241
Ser	Trp	Arg	Asn	Arg	Asn	Asn	Pro	Ser	Phe	Ile	Met	Gly	Ser	Ile	Thr	
325					330					335					340	
ccc	aca	gac	tac	acc	ctc	tcc	aag	tgc	tac	ctc	cca	cgt	gag	gat	gtg	1289
Pro	Thr	Asp	Tyr	Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro	Arg	Glu	Asp	Val	
				345					350					355		
gtt	ttg	atc	atc	tac	tgt	gga	gtg	gtg	ggc	ttc	ctt	gtg	gtc	ctc	aca	1337
Val	Leu	Ile	Ile	Tyr	Cys	Gly	Val	Val	Gly	Phe	Leu	Val	Val	Leu	Thr	
				360				365					370			
ctc	act	cac	ttt	ggg	ctt	cta	gcc	tca	cct	ttt	ctt	tct	ggg	ttg	aac	1385
Leu	Thr	His	Phe	Gly	Leu	Leu	Ala	Ser	Pro	Phe	Leu	Ser	Gly	Leu	Asn	
				375			380					385				
ttg	ctc	gga	aag	cgt	aag	aca	aga	tgaagagcag	gcgccattat	a						1430
Leu	Leu	Gly	Lys	Arg	Lys	Thr	Arg									

```

390
aatatcaaag cccaagaaat ggaacttttg gcagagatca tgttagaatc aagtggatga 1490
tgagaccaat tacaggccgt ctctctgcac agcacagaaa ttctcaatca ctgaaatgag 1550
taactgcaaa ataaatagtt gattgtactg ttctcatgct ataaaagtgg acagggtactc 1610
tacaac 1616

<210> 89
<211> 1860
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (69)...(1121)

<400> 89
gagaagtgtc gcgtccgtgc gccgcgggct ggggcgggtct caggtgtgcc gaagctctgg 60
tcagtgcc atg atc cgg cag gag cgc tcc aca tcc tac cag gag ctg 107
      Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu
      1           5           10
agt gag gag ttg gtc cag gtg gtt gag aac tca gag ctg gca gac gag 155
Ser Glu Glu Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu
      15           20           25
cag gac aag gag acg gtc aga gtc caa ggt ccg ggt atc tta cca ggc 203
Gln Asp Lys Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly
      30           35           40           45
ctg gac agc gag tcc gcc tcc agc agc atc cgc ttc agc aag gcc tgc 251
Leu Asp Ser Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys
      50           55           60
ctg aag aac gtc ttc tcg gtc cta ctc atc ttc atc tac ctg ctg ctc 299
Leu Lys Asn Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu
      65           70           75
atg gct gtg gcc gtc ttc ctg gtc tac cgg acc atc aca gac ttt cgt 347
Met Ala Val Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg
      80           85           90
gag aaa ctc aag cac cct gtc atg tct gtg tct tac aag gaa gtg gat 395
Glu Lys Leu Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp
      95           100           105
cgc tat gat gcc cca ggt att gcc ttg tac ccc ggt cag gcc cag ttg 443
Arg Tyr Asp Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu
      110           115           120           125
ctc agc tgt aag cac cat tac gag gtc att cct cct ctg aca agc cct 491
Leu Ser Cys Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro
      130           135           140
ggc cag ccg ggt gac atg aat tgc acc acc cag agg atc aac tac acg 539
Gly Gln Pro Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr
      145           150           155
gac ccc ttc tcc aat cag act gtg aaa tct gcc ctg att gtc cag ggg 587
Asp Pro Phe Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly
      160           165           170
ccc cgg gaa gtg aaa aag cgg gag ctg gtc ttc ctc cag ttc cgc ctg 635
Pro Arg Glu Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu
      175           180           185
aac aag agt agt gag gac ttc agc gcc att gat tac ctc ctc ttc tct 683
Asn Lys Ser Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser
      190           195           200           205
tct ttc cag gag ttc ctg caa agc cca aac agg gta ggc ttc atg cag 731
Ser Phe Gln Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln
      210           215           220
gcc tgt gag agt gcc tat tcc agc tgg aag ttc tct ggg ggc ttc cgc 779
Ala Cys Glu Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg

```

225								230				235				
acc	tgg	gtc	aag	atg	tca	ctg	gta	aag	acc	aag	gag	gag	gat	ggg	cgg	827
Thr	Trp	Val	Lys	Met	Ser	Leu	Val	Lys	Thr	Lys	Glu	Glu	Asp	Gly	Arg	
240								245				250				
gaa	gca	gtg	gag	ttc	cgg	cag	gag	aca	agt	gtg	gtt	aac	tac	att	gac	875
Glu	Ala	Val	Glu	Phe	Arg	Gln	Glu	Thr	Ser	Val	Val	Asn	Tyr	Ile	Asp	
255								260				265				
cag	agg	cca	gct	gcc	aaa	aaa	agt	gct	caa	ttg	ttt	ttt	gtg	gtc	ttt	923
Gln	Arg	Pro	Ala	Ala	Lys	Lys	Ser	Ala	Gln	Leu	Phe	Phe	Val	Val	Phe	
270								275				280				285
gaa	tgg	aaa	gat	cct	ttc	atc	cag	aaa	gtc	caa	gat	ata	gtc	act	gcc	971
Glu	Trp	Lys	Asp	Pro	Phe	Ile	Gln	Lys	Val	Gln	Asp	Ile	Val	Thr	Ala	
290								295				300				
aat	cct	tgg	aac	aca	att	gct	ctt	ctc	tgt	ggc	gcc	ttc	ttg	gca	tta	1019
Asn	Pro	Trp	Asn	Thr	Ile	Ala	Leu	Leu	Cys	Gly	Ala	Phe	Leu	Ala	Leu	
305								310				315				
ttt	aaa	gca	gca	gag	ttt	gcc	aaa	ctg	agt	ata	aaa	tgg	atg	atc	aaa	1067
Phe	Lys	Ala	Ala	Glu	Phe	Ala	Lys	Leu	Ser	Ile	Lys	Trp	Met	Ile	Lys	
320								325				330				
att	aga	aag	aga	tac	ctt	aaa	aga	aga	ggg	cag	gca	acg	agc	cac	ata	1115
Ile	Arg	Lys	Arg	Tyr	Leu	Lys	Arg	Arg	Gly	Gln	Ala	Thr	Ser	His	Ile	
335								340				345				
agc	tga	agtcacc	tcgcgttggt	tagagaactg	tcacacatcaa	tgggagctgt	ca									1170
Ser																
350																
tcacttccac	tttgtaaacg	gagctatcaa	caatcctgta	ctcacttgaa	gaaatggggc			1230								
cttgctggga	ggaacagcat	gtaaaaactgg	aacttctaac	cccgtcccaa	aagaggcggt			1290								
gtagagccta	atagaagaga	ctaattggata	aacctacaag	ttattttaaat	atttaaatta			1350								
ttataaaact	ttttaaagag	ctggccaatg	acttttgaat	agggtttgta	gaagatgcct			1410								
ttcttccctgt	ttggttcatt	gtattgtatt	aggttaaagt	ctactagggt	aatgaaggct			1470								
ctacttttca	cttttttaaaa	gtggacaaaa	gagtggtgatt	ttctttttcc	aaaaattcct			1530								
gagtatcaag	acgtgcaggt	catgcttttg	agcctatgca	ctgtacacaa	aggcaaaaacc			1590								
ctatgacttt	ggcatcatct	gccattgatg	tcacagcctct	gacatgctct	ttgatttggt			1650								
aaatgttaaa	tgagacttta	aggctactag	aaactagtaa	ttaagtttct	taatggactg			1710								
agtggccacc	tacttgctcg	gctagaatgt	ttgttgatgt	atgagtttag	attaacactc			1770								
aaaagcacta	ggacagatgt	acatagaagg	tgccactca	ttgtattttg	atgatttcat			1830								
taacaggtaa	ataaaagtta	atacaaaaag						1860								

```
<210> 90
<211> 783
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (245)...(706)
```

<400>	90																		
acacacccag	tgaggtctct	ggagccgcgg	tgcgggaagc	ggggaccggg	gtttgaatcc														60
tgcccctctg	gtgtggtgcg	gcctcttccc	acagactttt	ggcctcagtg	ttccccgcct														120
gggaagtggg	gactggccct	ggtacctggc	tccagagctg	caccacagagg	cgatcagccc														180
ggtgcgggaa	cggggcgggg	tgccgcgaac	tacggggccac	ggatcctgac	ccgccctgcc														240
cacg	atg	act	atc	cac	atc	ctc	atc	ctg	ctg	ttg	ctc	ctc	gcc	ttc					286
Met	Thr	Ile	His	Ile	Leu	Ile	Leu	Leu	Leu	Leu	Leu	Ala	Phe						
1				5						10									
tcc	gcc	caa	ggg	gac	ctg	gac	act	gca	gcc	agg	cga	ggc	cag	cac	cag				334
Ser	Ala	Gln	Gly	Asp	Leu	Asp	Thr	Ala	Ala	Arg	Arg	Gly	Gln	His	Gln				
15					20					25				30					
gtc	ccc	cag	cac	cgc	ggg	cac	gtc	tgc	tac	ctg	ggc	gta	tgc	cgg	acc				382
Val	Pro	Gln	His	Arg	Gly	His	Val	Cys	Tyr	Leu	Gly	Val	Cys	Arg	Thr				
				35				40					45						

cac cgc ctg gcg gag atc ata tac tgg att cgc tgt ctc cac caa gga	430
His Arg Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly	
50 55 60	
gcc ctc ggg gaa ggc cag cca cga gcc cca gga ccc cta cag cta tgg	478
Ala Leu Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp	
65 70 75	
gcg ccg ccg gtg gcg cga ggc gga agc ccg gct cgg ttc cca gga ttc	526
Ala Pro Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe	
80 85 90	
cgg cct gca gcg agg ggg cta gcg cag tgc cca gct cgc tgg gtg acc	574
Arg Pro Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr	
95 100 105 110	
tcg ggc acg gct cgt ccc ctc ctc ggc ttc agt ttg cct atc tgt atg	622
Ser Gly Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met	
115 120 125	
ttg gag ctt cta ctc cac att tct tct ccc cta act cca gcc cct gaa	670
Leu Glu Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu	
130 135 140	
acc gtc ttc ccc agt ccc tcc ccg ggc tgc gac taggttggac ctagaag	720
Thr Val Phe Pro Ser Pro Ser Pro Gly Cys Asp	
145 150	
cacacgggac caggctgggc gaagaacact gacgcccaga gccgaataaaa caagagttcc	780
gtg	783

<210> 91
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 91

Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr	
1 5 10 15	
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala	
20 25 30	
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His	
35 40 45	
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val	
50 55 60	
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser	
65 70 75 80	
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp	
85 90 95	
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro	
100 105 110	
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val	
115 120 125	
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn	
130 135 140	
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala	
145 150 155 160	
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp	
165 170 175	
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu	
180 185 190	
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg	
195 200 205	
Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu	
210 215 220	
Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met	
225 230 235 240	
Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly	

245 250 255
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
 290 295 300

<210> 92
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 92
 Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser
 1 5 10 15
 Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala
 20 25 30
 Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
 35 40 45
 Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
 50 55 60
 Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
 65 70 75 80
 Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
 85 90 95
 Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
 100 105 110
 Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
 115 120 125
 Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu
 130 135 140
 Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser
 145 150 155 160
 Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser
 165 170 175
 Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val
 180 185 190
 Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met
 195 200 205
 Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys
 210 215 220
 Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile
 225 230 235 240
 Leu Ala Asp Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn
 245 250 255
 Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met
 260 265 270
 Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg
 275 280

<210> 93
 <211> 488
 <212> PRT
 <213> Homo sapiens

<400> 93
 Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu
 1 5 10 15
 Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys
 20 25 30

$\langle 210 \rangle$	94
$\langle 211 \rangle$	182

<212> PRT
<213> Homo sapiens

<400> 94

```

Met Trp Pro Pro Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly
 1           5           10           15
Gly Ser Arg Pro Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro
          20           25           30
Ala Arg Ala Phe Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu
          35           40           45
Ser Gly Leu Ser Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala
          50           55           60
Ser Ala Phe Leu Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr
          65           70           75           80
Phe Leu Phe Ala Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu
          85           90           95
Cys Trp Pro Met Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile
          100          105          110
Tyr Phe Ala Ile Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala
          115          120          125
Ser Lys Ala Ala Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala
          130          135          140
Thr Asp Phe Tyr Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln
          145          150          155          160
Gly Asp Ser Ala Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn
          165          170          175
Ser Asp Ser Asp Ser Asp
          180

```

<210> 95
<211> 184
<212> PRT
<213> Homo sapiens

<400> 95

```

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn
 1           5           10           15
Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu
          20           25           30
Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu
          35           40           45
Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val
          50           55           60
Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp
          65           70           75           80
Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly
          85           90           95
Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr
          100          105          110
Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro
          115          120          125
Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe
          130          135          140
Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly
          145          150          155          160
Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser
          165          170          175
Gln Thr Pro Gln Pro Lys Asp Lys
          180

```

<210> 96

145

150

155

<210> 101
<211> 909
<212> DNA
<213> Homo sapiens

<400> 101
atggaggcag agcagcgggc ggcgggcggg gccagcgaag gggcgacccc tggactggag 60
gcggtgcctc ccgttgctcc cccgcctgcg accgcggcct caggtcogat ccccaaattct 120
gggcctgagc ctaagaggag gcaccttggg acgctgctcc agcctacggg caacaagtctc 180
tcccttcggg tggtcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
cggggggcct ggatcatcca cccctacagc gacttcgggt ttactggga cctgatcatg 300
ctgctgctga tgggggggaa cctcatcgtc ctgctgtgg gcatacctt cttcaaggag 360
gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420
ctggtgctca acttcgaac gggcatcggt gtggaggagg gtgctgagat cctgctggca 480
ccgcgggcca tccgcacgcg ctacctgcgc acctggttcc tgggtgacct catctcttct 540
atccctgtgg attacatctt cctagtgttg gagctggagc cacggttggg cgtgagggtc 600
tacaaaacgg caggggcctt acgcatcggt cgcttcacca agatcctaag cctgctgagg 660
ctgctccgct. tctccgcct catccgctac atacaccagt gggaggagat ctttcacatg 720
acctatgacc tggccagtgc tgtggttcgc atgctcaacc tcattgggat gatgctgtg 780
ctatgtcact gggatggctg tctgcagttc ctgggtgccca tgctgcagga cttccctccc 840
gactgctggg tctccatcaa ccacatggtg gtgagaagtc cccacagctc tgcctttcct 900
gggccttct 909

<210> 102
<211> 849
<212> DNA
<213> Homo sapiens

<400> 102
atggccgacc cccaccagct ttctgatgac acaagttcag cccagagccg gggctatggg 60
gccacgcggg cacctgggtg cctgagttat cctgcagcct ctcccacgcc ccatgcagcc 120
ttcctggctg acccggtgtc caacatggcc atggcctatg ggagcagcct ggccgcgcag 180
ggcaaggagc tgggtggataa gaacatcgac cgcttcaccc ccatcaccaa gctcaagtat 240
tactttgctg tggacaccat gtatgtgggc agaaagctgg gcctgctgtt ctcccctac 300
ctacaccagg actgggaagt gcagtaccaa caggacaccc cgggtggccc ccgctttgac 360
gtcaatgccc cggacctcta cattccagca atggctttca tcacctacgt tttgggtggc 420
ggctcttgcgc tggggagccca ggataggttc tcccagacc tcctgggggt gcaagcgagc 480
tcagccctgg cctggctgac cctggagggt ctggccatcc tgctcagcct ctatctgggt 540
actgtcaaca ccgacctcac caccatcgac ctggtggcct tcttgggcta caaatatgtc 600
gggatgattg gcggggctct catgggcctg ctcttcggga agattggcta ctacctggtg 660
ctgggctggt gctgcgtagc catctttgtg ttcatgatcc ggacgctgcg gctgaagatc 720
ttggcagacg cagcagctga gggggctccc gtgcgtgggg cccggaacca gctgcgcagt 780
tacctgacca tggcggtggc ggcggcgag cctatgctca tgtactgggt caccttccac 840
ctgggtgcgg 849

<210> 103
<211> 1464
<212> DNA
<213> Homo sapiens

<400> 103
atggctggaa aggggtcatc aggcaggcgg cccctgctgc tggggctgct ggtggccgta 60
gccactgtcc acctggtcat ctgtccctac accaaagtgg aggagagctt caacctgcag 120
gccacacatg acctgctcta ccactggcaa gacctggagc agtacgacca tcttgagttc 180
cccgagctcg tcccagagac gttcctcggg ccagtgggtg tcgcagtgtt ctccagcccc 240
gcggttttac tgctttcgct gttagaaatg tccaagtttt actctcagct aatagttaga 300
ggagtgcctt gactcggcgt gattttttgga ctctggacgt tacaaaagga agtgagacgg 360
cacttcgggg ccatggtggc caccatgttc tgctgggtga cggccatgca gttccacctg 420
atgttctact gcacgcggac actgccaat gtgctggccc tgctgtagt cctgctggcc 480

tcagtgattc	gctgcctctg	tgccattgac	attcacaaca	agacgctcta	tcacatcaca	240
ctctggacct	tcctccttgc	cctggggcat	ttcctctctg	agttgtttgt	ctatggaaact	300
gcagctccca	cgattggcgt	cctggcacc	ctgatgggtg	caagttttct	catcctgggt	360
atgctggctg	ggctccggta	tctagaagta	gaaccagtat	ccagacagaa	gaagagaaac	420

<210> 107
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 107						
atgaacgttg	gagttgcccc	cagtgaagtg	aatccaaata	cccggtgcat	gaacagccgg	60
ggtatgtggc	tgacatatgc	attgggagtt	ggcttgcttc	atattgtctt	actcagcatt	120
cccttcttca	gtgttcctgt	tgcttggaact	ttaaacaaata	ttatacataa	tctggggatg	180
tacgtatttt	tgcatgcagt	gaaaggaaca	cttttcgaaa	ctcctgacca	gggtaaagca	240
aggctcctaa	ctcattggga	acaactggac	tatggagtac	agtttacatc	ttcacggaag	300
tttttcacaa	tttctccaat	aattctatat	tttctggcaa	gtttctatac	gaagtatgat	360
ccaactcact	tcatectaaa	cacagcttct	ctcctgagtg	tactaattcc	caaatgccaa	420
caactacatg	gtgttcggat	ctttggaatt	aataagtat			459

<210> 108
 <211> 519
 <212> DNA
 <213> Homo sapiens

<400> 108						
atggctgcct	tcctgataca	gaccaaggac	aaccccatga	aggccgtggg	tgtgctggcc	60
ggcaccatgg	ccaccgtcgt	ggccatcact	gtcctcatct	ccaccgccac	cttctggcgc	120
aacaagaagt	ctaacaaggt	cctgccaatg	cgcggggtgc	tcgcgaagcg	gccagccct	180
gcgccccgca	ccatccgcat	tgagtggctc	aagtccaaga	gcaccaaagc	cgctaccaag	240
ttcatgctca	aagagaaaacc	tcccaatgag	aactgttaaca	acaacagccc	agaaagctct	300
ctgetccccga	gagctccggc	tctccctcca	ccaccagcg	tggcgcccag	cactggcgca	360
gcccagtgga	ccgtgcctac	tgtctctggc	tctctcactc	cgcagccgac	ccaacccccg	420
ccaaaaccca	aaactatggg	aagccccgtc	cagtcaactc	tgatctctga	gctcaagcaa	480
aagtttgaga	agaagagtgt	gcacaacaag	gcttacttc			519

<210> 109
 <211> 225
 <212> DNA
 <213> Homo sapiens

<400> 109						
atgatcggag	acatcctgct	gttcgggacg	ttgctgatga	atgccggggc	ggtgctgaac	60
tttaagctga	aaaagaagga	cacgcagggc	tttggggagg	agtccaggga	gccagcaca	120
ggtgacaaca	tccgggaatt	cttgctgagc	ctcagatact	ttcgaatctt	catcgccctg	180
tggaacatct	tcattgatgtt	ctgcatgatt	gtgctgttcg	gctct		225

<210> 110
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 110						
atggagctgc	ctgctgtgaa	cctgaagggtg	attctcctag	gtcactggct	gctgacaacc	60
tggggctgca	ttgtattctc	aggctcctat	gcctgggcca	acttcacat	cctggccttg	120
ggcgtgtggg	ctgtggctca	gcgggactcc	atcgacgcca	taagcatgtt	tctgggtggc	180
ttgctggcca	ccatcttctc	ggacatcgtg	cacatcagca	tcttctaccc	gcgggtcagc	240
ctcacggaca	cgggccgctt	tggcgtgggc	atggccatcc	tcagcttgct	gctcaagccg	300
ctctcctgct	gcttcgtcta	ccacatgtac	cgggagcgcg	ggggtgagct	cctgggtccac	360
actggtttcc	ttgggtcttc	tcaggaccgt	agtgccctacc	agacgattga	ctcagcagag	420
gcgccccgag	atccctttgc	agtcccagag	ggcaggagtc	aagatgcccg	aggggtac	477


```
<210> 111
<211> 3438
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (121)...(1032)
```

<400> 111																	
gcctacgacg cctccgctag agccccgcggg gctgcgcgcga ctcctgctct ggagggggttg																	60
cgggtacctg atggccacag agggctctag gaggccgagc gtgtaagcgg ggtgggcgcc																	120
atg gag gca gag cag cgg ccg gcg gcg ggg gcc agc gaa ggg gcg acc																	168
Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr																	
1 5 10 15																	
cct gga ctg gag gcg gtg cct ccc gtt gct ccc ccg cct gcg acc gcg																	216
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala																	
20 25 30																	
gcc tca ggt ccg atc ccc aaa tct ggg cct gag cct aag agg agg cac																	264
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His																	
35 40 45																	
ctt ggg acg ctg ctc cag cct acg gtc aac aag ttc tcc ctt cgg gtg																	312
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val																	
50 55 60																	
ttc ggc agc cac aaa gca gtg gaa atc gag cag gag cgg gtg aag tca																	360
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser																	
65 70 75 80																	
gcg ggg gcc tgg atc atc cac ccc tac agc gac ttc cgg ttt tac tgg																	408
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp																	
85 90 95																	
gac ctg atc atg ctg ctg ctg atg gtg ggg aac ctc atc gtc ctg cct																	456
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro																	
100 105 110																	
gtg ggc atc acc ttc ttc aag gag gag aac tcc ccg cct tgg atc gtc																	504
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp ile Val																	
115 120 125																	
ttc aac gta ttg tct gat act ttc cta ctg gat ctg gtg ctc aac																	552
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn																	
130 135 140																	
ttc cga acg ggc atc gtg gtg gag gag ggt gct gag atc ctg ctg gca																	600
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala																	
145 150 155 160																	
ccg cgg gcc atc cgc acg cgc tac ctg cgc acc tgg ttc ctg gtt gac																	648
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp																	
165 170 175																	
ctc atc tct tct atc cct gtg gat tac atc ttc cta gtg gtg gag ctg																	696
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu																	
180 185 190																	
gag cca cgg ttg gac gct gag gtc tac aaa acg gca cgg gcc cta cgc																	744
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg																	
195 200 205																	
atc gtt cgc ttc acc aag atc cta agc ctg ctg agg ctg ctc cgc ctc																	792
Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu																	
210 215 220																	
tcc cgc ctc atc cgc tac ata cac cag tgg gag gag atc ttt cac atg																	840
Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met																	
225 230 235 240																	
acc tat gac ctg gcc agt gct gtg gtt cgc atc ttc aac ctc att ggg																	888
Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly																	
245 250 255																	

```

atg atg ctg ctg cta tgt cac tgg gat ggc tgt ctg cag ttc ctg gtg      936
Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
                260                265                270
ccc atg ctg cag gac ttc cct ccc gac tgc tgg gtc tcc atc aac cac      984
Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
                275                280                285
atg gtg gtg aga agt ccc cac agc tct gcc ttt cct ggg cct tct t      1030
Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
                290                295                300
agggctcttc tgccctgagta gcagggatgg ccacagggag caggaggtgg gagatgatca 1090
caacagaaaa taggagcgag gaggtgggga ggagggagga aaggggaagg agaccagaa 1150
gaagtgcctcg tgtgttgag ggagcaggca aaggaagggt acctaccgg aagctgaggg 1210
ccccaagtgtg caatagagga ccccttttgcc tcagggcccc ccagaaccaa acttaagtgc 1270
ctgccaggag gaaggcctgc agtagaagg gcagacagaa agaccaaaga aggaaaagg 1330
gcaggcagag aatgaggctc cgaggggccc atgccagct ctgcaatata ctctgccct 1390
cagaaccact cgtggggccg ccagtattcc catgccctgt tcaaggccat gagccacatg 1450
ctgtgcattg gctatgggca gcaggcacct gtaggcattg ccgacgtctg gctcaccatg 1510
ctcagcatga tcgtaggtgc cacatgctac gccatgttca tcggccatgc cacggcactc 1570
atccagctccc tggcacttc ccggcgctcag taccaggaga agtacaagca ggtggagcag 1630
tactgtcctt tcacacagct gccagcagac acggcgagc gcattccaga gtactatgag 1690
caccgctacc agggcaagat gttcgatgag gaaagcatcc tgggcgagct gagcgagccg 1750
cttcgcgagg agatcattaa cttcacctgt cggggcctgg tggcccacat gccgctgttt 1810
gcccatgccg accccagctt cgtcactgca gttctcacca agctgcgctt tgaggctctc 1870
cagccggggg atctcgtggt gcgtgagggc tccgtgggga ggaagatgta cttcatccag 1930
catgggctgc tcagtgtgct ggcccgcggc gcccgggaca cagccctcac cgatggatcc 1990
tactttgggg agatctgctt gctaactagg ggccggcgca cagccagtgt tcgggctgac 2050
acctactgcc gcccttactc actcagcgtg accatttca atgctgtgct tgaggagttc 2110
cccatgatgc gccgggacct tgagactgtg gccatggatc ggctgctccg catcggaag 2170
aagaattcca tactgcagcg gaagcgctcc gagccaagtc caggcagcag tgggtggcatc 2230
atggagcagc acttggtgca acatgacaga gacatggctc ggggtgttcg gggtcgggcc 2290
ccgagcacag gagctcagct tagtggaag ccagtactgt gggagccact ggtacatgcg 2350
ccccttcagg cagctgctgt gacctccaat gtggccattg cctgactca tcagcggggc 2410
cctctgcccc tctcccctga ctctccagcc acctccttg ctgcctctgc ttggcgctca 2470
gcaggctctc cagcttcccc gctggtgccc gtccgagctg gcccatgggc atccacctcc 2530
cgctgccccg ccccacctgc ccgaacctg cagccagcc tatcccgggc agggcgctcc 2590
caggctctcc tgctgggtcc cctccagga ggaggtggac ggcggtagg acctcggggc 2650
cgccactct cagcctccca accctctctg cctcagcgg caacaggcga tggctctct 2710
gggcgtaaag gatcaggaag tgagcggctg cctccctcag ggctcctggc caaacctcca 2770
aggacagccc agccccccag gccaccagt cctgagccag ccacacccc gggtctccag 2830
ctttctgcca acatgtaaaa cctttgagta catccagcct tagttcttgg ggtgcagtag 2890
tatgtaccca agggcagatg cctcttggg aaggccatgg ggacctgaaa cattgcccc 2950
tggaatatgt gacctgtgtc ggacattccg catactgcca tgaagacgg ctctgtgtcc 3010
tcagctcaag aatcctgtag cttgtcccat cataatccat tcaccggttc atcatgtgta 3070
ctgagcagct accatgttca aggtaaggag acaggaggag taggaggagg cagggcctct 3130
ccatgccagc ctctgtggtc cttgccc aaa cccatcagcg caatacttga acctctctcc 3190
aggtaggggc aggaggagcc acatgagaga gggagaagga ccgcgtttac ctttagagtt 3250
ttgttttgtt ttttcttct gagtttgctg ttggtgcagg aataagggaagg aggcccaagg 3310
tatccaagcc tggggaaggg caggccagcc agcacctctg ccttctcagg gacaagagta 3370
gtcctttacc acctcactc tgccctgtccc ctctctact ctacagcatt aaagactgtg 3430
ggaccagg

```

```

<210> 112
<211> 1144
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)...(907)

<400> 112

```

```

caaggatctg gaaccctgag cctcgaagcg gaggatccct gtgtcccagc cgggc      55
atg gcc gac ccc cac cag ctt ttc gat gac aca agt tca gcc cag agc      103
Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser
1      5      10      15
cgg ggc tat ggg gcc cag cgg gca cct ggt ggc ctg agt tat cct gca      151
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala
20      25      30
gcc tct ccc acg ccc cat gca gcc ttc ctg gct gac ccg gtg tcc aac      199
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
35      40      45
atg gcc atg gcc tat ggg agc agc ctg gcc gcg cag ggc aag gag ctg      247
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
50      55      60
gtg gat aag aac atc gac cgc ttc atc ccc atc acc aag ctc aag tat      295
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
65      70      75      80
tac ttt gct gtg gac acc atg tat gtg ggc aga aag ctg ggc ctg ctg      343
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
85      90      95
ttc ttc ccg tac cta cac cag gac tgg gaa gtg cag tac caa cag gac      391
Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
100      105      110
acc ccg gtg gcc ccc cgc ttt gac gtc aat gcc ccg gac ctc tac att      439
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
115      120      125
cca gca atg gct ttc atc acc tac gtt ttg gtg gct ggt ctt gcg ctg      487
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu
130      135      140
ggg acc cag gat agg ttc tcc cca gac ctc ctg ggg ctg caa gcg agc      535
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser
145      150      155      160
tca gcc ctg gcc tgg ctg acc ctg gag gtg ctg gcc atc ctg ctc agc      583
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser
165      170      175
ctc tat ctg gtc act gtc aac acc gac ctc acc acc atc gac ctg gtg      631
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val
180      185      190
gcc ttc ttg ggc tac aaa tat gtc ggg atg att ggc ggc gtc ctc atg      679
Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met
195      200      205
ggc ctg ctc ttc ggg aag att ggc tac tac ctg gtg ctg ggc tgg tgc      727
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys
210      215      220
tgc gta gcc atc ttt gtg ttc atg atc cgg acg ctg cgg ctg aag atc      775
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile
225      230      235      240
ttg gca gac gca gca gct gag ggg gtc ccg gtg cgt ggg gcc cgg aac      823
Leu Ala Asp Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn
245      250      255
cag ctg cgc atg tac ctg acc atg gcg gtg gcg gcg gcg cag cct atg      871
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met
260      265      270
ctc atg tac tgg ctc acc ttc cac ctg gtg cgg tgagcgcgcc cgctga      920
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg
275      280
acctcccgtc gctgctgctg ctgctggggc ccactgtggc cgccgaactc atctcctgcc      980
tgcaggcccc aagggtccacc ctgtctggcc acaggcaccg cctccatccc atgtcccgcc      1040
cagccccgcc cccaacccaa ggtgctgaga gatctccagc tgcacaggcc accgccccag      1100
ggcgtggccg ctgttacaga aacaataaac cctgatgggc atgg      1144

```

<210> 113

<211> 2339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (253)...(1719)

<400> 113

```

ctttactcag ggcacagagg gtctctgccc ccgtageggc cggggctgcg gtagccactt      60
tagatttggg caaggacttt agattcgggc tctgttctgt ttccgccgtc ctgcttccctg      120
ccgaggctgg cccaggcagc cgcgcttcga aggacgccgc cgggagctgc ggagcatgcg      180
tggagtggca gtgctaaccg ctggtgtctc gcaactgttg cctgtgaagg tacgtgaagc      240
tgaaagcctg ga atg gct gga aag ggg tca tca ggc agg cgg ccc ctg      288
          Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu
                1             5             10
ctg ctg ggg ctg ctg gtg gcc gta gcc act gtc cac ctg gtc atc tgt      336
Leu Leu Gly Leu Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys
                15             20             25
ccc tac acc aaa gtg gag gag agc ttc aac ctg cag gcc aca cat gac      384
Pro Tyr Thr Lys Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp
                30             35             40
ctg ctc tac cac tgg caa gac ctg gag cag tac gac cat ctt gag ttc      432
Leu Leu Tyr His Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe
                45             50             55             60
ccc gga gtc gtc ccc agg acg ttc ctc ggg cca gtg gtg atc gca gtg      480
Pro Gly Val Val Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val
                65             70             75
ttc tcc agc ccc gcg gtt tac gtg ctt tcg ctg tta gaa atg tcc aag      528
Phe Ser Ser Pro Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys
                80             85             90
ttt tac tct cag cta ata gtt aga gga gtg ctt gga ctc ggc gtg att      576
Phe Tyr Ser Gln Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile
                95             100             105
ttt gga ctc tgg acg tta caa aag gaa gtg aga cgg cac ttc ggg gcc      624
Phe Gly Leu Trp Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala
                110             115             120
atg gtg gcc acc atg ttc tgc tgg gtg acg gcc atg cag ttc cac ctg      672
Met Val Ala Thr Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu
                125             130             135             140
atg ttc tac tgc acg cgg aca ctg ccc aat gtg ctg gcc ctg cct gta      720
Met Phe Tyr Cys Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val
                145             150             155
gtc ctg ctg gcc ctc gcg gcc tgg ctg cgg cac gag tgg gcc cgc ttc      768
Val Leu Leu Ala Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe
                160             165             170
atc tgg ctg tca gcc ttc gcc atc atc gtg ttc agg gtg gag ctg tgc      816
Ile Trp Leu Ser Ala Phe Ala Ile Val Phe Arg Val Glu Leu Cys
                175             180             185
ctg ttc ctg ggc ctc ctg ctg ctg ctg gcc ttg ggc aac cga aag gtt      864
Leu Phe Leu Gly Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val
                190             195             200
tct gta gtc aga gcc ctt cgc cac gcc gtc ccg gca ggg atc ctc tgt      912
Ser Val Val Arg Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys
                205             210             215             220
tta gga ctg acg gtt gct gtg gac tct tat ttt tgg cgg cag ctc act      960
Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr
                225             230             235
tgg ccg gaa gga aag gtg ctt tgg tac aac act gtc ctg aac aaa agc      1008
Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser
                240             245             250

```

tcc aac tgg ggg acc tcc ccg ctg ctg tgg tac ttc tac tca gcc ctg 1056
 Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu
 255 260 265

ccc cgc ggc ctg ggc tgc agc ctg ctc ttc atc ccc ctg ggc ttg gta 1104
 Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val
 270 275 280

gac aga agg acg cac gcg ccg acg gtg ctg gca ctg ggc ttc atg gca 1152
 Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala
 285 290 295 300

ctc tac tcc ctc ctg cca cac aag gag cta cgc ttc atc atc tat gcc 1200
 Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala
 305 310 315

ttc ccc atg ctc aac atc acg gct gcc aga ggc tgc tcc tac ctg ctg 1248
 Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu
 320 325 330

aat aac tat aaa aag tct tgg ctg tac aaa gca ggg tct ctg ctt gtg 1296
 Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val
 335 340 345

atc gga cac ctc gtg gtg aat gcc ggc tac tca gcc acg gcc ctg tat 1344
 Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr
 350 355 360

gtg tcc cat ttc aac tac cca ggt ggc gtc gca atg cag agg ctg cac 1392
 Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His
 365 370 375 380

cag ctg gtg ccc ccc cag aca gac gtc ctt ctg cac att gac gtg gca 1440
 Gln Leu Val Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala
 385 390 395

gcc gcc cag aca ggt gtg tct cgg ttt ctc caa gtc aac agc gcc tgg 1488
 Ala Ala Gln Thr Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp
 400 405 410

agg tac gac aag agg gag gat gtg cag ccg ggg aca ggc atg ctg gca 1536
 Arg Tyr Asp Lys Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala
 415 420 425

tac aca cac atc ctc atg gag gcg gcc cct ggg ctc ctg gcc ctc tac 1584
 Tyr Thr His Ile Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr
 430 435 440

agg gac aca cac cgg gtc ctg gcc agc gtc gtg ggg acc aca ggt gtg 1632
 Arg Asp Thr His Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val
 445 450 455 460

agt ctg aac ctg acc caa ctg ccc ccc ttc aac gtc cac ctg cag aca 1630
 Ser Leu Asn Leu Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr
 465 470 475

aag ctg gtg ctt ctg gag agg ctc ccc cgg ccg tcc tgagggggac cagg 1730
 Lys Leu Val Leu Leu Glu Arg Leu Pro Arg Pro Ser
 480 485

cagccctcag cagccacagg ccttccagga gctgttatca ctaccagttt ctggcacaat 1790
 tccagcaciaa ttatgacaaat tcagagaagc aagtcaaagg actgggcacc tgcctctgac 1850
 agacaccaga ccagggtccag ggcctcctcc acagcctcag ctggggctct cagcaccaaa 1910
 gaacgagggg cccagggtctt gttggcacc cgggagccac tgcccagggt gatggtggcc 1970
 agctcagggc ttcctgcggg tgactgtcgc ccagaccagg tgccattcat gactaatcag 2030
 gagcagcggg ctcaccacagg cacctgtctg ccaggaggcc acgtgtgtcc tgcccaccca 2090
 gggggagctg tatttttgga gcacccacg cttgctgccc gagggcctct tggggcacct 2150
 aagacagcac cccctctcag gggagacat ggtggccccg gccgcacccc cccaccctgg 2210
 tgccaccact gcaacttttg tattcacagg catcccatct ccatcacaga taaaatctta 2270
 ggagataaac acattcaaaa aggaatgaga taaaaagaat aaggcaataa atgttgattg 2330
 gaacctctc 2339

<210> 114
 <211> 1756
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (102)...(650)

<400> 114

```

gtgtcgcttg cctccttcc gcacagcccg ggtttccgct tccctccggg cgcgagaaga      60
ggggagccag gccgagcccc ggccctaccg ccgccgccgc c atg tgg ccc cca      113
                                   Met Trp Pro Pro
                                   1
gac ccc gac ccc gac ccg gac ccc gag cct gcc ggc ggc tcc cgt ccc      161
Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly Gly Ser Arg Pro
   5                               10                               15                               20
ggc ccc gcg gtc ccc ggg ctg cgc gcc ctg ctg ccg gcg cgg gct ttc      209
Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro Ala Arg Ala Phe
                               25                               30                               35
ctc tgc tct ctc aaa ggc cgc ctc ctg ctg gcc gag tgc ggt ctc tca      257
Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu Ser Gly Leu Ser
   40                               45                               50
ttc atc act ttt atc tgc tat gtg gcg tcc tca gca tct gcc ttc ctc      305
Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala Ser Ala Phe Leu
   55                               60                               65
aca gcg cct ctg ctg gag ttc ctg ctg gcc ttg tac ttc ctc ttt gct      353
Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr Phe Leu Phe Ala
   70                               75                               80
gat gcc atg cag ctg aat gac aag tgg cag ggc ttg tgc tgg ccc atg      401
Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu Cys Trp Pro Met
   85                               90                               95                               100
atg gac ttc ctg cgc tgt gtc acc gcg gcc ctc atc tac ttt gct atc      449
Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile Tyr Phe Ala Ile
                               105                               110                               115
tcc atc acg gcc atc gcc aag tac tgc gat ggg gct tcc aaa gcc gct      497
Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala Ser Lys Ala Ala
                               120                               125                               130
ggg gtg ttt ggc ttc ttt gct acc atc gtg ttt gca act gat ttc tac      545
Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala Thr Asp Phe Tyr
                               135                               140                               145
ctg atc ttt aac gac gtg gcc aaa ttc ctc aaa caa ggg gac tct gca      593
Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln Gly Asp Ser Ala
                               150                               155                               160
gat gag acc aca gcc cac aag aca gaa gaa gag aat tcc gac tgc gac      641
Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn Ser Asp Ser Asp
   165                               170                               175                               180
tct gac tgaaggcctg gcgggtgcct tggcaacctg agccacacag gcc      690
Ser Asp

tccacccctg cgcctcacag gggtcgctgg cgttggagcg gaggcctgga cttctgagtt      750
gcagaggggg ctgcggacac agcaggcccc ctacagcctc aggttctgcc tgagcccagc      810
ctaccaggct tgcccctcag ctcagcactg ttgaccacgc tgcgtatgag ggcattcttg      870
gtatcccact ccttctcccc atttctgtcc cacaggcctt cagcccttta acgtctctgc      930
caaaaaccag cacaaggaga caaagcagag ccttgtctgt atctgggcag caggtgttcc      990
atgctgctag gtggcggggg tcgggggtct tctgtttcac taacaggaac aaagacagaa     1050
accatgacag ggctgccccg ccaggccccg gtgggtttgt ctgcacttgg tgctcctgcc     1110
cacaccagcc actttggtga caatgaccct tccaagaatc tttggttcaa ggagcaccag     1170
ttccctcttc attcttgaag caggagaaaa ttgacctttg ccttgtcgcc caggaagtgg     1230
ggctcggcac ccataactaa cacctcccac ccttgaaac catgtcttct gggggtgaga     1290
tgaccattct gggtctaaga ctgtttcaaa gaagagctca tagactgact ggtccagaag     1350
acagagggtg caacagtggc atcacagtga cagtgtcatg gggagctggg cgggccagc      1410
caaaccctcc ttcttcttag agcccagcca gcaggcagga gttcctggac cctcaggaca     1470
gtgaacttcc agacctcagg gcaggtctat gggccactgc aggagatgag accagccttc     1530
tgtgttcacc taacgattta tactgtgtat ctgtctttga tggaattttg taacttttta     1590

```

tattttttta tgcaaaagca gcttcttaac agatggcatt ttctgtgact ctaggcctca 1650
 caaaagagcc agagttcttg acccatgttt ggagcatttg tagccttatt ctcttgctg 1710
 tgaatctctt accctgaaaa aaagccataa tgaattaagc caaaag 1756

<210> 115
 <211> 1418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (149)...(703)

<400> 115
 attggtccta gcggggggcc gggggcggac accgggcggg ggccggagca gcgcggctca 60
 ggctgcggga aagcgggtgc cgtgcagcgg ggtgggtgcc ctggtcgcgc gccgagctcg 120
 agcagccaac cccgggcgcg tcggggcc atg gac ggc ctg agg cag cgc gtg 172
 Met Asp Gly Leu Arg Gln Arg Val
 1 5
 gag cac ttc ctg gag caa agg aac ctg gtc acc gaa gtg ctg ggg gcg 220
 Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu Val Leu Gly Ala
 10 15 20
 ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg gct gca gga gcc 268
 Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu Ala Ala Gly Ala
 25 30 35 40
 gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac gga gcg tct ctg 316
 Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr Gly Ala Ser Leu
 45 50 55
 ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat gcc tca atc aaa 364
 Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr Ala Ser Ile Lys
 60 65 70
 gct atc gag agc cca agc aag gac gac gac act gtg tgg ctc acc tac 412
 Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val Trp Leu Thr Tyr
 75 80 85
 tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc ttc agc gat cta 460
 Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe Phe Ser Asp Leu
 90 95 100
 ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag tgc gcc ttc ctg 503
 Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys Cys Ala Phe Leu
 105 110 115 120
 ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct ctc atg ctg tat 556
 Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala Leu Met Leu Tyr
 125 130 135
 cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac ggg gcc gta gac 604
 Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His Gly Ala Val Asp
 140 145 150
 aga atc atg aac gac ctc agc ggg cga gcc ctg gac gcg gcg gcc gga 652
 Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp Ala Ala Ala Gly
 155 160 165
 ata acc agg aac gtc aag cca agc cag acc ccg cag ccg aag gac aag 700
 Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln Pro Lys Asp Lys
 170 175 180
 tgaagcagcc ccctgagcct cacaaggacc tcctggctgg tgaggagggg gccgcgccag 760
 gctcccaggc ctccacagag tcttcagcgc atcccccaac agcagcccct gccagtcct 820
 cgggtccagg caaggccctg ggggtctcct taaatgccac ctccgggcaag tcccagtcct 880
 agtccctggc caccctcagc tctggatccc agggccagct gccctctggc tctggctgtg 940
 gctcccgcc gtccggcagg gccagggcc agcgtcgggc acagggcagc tccactggg 1000
 ctccggcaaca caccagccg cctggtaact cctccggccc ctcccagtc gccctcccg 1060
 cctccggggcc cctgcagcca cccaacgtca cctccagccc ggtctcacc atgggtccagt 1120
 ctcccagcag cagcaacatc cccacgcagc ccccagcaa gtcctctggc aagccggagg 1180
 acgcagcccc caagaccagc ggacagcgcc agaaggaatc gtcgaaacag cctgccagca 1240

gagcctcagt	gcccagactg	gtccctgcc	attccgggac	ctctctggag	tacacttcgg	1300
agtccaccac	cgagatcacc	tgcagctggc	cacaccacag	gcccccgtag	ctgcagcact	1360
actggtgcct	gaaacacctg	gcctgctagg	aggctccaat	aaagctaacc	cggaccag	1418

```
<210> 116
<211> 1211
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (133) ... (555)

<400>	116	
gaaaatggct	caggtggact	ccgggctgga gctgtccttg gggagcttgt ttgcggcagc 60
ggctgctgct	gccactgctg	tgctgggggc ceggtcgcca ggcaaaaagc cctcccacgt 120
ttgaggggag	tc atg agc cgt ttc ctg aat gtg tta aga agt tgg ctg	168
	Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu	
	1 5 10	
gtt atg gtg tcc atc ata gcc atg ggg aac acg ctg cag agc ttc cga		216
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg		
	15 20 25	
gac cac act ttt ctc tat gaa aag ctc tac act ggc aag cca aac ctt		264
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu		
	30 35 40	
gtg aat ggc ctc caa gct cgg acc ttt ggg atc tgg acg ctg ctc tca		312
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser		
	45 50 55 60	
tca gtg att cgc tgc ctc tgt gcc`att gac att cac aac aag acg ctc		360
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu		
	65 70 75	
tat cac atc aca ctc tgg acc ttc ctc ctt gcc ctg ggg cat ttc ctc		408
Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu		
	80 85 90	
tct gag ttg ttt gtc tat gga act gca gct ccc acg att ggc gtc ctg		456
Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu		
	95 100 105	
gca ccc ctg atg gtg gca agt ttc tcc atc ctg ggt atg ctg gtc ggg		504
Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly		
	110 115 120	
ctc cgg tat cta gaa gta gaa cca gta tcc aga cag aag aag aga aac		552
Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn		
	125 130 135 140	
tgaggcca gcattatcac ctccaggact ttctcgTTTT ccaccttggc catcttcttc		610
cttcctgcgc tctctctctt aatttctttt ctattccatc atctgccctt ttattcactt		670
ttagcctctt tttttaattt ttaaaattta aagatatgca tactgaaaag tatataacat		730
gtacgtacaa tttaaagaat aattttaaag tgaatactac gtaactccat ccaagtcaag		790
aaattgccag ctctctggaa gccactgtg tctccttccc ctacctgcaa cctcttcag		850
gctccccctt ccagccttcc cctttttccc ttttatTTTc atgccttgat ttgacttgtg		910
tgggtgggaac atgtgaacta tgaaacttaa acctgctgcc caccagagc agctgtgacc		970
aagggtgcc tcaaggggtt gtccacgcag gttgggctcc tctetgctgc tggaccaag		1030
actctgaacc ttccaaggga caggcagttc ttctaagaag ggctccccctg tgtgtgagca		1090
agaccacagc tctccttcta tctacagatg catgagggtt ggaagagtct gggetgtttt		1150
tagaccttct ggtcagctgt atttgtgtaa caacttttgt aataaataga aaaacctct		1210
g		1211

```
<210> 117
<211> 1099
<212> DNA
<213> Homo sapiens
```


<220>
<221> CDS
<222> (183)...(644)

<400> 117
gtatccgagg ccgtagcagc cgggctgggc ctgctgcgag ccggcgggccc ggagtggggc 60
ggcggcattgt accttcacac ttgagtattc agaaagaagt gatctgaact ctgaccattc 120
tttatggata cattaagtca aatataagag tctgactact tgacacactg gctcgagcaa 180
ac atg aac gtt gga gtt gcc cac agt gaa gtg aat cca aat acc cgt 227
Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg
1 5 10 15
gtc atg aac agc cgg ggt atg tgg ctg aca tat gca ttg gga gtt ggc 275
Val Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly
20 25 30
ttg ctt cat att gtc tta ctc agc att ccc ttc ttc agt gtt cct gtt 323
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val
35 40 45
gct tgg act tta aca aat att ata cat aat ctg ggg atg tac gta ttt 371
Ala Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe
50 55 60
ttg cat gca gtg aaa gga aca cct ttc gaa act cct gac cag ggt aaa 419
Leu His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
65 70 75
gca agg ctc cta act cat tgg gaa caa ctg gac tat gga gta cag ttt 467
Ala Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe
80 85 90 95
aca tct tca cgg aag ttt ttc aca att tct cca ata att cta tat ttt 515
Thr Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe
100 105 110
ctg gca agt ttc tat acg aag tat gat cca act cac ttc atc cta aac 563
Leu Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn
115 120 125
aca gct tct ctc ctg agt gta cta att ccc aaa atg cca caa cta cat 611
Thr Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His
130 135 140
ggg gtt cgg atc ttt gga att aat aag tat tgaaatgttt tgaaactga 660
Gly Val Arg Ile Phe Gly Ile Asn Lys Tyr
145 150
aaaaaaaaattt tacagctact gaattttctta taaggaagga gtggttagta aactgcactg 720
tttctctgat aatgtgaaat gagaagtatt tacattggag ggccaatggc tggctcttca 750
agtgtgtgtt tgaagtgcag atttccatta aatgatgcct ctgtttaata cacctggtag 840
atttctgaag aggggcttta taagcaggct gggcaggccc agcttataag ttaaagggca 900
tcacagttag ggtgtagtag ataaattcaa ggaaataaga gatttgaag aaactaggac 960
cagcttaact tataatgaat gggcattgtg ttaagaaaag aacatttcca gtcattcagc 1020
tgtgtgttatt taaagcagac ttacatgtaa accggaatcc tctctatata agtttattaa 1080
agattatttt tattaccgt 1099

<210> 118
<211> 3489
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (227)...(748)

<400> 118
gcgtgcattt ttctggagaa ctgcatgcat catgctctct ctgtgtgcat tttctggac 60
aaaagcccat agtgccatc agattctcaa agggactcct gactccagaa agtttaaaaa 120
ccattaggct taaggaagca catacctact ctgtactcca gggaccaggt gggaacagct 180
gagtgcaggg agtggtcttc tctttcagac cctctcccg agcccc atg gct gcc 235

															Met	Ala	Ala		
															1				
ttc	ctg	ata	cag	acc	aag	gac	aac	ccc	atg	aag	gcc	gtg	ggt	gtg	ctg	283			
Phe	Leu	Ile	Gln	Thr	Lys	Asp	Asn	Pro	Met	Lys	Ala	Val	Gly	Val	Leu				
5						10				15									
gcc	ggc	acc	atg	gcc	acc	gtc	gtg	gcc	atc	act	gtc	ctc	atc	tcc	acc	331			
Ala	Gly	Thr	Met	Ala	Thr	Val	Val	Ala	Ile	Thr	Val	Leu	Ile	Ser	Thr				
20				25				30				35							
gcc	acc	ttc	tgg	cgc	aac	aag	aag	tct	aac	aag	gtc	ctg	cca	atg	cgg	379			
Ala	Thr	Phe	Trp	Arg	Asn	Lys	Lys	Ser	Asn	Lys	Val	Leu	Pro	Met	Arg				
		40				45				50									
cgg	gtg	ctc	cgc	aag	cgg	ccc	agc	cct	gcg	ccc	cgc	acc	atc	cgc	att	427			
Arg	Val	Leu	Arg	Lys	Arg	Pro	Ser	Pro	Ala	Pro	Arg	Thr	Ile	Arg	Ile				
		55				60				65									
gag	tgg	ctc	aag	tcc	aag	agc	acc	aaa	gcc	gct	acc	aag	ttc	atg	ctc	475			
Glu	Trp	Leu	Lys	Ser	Lys	Ser	Thr	Lys	Ala	Ala	Thr	Lys	Phe	Met	Leu				
70				75				80											
aaa	gag	aaa	cct	ccc	aat	gag	aac	tgt	aac	aac	aac	agc	cca	gaa	agc	523			
Lys	Glu	Lys	Pro	Pro	Asn	Glu	Asn	Cys	Asn	Asn	Asn	Ser	Pro	Glu	Ser				
85				90				95											
tct	ctg	ctc	ccg	aga	gct	ccg	gct	ctc	cct	cca	cca	ccc	agc	gtg	gcg	571			
Ser	Leu	Leu	Pro	Arg	Ala	Pro	Ala	Leu	Pro	Pro	Pro	Pro	Ser	Val	Ala				
100				105				110				115							
ccc	agc	act	ggc	gca	gcc	cag	tgg	acc	gtg	cct	act	gtc	tct	ggc	tct	619			
Pro	Ser	Thr	Gly	Ala	Ala	Gln	Trp	Thr	Val	Pro	Thr	Val	Ser	Gly	Ser				
		120				125				130									
ctc	act	ccg	cag	ccg	acc	caa	ccc	ccg	cca	aaa	ccc	aaa	act	atg	gga	667			
Leu	Thr	Pro	Gln	Pro	Thr	Gln	Pro	Pro	Pro	Lys	Pro	Lys	Thr	Met	Gly				
		135				140				145									
agc	ccc	gtc	cag	tca	act	ctg	atc	tct	gag	ctc	aag	caa	aag	ttt	gag	715			
Ser	Pro	Val	Gln	Ser	Thr	Leu	Ile	Ser	Glu	Leu	Lys	Gln	Lys	Phe	Glu				
150				155				160											
aag	aag	agt	gtg	cac	aac	aag	gct	tac	ttc	tagt	gtat	gc	cctat			760			
Lys	Lys	Ser	Val	His	Asn	Lys	Ala	Tyr	Phe										
165				170															
gaccccccat		ctttcctcctcg		cccctgaccc		ccaccaccct		gctgctcgga		ctatgctccc						820			
cttcctctgc		tccttaaggt		cactgacccc		tgttttgcac		aatgggtataa		tccccactgt						880			
cctcatctct		accgccacct		tctggcgcaa		caagaagttg		cgctctgaca		gggctctagt						940			
cagggccttg		ggcaagacat		tgggctctag		gatgcaattg		gcaaatacgt		ccccgttaact						1000			
caaatcccttg		gcactactac		aatgcctctc		attcttcag		gctgagaatt		gacgagaagc						1060			
cagctcaccc		atcccagacc		tcacagtcctc		tcagggttcta		ctgggactctc		atcatcatcc						1120			
ttagtcaagc		agcagggcc		tggccacgtg		gagcaacact		gactagaate		tggatcctga						1180			
cgcttgacgc		tgagagcagg		agcaggaaaa		ggaggctcag		cactgtctca		ggctggaggt									

ctagaataca	ttggtgattt	catttaaaga	gattgtatgc	atttgtggct	ttcctgattt	2380
ctgagctctgt	gtttggaggt	gttactgaga	tgtgccagtg	tgcagaatcc	ttgctggggg	2440
ttctacagtc	cccaacgtga	acagtattaa	gcaagagggtg	gactcgagca	atccaggagc	2500
ccagactgag	caaataagta	ctttccagcc	tgtgtttcag	gagaggactg	tgctggatca	2560
tgcttgcct	ccacagggaa	tacagcatcc	ttacagcttg	catgcaatca	acctcttttg	2620
taaatggaaa	ataaagtctg	ttaccctaaag	gccatgctga	tccctgctc	cctgctttca	2680
tttatgtttg	ctgacctgtg	gagaccagtc	tttctgacac	acagtgaagc	tcaacttgcc	2740
tcttggctgc	ttcagcaggt	ggatccattc	ttcgaccccc	agatgtgact	ctaaagaagg	2800
ctgaaaattt	ttgtccaaat	tgccatgcag	atatcttgaa	cagcaggaca	tttgaggcc	2860
ttgtctactg	gacttttctc	ccaaacagga	caagcccagg	cagggctgca	tggagaggaa	2920
tggaaacctg	agctagaatt	aattgcccac	tetcccaccc	taccagtgc	gcccggcaag	2980
ggcaggaatt	gggaggccta	gggtgggcat	gaaagcttgg	gaagcactgt	cgtctctcag	3040
acaggcgctcc	taaaagacctc	taggctggaa	gcttgggctt	gcaagtggat	ccgggaccga	3100
gggtggtctc	ttggacaacc	ccaggaactt	ggaccaaggc	agagccaatc	ttgcaaactg	3160
gccatggatg	gggaagtgcc	cggtagccag	catgagccac	actaggaaag	aggaggaggg	3220
tgcagccaaa	cttaaggcac	cggcaagtgt	tgtcagcact	ggaggagacc	ccgccagtgg	3280
ggtgaggcca	gccaagtccc	tgtgttacga	atggtgggcc	aaggggctgt	ctgctaggtc	3340
cagtaggaca	ggcagagctc	caggctggca	ccatggtagg	cctccaggga	aagagctggg	3400
aggcaggaat	ggcacactgg	gcaggcttgg	ccattcctgg	ccctgagaat	ggagctgtag	3460
cctcatggac	aataaatgga	tgtgacacc				3489

<210> 119
 <211> 931
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (25)...(252)

<400> 119	
ctgacggacg cttcggccgt aacg atg atc gga gac atc ctg ctg ttc ggg	51
	Met Ile Gly Asp Ile Leu Leu Phe Gly
	1 5
acg ttg ctg atg aat gcc ggg gcg gtg ctg aac ttt aag ctg aaa aag	99
Thr Leu Leu Met Asn Ala Gly Ala Val Leu Asn Phe Lys Leu Lys Lys	
10 15 20 25	
aag gac acg cag ggc ttt ggg gag gag tcc agg gag ccc agc aca ggt	147
Lys Asp Thr Gln Gly Phe Gly Glu Glu Ser Arg Glu Pro Ser Thr Gly	
30 35 40	
gac aac atc cgg gaa ttc ttg ctg agc ctc aga tac ttt cga atc ttc	195
Asp Asn Ile Arg Glu Phe Leu Leu Ser Leu Arg Tyr Phe Arg Ile Phe	
45 50 55	
atc gcc ctg tgg aac atc ttc atg atg ttc tgc atg att gtg ctg ttc	243
Ile Ala Leu Trp Asn Ile Phe Met Met Phe Cys Met Ile Val Leu Phe	
60 65 70	
ggc tct tgaatcccag cgatgaaacc aggaactcac tttcccggga tgccgagtct c	300
Gly Ser	
75	
cattcctcca ttcctgatga cttcaagaat gtttttgacc agaaaaccga caaccttccc	360
agaaagtcca agctcgtggt gggtggaaaa gtgttcgccca aggtgtgcat ggtttcccag	420
ccacgtccct gttttctaaag atagtttcac tttggtctct gaattgaaat gctgtctact	480
gaaaggggtt caggagcggt tatgtaagggt gctgtgatga aattgcattc cccatagata	540
aaagaaaaat catttctatc cagagatctg agcagaagga ttggcttggt agtttaacac	600
agccgtgttt ttggacattc agtgttactt cctgagctctg acagcctctg ggcccggcca	660
ggggccctgt taacaaaactg cttcacatc ccaacagggt ctgcttggcc actcagtgc	720
gctgcgatta accctaaagg ctttaaggaa cgggccacct gtaacagaga caccagcctt	780
cctgtataga cactaaattg ttagcaagag tgttgagcta gttcctgggt aagtgtttcc	840
acagaagaca tgtggagcag ttgtggggat attaagggaa actttcctct gccttgaccc	900
ctttgttaaa taaaatgact ttgggagcca t	931

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510
 Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525
 Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro Glu Thr
 530 535 540
 Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560
 Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575
 Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590
 Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605
 Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620
 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 122
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 122
 Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1 5 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
 145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
 195 200 205
 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
 210 215 220
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
 225 230 235 240
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
 245 250 255
 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
 260 265 270
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
 275 280 285

Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
 290 295 300
 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
 305 310 315

<210> 123
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Ala Phe Thr Leu Tyr Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
 1 5 10 15
 Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
 20 25 30
 Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
 35 40 45
 Lys Ser Gln Leu Met Asn Leu Ile Arg Ser Val Arg Thr Val Met Arg
 50 55 60
 Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
 65 70 75 80
 Phe Gly

<210> 124
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu
 1 5 10 15
 Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
 20 25 30
 Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
 35 40 45
 Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
 50 55 60
 Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
 65 70 75 80
 Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
 85 90 95
 Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
 100 105 110
 Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala Gly Lys
 115 120 125
 Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Gln Ala
 130 135 140
 Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala Ala Asp
 145 150 155 160
 Gln Ala Gly Lys Glu Val Glu Lys Leu Gly Gln Gly Ala His His Ala
 165 170 175
 Ala Gly Gln Ala Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn
 180 185 190
 Gln Ala Ser Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser
 195 200 205
 Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
 210 215 220
 Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
 225 230 235 240
 Ser Val Ala Asn Ile Met Pro


```

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
      165      170      175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
      180      185      190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
      195      200      205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
      210      215      220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
      225      230      235      240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
      245      250      255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
      260      265      270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
      275      280      285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
      290      295      300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
      305      310      315      320
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
      325      330      335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
      340      345      350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
      355      360      365
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
      370      375      380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
      385      390      395      400
Val Phe Ala Ala Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
      405      410      415
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
      420      425      430

```

<210> 127

<211> 306

<212> PRT

<213> Homo sapiens

<400> 127

```

Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys
  1      5      10      15
Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala
      20      25      30
Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly
      35      40      45
Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly
      50      55      60
Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
      65      70      75      80
Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
      85      90      95
Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
      100      105      110
Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
      115      120      125
Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
      130      135      140
Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
      145      150      155      160

```

[illegible]

```
<210> 128
<211> 555
<212> PRT
<213> Homo sapiens
```

<400> 128															
Met	Gln	Ser	Cys	Glu	Ser	Ser	Gly	Asp	Ser	Ala	Asp	Asp	Pro	Leu	Ser
1				5					10					15	
Arg	Gly	Leu	Arg	Arg	Arg	Gly	Gln	Pro	Arg	Val	Val	Val	Ile	Gly	Ala
			20					25					30		
Gly	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Lys	Ala	Leu	Leu	Glu	Gln	Gly	Phe
		35					40					45			
Thr	Asp	Val	Thr	Val	Leu	Glu	Ala	Ser	Ser	His	Ile	Gly	Gly	Arg	Val
	50					55					60				
Gln	Ser	Val	Lys	Leu	Gly	His	Ala	Thr	Phe	Glu	Leu	Gly	Ala	Thr	Trp
65					70					75					80
Ile	His	Gly	Ser	His	Gly	Asn	Pro	Ile	Tyr	His	Leu	Ala	Glu	Ala	Asn
				85					90					95	
Gly	Leu	Leu	Glu	Glu	Thr	Thr	Asp	Gly	Glu	Arg	Ser	Val	Gly	Arg	Ile
			100					105					110		
Ser	Leu	Tyr	Ser	Lys	Asn	Gly	Val	Ala	Cys	Tyr	Leu	Thr	Asn	His	Gly
		115					120					125			
Arg	Arg	Ile	Pro	Lys	Asp	Val	Val	Glu	Glu	Phe	Ser	Asp	Leu	Tyr	Asn
		130				135					140				
Glu	Val	Tyr	Asn	Leu	Thr	Gln	Glu	Phe	Phe	Arg	His	Asp	Lys	Pro	Val
145					150					155					160
Asn	Ala	Glu	Ser	Gln	Asn	Ser	Val	Gly	Val	Phe	Thr	Arg	Glu	Glu	Val
				165					170					175	
Arg	Asn	Arg	Ile	Arg	Asn	Asp	Pro	Asp	Asp	Pro	Glu	Ala	Thr	Lys	Arg
			180					185					190		
Leu	Lys	Leu	Ala	Met	Ile	Gln	Gln	Tyr	Leu	Lys	Val	Glu	Ser	Cys	Glu
		195					200					205			
Ser	Ser	Ser	His	Ser	Met	Asp	Glu	Val	Ser	Leu	Ser	Ala	Phe	Gly	Glu
		210				215					220				
Trp	Thr	Glu	Ile	Pro	Gly	Ala	His	His	Ile	Ile	Pro	Ser	Gly	Phe	Met
225					230					235					240
Arg	Val	Val	Glu	Leu	Leu	Ala	Glu	Gly	Ile	Pro	Ala	His	Val	Ile	Gln
				245					250					255	
Leu	Gly	Lys	Pro	Val	Arg	Cys	Ile	His	Trp	Asp	Gln	Ala	Ser	Ala	Arg
			260					265						270	

Pro	Arg	Gly	Pro	Glu	Ile	Glu	Pro	Arg	Gly	Glu	Gly	Asp	His	Asn	His
		275					280					285			
Asp	Thr	Gly	Glu	Gly	Gly	Gln	Gly	Gly	Glu	Glu	Pro	Arg	Gly	Gly	Arg
	290					295					300				
Trp	Asp	Glu	Asp	Glu	Gln	Trp	Ser	Val	Val	Val	Glu	Cys	Glu	Asp	Cys
305					310					315					320
Glu	Leu	Ile	Pro	Ala	Asp	His	Val	Ile	Val	Thr	Val	Ser	Leu	Gly	Val
				325					330					335	
Leu	Lys	Arg	Gln	Tyr	Thr	Ser	Phe	Phe	Arg	Pro	Gly	Leu	Pro	Thr	Glu
			340					345					350		
Lys	Val	Ala	Ala	Ile	His	Arg	Leu	Gly	Ile	Gly	Thr	Thr	Asp	Lys	Ile
		355					360					365			
Phe	Leu	Glu	Phe	Glu	Glu	Pro	Phe	Trp	Gly	Pro	Glu	Cys	Asn	Ser	Leu
	370					375					380				
Gln	Phe	Val	Trp	Glu	Asp	Glu	Ala	Glu	Ser	His	Thr	Leu	Thr	Tyr	Pro
385					390					395					400
Pro	Glu	Leu	Trp	Tyr	Arg	Lys	Ile	Cys	Gly	Phe	Asp	Val	Leu	Tyr	Pro
				405					410					415	
Pro	Glu	Arg	Tyr	Gly	His	Val	Leu	Ser	Gly	Trp	Ile	Cys	Gly	Glu	Glu
			420					425					430		
Ala	Leu	Val	Met	Glu	Lys	Cys	Asp	Asp	Glu	Ala	Val	Ala	Glu	Ile	Cys
		435					440					445			
Thr	Glu	Met	Leu	Arg	Gln	Phe	Thr	Gly	Asn	Pro	Asn	Ile	Pro	Lys	Pro
	450					455					460				
Arg	Arg	Ile	Leu	Arg	Ser	Ala	Trp	Gly	Ser	Asn	Pro	Tyr	Phe	Arg	Gly
465					470					475					480
Ser	Tyr	Ser	Tyr	Thr	Gln	Val	Gly	Ser	Ser	Gly	Ala	Asp	Val	Glu	Lys
				485					490					495	
Leu	Ala	Lys	Pro	Leu	Pro	Tyr	Thr	Glu	Ser	Ser	Lys	Thr	Ala	Pro	Met
			500					505					510		
Gln	Val	Leu	Phe	Ser	Gly	Glu	Ala	Thr	His	Arg	Lys	Tyr	Tyr	Ser	Thr
		515					520					525			
Thr	His	Gly	Ala	Leu	Leu	Ser	Gly	Gln	Arg	Glu	Ala	Ala	Arg	Leu	Ile
	530					535					540				
Glu	Met	Tyr	Arg	Asp	Leu	Phe	Gln	Gln	Gly	Thr					
545					550					555					

```
<210> 129
<211> 250
<212> PRT
<213> Homo sapiens
```

<400> 129																
Met	Gly	Ser	Gln	His	Ser	Ala	Ala	Ala	Arg	Pro	Ser	Ser	Cys	Arg	Arg	
1				5					10					15		
Lys	Gln	Glu	Asp	Asp	Arg	Asp	Gly	Leu	Leu	Ala	Glu	Arg	Glu	Gln	Glu	
			20					25					30			
Glu	Ala	Ile	Ala	Gln	Phe	Pro	Tyr	Val	Glu	Phe	Thr	Gly	Arg	Asp	Ser	
		35					40					45				
Ile	Thr	Cys	Leu	Thr	Cys	Gln	Gly	Thr	Gly	Tyr	Ile	Pro	Thr	Glu	Gln	
	50					55					60					
Val	Asn	Glu	Leu	Val	Ala	Leu	Ile	Pro	His	Ser	Asp	Gln	Arg	Leu	Arg	
65					70					75					80	
Pro	Gln	Arg	Thr	Lys	Gln	Tyr	Val	Leu	Leu	Ser	Ile	Leu	Leu	Cys	Leu	
				85					90					95		
Leu	Ala	Ser	Gly	Leu	Val	Val	Phe	Phe	Leu	Phe	Pro	His	Ser	Val	Leu	
			100					105					110			
Val	Asp	Asp	Asp	Gly	Ile	Lys	Val	Val	Lys	Val	Thr	Phe	Asn	Lys	Gln	
		115					120					125				
Asp	Ser	Leu	Val	Ile	Leu	Thr	Ile	Met	Ala	Thr	Leu	Lys	Ile	Arg	Asn	
	130					135					140					

Ser	Asn	Phe	Tyr	Thr	Val	Ala	Val	Thr	Ser	Leu	Ser	Ser	Gln	Ile	Gln
145					150					155					160
Tyr	Met	Asn	Thr	Val	Val	Ser	Thr	Tyr	Val	Thr	Thr	Asn	Val	Ser	Leu
				165					170					175	
Ile	Pro	Pro	Arg	Ser	Glu	Gln	Leu	Val	Asn	Phe	Thr	Gly	Lys	Ala	Glu
			180					185					190		
Met	Gly	Gly	Pro	Phe	Ser	Tyr	Val	Tyr	Phe	Phe	Cys	Thr	Val	Pro	Glu
		195					200					205			
Ile	Leu	Val	His	Asn	Ile	Val	Ile	Phe	Met	Arg	Thr	Ser	Val	Lys	Ile
	210					215					220				
Ser	Tyr	Ile	Gly	Leu	Met	Thr	Gln	Ser	Ser	Leu	Glu	Thr	His	His	Tyr
225				230						235					240
Val	Asp	Cys	Gly	Gly	Asn	Ser	Thr	Ala	Ile						
				245					250						

```
<210> 130
<211> 174
<212> PRT
<213> Homo sapiens
```

```

<400> 130
Met Gln Ala Pro Ala Phe Arg Asp Lys Lys Gln Gly Val Ser Ala Lys
  1          5          10          15
Asn Gln Gly Ala His Asp Pro Asp Tyr Glu Asn Ile Thr Leu Ala Phe
          20          25          30
Lys Asn Gln Asp His Ala Lys Gly Gly His Ser Arg Pro Thr Ser Gln
          35          40          45
Val Pro Ala Gln Cys Arg Pro Ser Asp Ser Thr Gln Val Pro Cys
          50          55          60
Trp Leu Tyr Arg Ala Ile Leu Ser Leu Tyr Ile Leu Leu Ala Leu Ala
          65          70          75          80
Phe Val Leu Cys Ile Ile Leu Ser Ala Phe Ile Met Val Lys Asn Ala
          85          90          95
Glu Met Ser Lys Glu Leu Leu Gly Phe Lys Arg Glu Leu Trp Asn Val
          100          105          110
Ser Asn Ser Val Gln Ala Cys Glu Arg Gln Lys Arg Gly Trp Asp
          115          120          125
Ser Val Gln Gln Ser Ile Thr Met Val Arg Ser Lys Ile Asp Arg Leu
          130          135          140
Glu Thr Thr Leu Ala Gly Ile Lys Asn Ile Asp Thr Lys Val Gln Lys
          145          150          155          160
Ile Leu Glu Val Leu Gln Lys Met Pro Gln Ser Ser Pro Gln
          165          170

```

```
<210> 131
<211> 1908
<212> DNA
<213> Homo sapiens
```

<400> 131						
atgaccacgt	ggagcctccg	gcgaggcccg	gcccgcacgc	tgggactcct	gctgctggtc	60
gtcttgggct	tcctgggtgct	tcgcaggctg	gactggagca	ccctgggtccc	tctgcggtct	120
cgccatcgac	agctggggct	gcaggccaag	ggctggaact	tcattgctgga	ggattccacc	180
ttctggatct	tcgggggctc	catccactat	ttccgtgtgc	ccagggagta	ctggagggac	240
cgccgtctga	agatgaaggc	ctgtggcttg	aacacctca	ccacctatgt	tccgtggaac	300
ctgcatgagc	cagaaagagg	caaatttgac	ttctctggga	acctggacct	ggaggccttc	360
gtcctgatgg	ccgcagagat	cgggctgtgg	gtgattctgc	gtccaggccc	ctacatctgc	420
agtgagatgg	acctcggggg	cttgcccagc	tggctactcc	aagaccttg	catgaggctg	480
aggacaactt	acaaggcctt	caccgaagca	gtggaccttt	attttgacca	cctgatgtcc	540
aggggtgtgc	cactccagta	caagcgtggg	ggacctatca	ttgccgtgca	ggtggagaat	600
gaatatggtt	cctataataa	agaccccgca	tacatgccct	acgtcaagaa	ggcactggag	660

gaccgtggca	ttgtggaact	gctcctgact	tcagacaaca	aggatgggct	gagcaagggg	720
attgtccagg	gagtcttggc	caccatcaac	ttgcagtcaa	cacacgagct	gcagctactg	780
accacctttc	tcttcaacgt	ccaggggact	cagcccaaga	tggatgatgga	gtactggacg	840
gggtggtttg	actcgtgggg	aggccctcac	aatatctttg	attctttctga	ggttttgaaa	900
accgtgtctg	ccattgtgga	cgccggctcc	tccatcaacc	tctacatgtt	ccacggaggg	960
accaactttg	gcttcatgaa	tggagccatg	cacttccatg	actacaagtc	agatgtcacc	1020
agctatgact	atgatgctgt	gctgacagaa	gccggcgatt	acacggccaa	gtacatgaag	1080
cttcgagact	tcttcggctc	catctcaggc	atccctctcc	ctccccacc	tgaccttctt	1140
cccaagatgc	cgtatgagcc	cttaacgcca	gtcttgtacc	tgtctctgtg	ggacgccctc	1200
aagtacctgg	gggagccaat	caagtctgaa	aagcccatca	acatggagaa	cctgccagtc	1260
aatgggggaa	atggacagtc	cttcgggtac	attctctatg	agaccagcat	cacctcgtct	1320
ggcatctca	gtggccacgt	gcatgatcgg	gggcaggtgt	ttgtgaacac	agtatccata	1380
gatttcttgg	actacaagac	aacgaagatt	gctgtccccc	tgatccaggg	ttacaccgtg	1440
ctgaggatct	tgggtggagaa	tcgtgggcga	gtcaactatg	gggagaatat	tgatgaccag	1500
cgcaaaggct	taattggaaa	tctctatctg	aatgattcac	ccctgaaaaa	cttcagaatc	1560
tatagcctgg	atatgaagaa	gagcttcttt	cagaggttcg	gcctggacaa	atggagttcc	1620
ctcccagaaa	caccacatt	acctgctttc	ttcttgggta	gcttgtccat	cagctccacc	1680
ccttgtgaca	cctttctgaa	gctggagggc	tgggagaagg	gggttgtatt	catcaatggc	1740
cagaaccttg	gacgttactg	gaacattgga	ccccagaaga	cgctttacct	cccaggtccc	1800
tggttgagca	gcggaatcaa	ccaggtcatc	gtttttgagg	agacgatggc	gggccttgca	1860
ttacagttca	cggaaacccc	ccacctgggc	aggaaccagt	acattaag		1908

<210> 132

<211> 954

<212> DNA

<213> Homo sapiens

<400> 132

atggttgagc	tcattgttccc	gctgttgcct	ctccttctgc	ccttccttct	gtatatggct	60
gcgccccaaa	tcaggaaaat	gctgtccagt	gggggtgtga	catcaactgt	tcagcttctc	120
gggaaagtag	ttgtgggcac	aggagctaatt	acaggtatcg	ggaaggagac	agccaaagag	180
ctggctcaga	gaggagctcg	agtatattta	gcttgccggg	atgtggaaaa	gggggaattg	240
gtggccaaaag	agatccagac	cacgacaggg	aaccagcagg	tgttgggtgcg	gaaactggac	300
ctgtctgata	ctaagtctat	tcgagctttt	gctaagggct	tcttagctga	ggaaaagcac	360
ctccacgttt	tgatcaacaa	tgacaggagt	atgatgtgtc	cgtactcgaa	gacagcagat	420
ggctttgaga	tgacacatagg	agtcaaccac	ttgggtcact	tcctcctaac	ccatctgctg	480
ctagagaaac	taaaggaatc	agccccatca	aggatagtaa	atgtgtcttc	cctcgcacat	540
cacctgggaa	ggatccactt	ccataacctg	cagggcgaga	aattctacaa	tgacggcctg	600
gcctactgtc	acagcaagct	agccaacatc	ctcttcaccc	aggaactggc	ccggagacta	660
aaaggctctg	gcgttacgac	gtattctgta	caccttgcca	cagtcctaac	tgaactgggt	720
cggcactcat	cttctcatgag	atggatgtgg	tggcttttct	cctttttcat	caagactcct	780
cagcagggag	cccagaccag	cctgcactgt	gccttaacag	aaggtcttga	gattctaagt	840
gggaatcatt	tcagtgactg	tcattgtggca	tgggtctctg	cccaagctcg	taatgagact	900
atagcaaggc	ggctgtggga	cgtcagttgt	gacctgctgg	gcctcccaat	agac	954

<210> 133

<211> 246

<212> DNA

<213> Homo sapiens

<400> 133

atggccttta	ccctgtactc	actgctgcag	gcagccctgc	tctgcgtcaa	cgccatcgca	60
gtgctgcacg	aggagcgatt	cctcaagaac	attggctggg	gaacagacca	gggaattggg	120
ggattttggag	aagagccggg	aattaaatca	cagctaattg	accttatctg	atctgtaaga	180
accgtgatga	gagtgccatt	gataaatagta	aactcaattg	caattgtgtt	acttttatta	240
tttggga						246

<210> 134

<211> 741

<212> DNA

<213> Homo sapiens

<400> 134
atgcatcttg cacgtctggt cggctcctgc tccctccttc tgctactggg ggccctgctt 60
ggatggggcg ccagcgatga cccatttgag aaggtcattg aagggatcaa ccgagggctg 120
agcaatgcag agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 180
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag ccacaccggc 240
aaggagttag acaaaggcgt ccaggggctc aaccacggca tggacaagggt tgcccatgag 300
atcaaccatg gtattggaca agcaggaaaag gaagcagaga agcttggcca tggggtcaac 360
aacgtgctg gacaggccgg gaaggaagca gacaaagcgg tccaagggtt ccacactggg 420
gtccaccagg ctgggaagga agcagagaaa cttggccaag gggtaacca tgetgctgac 480
caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc tggccaggcc 540
gggaaggagc tgcagaatgc tcataatggg gtcaaccaag ccagcaagga ggccaaccag 600
ctgctgaatg gcaaccatca aagcggatct tccagccatc aaggaggggc cacaaccacg 660
cgttagcct ctggggcctc ggtcaacacg ctttcatca accttccgc cctgtggagg 720
agcgtcgcca acatcatgcc c 741

<210> 135

<211> 618

<212> DNA

<213> Homo. sapiens

<400> 135
atggccccca gccacctgtc agtgcgggag atgagggaa atgagaagcc cctgggtgctg 60
gagatgctga aggccggcgt gaaggacacg gaaaaccgcg tggccctcca tgctttgaca 120
cggccgcggg cctgctcctt cctggcgggc gccagcagcg gctgctgctt tgctctggct 180
tccttcgccc tggccctcct cctgccgggtg ttcttggtg tggccgcccgt gaagctgggc 240
ctgcggggccc gatggggctc gctgcctccg ccgggtggcc tggggggccc ctgggtggcc 300
gtgcggggct ccggtgacgt gtgtggggtc ctggtctggt tctgctggc cccttggcac aaatgcaggg 360
gacggggggc gggtcaaccg cctgtctgtc tctgctggc accgcggcg gggcgtgggc 420
aggagctgc tggccttcgc ggaggcccg gctcgggctt gggctgggg catgggggag 480
ccccggggccc ggctcgtgtt ccccggtggt gtggccgctt ggggggtggg agggatgctg 540
gagggctgtg gctaccaggc cgagggggggc tggggtgctc tgggctacac gctggtgagg 600
gaattcagca aagacctg 618

<210> 136

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 136
atggacgcca gatgggtggg agtggtggtg ctggtgctg tccctcctt aggggcaggt 60
ggggagactc ccgaagcccc tccggagtca tggaccagc tatggttctt ccgatttgtg 120
gtgaatgctg ctggttatgc cagctttatg gtacctggct acctcctggt gcagtacttc 180
aggcggaaga actacctgga gaccggtagg ggctctgctt ttcccctggt gaaagcttgt 240
gtgtttggca atgagcccaa ggctctgat gaggttcccc tggcgccccg aacagaggcg 300
gcagagacca ccccgatgtg gcaggccctg aagctgctct tctgtgccac agggctccag 360
gtgtcttata tgacttgggg tgtgctgcag gaaaagagtga tgaccgcag ctatggggcc 420
acagccacat caccgggtga gcgctttacg gactcgagct tctggtgctt aatgaaccga 480
gtgctggcac tgattgtggc tggcctctcc tgtgttctct gcaagcagcc ccggcatggg 540
gcacccatgt accggctact ctttgccag ctgtccaatg tgcttagcag ctggtgccaa 600
tacgaagctc ttaagttcgt cagcttcccc acccaggtgc tggccaaggc ctctaagggtg 660
atccctgtca tgetgatggg aaagcttgtg tctcgcgcca gctacgaaca ctgggagtag 720
ctgacagcca cactcatctc cattgggggtc agcatgttct tgctatccag cggaccagag 780
ccccgcagct cccagccac cactctctca ggctcatct tactggcagg ttatattgct 840
tttgacagct tcacctcaaa ctggcaggat gccctgtttg cctataagat gtcacgggtg 900
cagatgatgt ttgggtgcaa tttcttctcc tgctcttcca cagtgggctc actgctagaa 960
cagggggggc tactggaggg aaccgcctc atggggcgac acagtgaagt tgctgcccac 1020
gccctgctac tctccatctg ctccgcatgt ggcagctct tcatctttta caccattggg 1080
cagtttgggg ctgccgtctt caccatcatc atgacctcc gccaggcctt tgccatcctt 1140
ctttcctgcc ttctctatgg ccacactgtc actgtggtgg gagggctggg ggtggctgtg 1200
gtctttgctg cctcctgctc cagagtctac gcgcggggcc gtctaaagca acggggaaag 1260

aaggctgtgc ctgttgagtc tcctgtgcag aaggtt

1296

<210> 137

<211> 918

<212> DNA

<213> Homo sapiens

<400> 137

atggggcacc	ggaccctggt	cctgccctgg	gtgctgctga	ccttgtgtgt	cactgcgggg	60
accccgagg	tgtgggttca	agttcggatg	gaggccaccg	agctctcgtc	cttcaccatc	120
cgttgtgggt	tcctggggtc	tggctccatc	tccttgggtg	ctgtgagctg	ggggggcccc	180
gacggtgctg	gggggaccac	gctggctgtg	ttgcacccag	aacgtggcat	ccggcaatgg	240
gcccctgctc	gccaggcccc	ctgggaaacc	cagagcagca	tctctctcat	cctggaaggc	300
tctggggcca	gcagcccttg	cgccaacacc	accttctgct	gcaagtttgc	gtccttccct	360
gagggctcct	gggaggcctg	tgggagcctc	ccgcccagct	cagacccagg	gctctctgcc	420
ccgccgactc	ctgcccccat	tctgcgggca	gacctggccg	ggatcttggg	ggtctcagga	480
gtcctcctct	ttggctgtgt	ctacctcctt	catctgctgc	gccgacataa	gcacgcacct	540
gcccctaggg	tccagccgtc	ccgcaccagc	ccccaggcac	cgagagcacg	agcatgggca	600
ccaagccagg	cctcccaggc	tgctcttcac	gtcccttatg	ccactatcaa	caccagctgc	660
cgcccagcta	ctttgggacg	agctcaccac	cctggggggc	cgctcctggg	ggcgctcact	720
cccacccacg	ctgcacaccg	gccccagggc	cctgcgcctt	gggcctccac	acccatccct	780
gcacgtggca	gctttgtctc	tggtgagaat	ggactctacg	ctcaggcagg	ggagaggcct	840
cctcacactg	gtcccggcct	cactcttttc	cctgaccctc	gggggcccag	ggccatggaa	900
ggacccttag	gagttcga					918

<210> 138

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 138

atgcaaagtt	gtgaatccag	tggtgacagt	gcggatgacc	ctctcagtcg	cggcctacgg	60
agaaggggac	agcctcgtgt	ggtggtgatc	ggcgccggct	tggctggcct	ggctgcagcc	120
aaagcacttc	ttgagcaggg	tttcacggat	gtcactgtgc	ttgaggcttc	cagccacatc	180
ggaggccgtg	tgcagagtgt	gaaacttgga	cacgccacct	ttgagctggg	agccacctgg	240
atccatggct	cccatgggaa	ccctatctat	catctagcag	aagccaacgg	cctcctggaa	300
gagacaaccg	atggggaaac	cagcgtgggc	cgcacagacc	tctattccaa	gaatggcgtg	360
gcctgctacc	ttaccaacca	cggccgcagg	atccccaagg	acgtggttga	ggaattcagc	420
gatttatata	acgaggtcta	taacttgacc	caggagttct	tccggcacga	taaaccagtc	480
aatgctgaaa	gtcaaaaatg	cgtggggggt	ttcaccagag	aggaggtgct	taaccgcctc	540
aggaatgacc	ctgacgaccc	agaggtctac	aagcgctga	agctcgccat	gacccagcag	600
tacctgaagg	tggagagctg	tgagagcagc	tcacacagca	tggacgaggt	gtccctgagc	660
gccttcgggg	agtggaccga	gatccccggc	gctcaccaca	tcaccccttc	gggcttcatg	720
cgggttgttg	agctgctggc	ggagggcctc	cctgcccacg	tcacccagct	agggaaacct	780
gtccgctgca	ttcactggga	ccaggcctca	gcccgcacca	gaggccctga	gattgagccc	840
cggggtgagg	gcgaccacaa	tcacgacact	ggggagggtg	gccagggtgg	agaggagccc	900
cggggggggc	ggtgggatga	ggatgagcag	tggctcgggtg	tgggtggagt	cgaggactgt	960
gagctgatcc	cggcggaacca	tgtgattgtg	accgtgtcgc	taggtgtgct	aaagaggcag	1020
tacaccagtt	tcttccggcc	aggcctgccc	acagagaagg	tggctgccat	ccaccgcctg	1080
ggcattggca	ccaccgacaa	gatctttctg	gaattcgagg	agcccttctg	gggcccctgag	1140
tgcaacagcc	tacagtttgt	gtgggaggac	gaagcggaga	gccacaccct	cacctaccca	1200
cctgagctct	ggtaccgcaa	gatctgcggc	tttgatgtcc	tctaccgcgc	tgagcgctac	1260
ggccatgtgc	tgagcggctg	gatctgcggg	gaggaggccc	tcgtcatgga	gaagtgtgat	1320
gacgaggcag	tggccgagat	ctgcacggag	atgctgcgtc	agttcacagg	gaaccccaac	1380
attccaaaac	ctcggcgaaat	cttgcgctcg	gcttggggca	gcaaccctta	cttccgcggc	1440
tcctattcat	acacgcagggt	gggctccagc	ggggcgagtg	tggagaagct	ggccaagccc	1500
ctgccgtaca	cggagagctc	aaagacagcg	cccatgcagg	tgctgttttc	cggtagggcc	1560
acccaccgca	agtactattc	caccacccac	ggtgctctgc	tgtccggcca	gcgtgaggct	1620
gcccgcctca	ttgagatgta	ccgagacctc	ttccagcagg	ggacc		1665

<210> 139

<211> 750
<212> DNA
<213> Homo sapiens

<400> 139
atgggggtctc agcatttcgc tgetgctcgc cctcctcct gcaggcgaaa gcaagaagat 60
gacagggacg gtttgctggc tgaacgagag caggaagaag ccattgctca gttcccatat 120
gtggaattca ccgggagaga tagcatcacc tgtctcact gccaggggac aggtacatt 180
ccaacagagc aagtaaataa gttggtggct ttgatccac acagtgatca gagattgctc 240
cctcagcgaa ctaagcaata tgtcctcctg tccatcctgc tttgtctcct ggcattctgt 300
ttggtggttt tcttcctggt tccgcattca gtcttgtgg atgatgacgg catcaaagtg 360
gtgaaagtca catttaataa gcaagactcc cttgtaattc tcaccatcat ggccaccctg 420
aaaatcagga actccaactt ctacacgggt gcagtgaacca gcctgtccag ccagattcag 480
tacatgaaca cagtggctcag tacatatgtg actactaacg tctcccttat tccacctcgg 540
agtgaagcaac tgggtgaattt taccgggaag gccgagatgg gaggaccgtt ttcctatgtg 600
tacttcttct gcacgggtacc tgagatcctg gtgcacaaca tagtgatctt catgcgaact 660
tcagtgaaga ttccatacat tggcctcatg acccagagct ccttgagagc acatcactat 720
gtggattgtg gaggaaattc cacagctatt 750

<210> 140
<211> 522
<212> DNA
<213> Homo sapiens

<400> 140
atgcaagcac cagccttcag ggacaagaaa caggggggtct cagccaagaa tcaaggtgcc 60
catgaccacg actatgagaa tatcaccttg gccttcaaaa atcaggacca tgcaaagggg 120
ggtcattcac gaccacagag ccaagtccca gccagtgca ggccgcctc agactccacc 180
caggtcccct gctggttgta cagagccatc ctgagcctgt acatcctcct ggccctggcc 240
tttgtcctct gcatcatcct gtcagccttc atcatggtga agaattgctga gatgtccaag 300
gagctgctgg gctttaaaag ggagctttgg aatgtctcaa actccgtaca agcatgcgaa 360
gagagacaga agagaggctg ggattccgtt cagcagagca tcaccatggg caggagcaag 420
attgatagat tagagacgac attagcaggc ataaaaaaca ttgacacaaa ggtacagaaa 480
atcttgaggg tgctgcagaa aatgccacag tcctcacctc aa 522

<210> 141
<211> 3234
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (129)...(2039)

<400> 141
aatgagcgcc ggcgggccgg ttgccaggc gaccagcgcg cggctccgcc ccccgcgcg 60
aggctcccgc gcgcggctga gtgcggactg gactgggaac ccgggtcccc gcgcttagag 120
aacacgcg atg acc acg tgg agc ctc cgg cgg agg ccg gcc cgc acg ctg 170
Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu
1 5 10
gga ctc ctg ctg ctg gtc gtc ttg ggc ttc ctg gtg ctt cgc agg ctg 218
Gly Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu
15 20 25 30
gac tgg agc acc ctg gtc cct ctg cgg ctc cgc cat cga cag ctg ggg 266
Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly
35 40 45
ctg cag gcc aag ggc tgg aac ttc atg ctg gag gat tcc acc ttc tgg 314
Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp
50 55 60
atc ttc ggg ggc tcc atc cac tat ttc cgt gtg ccc agg gag tac tgg 362
Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp


```

gcc ctc aag tac ctg ggg gag cca atc aag tct gaa aag ccc atc aac      1370
Ala Leu Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn
    400                      405                      410

atg gag aac ctg cca gtc aat ggg gga aat gga cag tcc ttc ggg tac      1418
Met Glu Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr
    415                      420                      425                      430

att ctc tat gag acc agc atc acc tcg tct ggc atc ctc agt ggc cac      1466
Ile Leu Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His
    435                      440                      445

gtg cat gat cgg ggg cag gtg ttt gtg aac aca gta tcc ata gga ttc      1514
Val His Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe
    450                      455                      460

ttg gac tac aag aca acg aag att gct gtc ccc ctg atc cag ggt tac      1562
Leu Asp Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr
    465                      470                      475

acc gtg ctg agg atc ttg gtg gag aat cgt ggg cga gtc aac tat ggg      1610
Thr Val Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly
    480                      485                      490

gag aat att gat gac cag cgc aaa ggc tta att gga aat ctc tat ctg      1658
Glu Asn Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu
    495                      500                      505                      510

aat gat tca ccc ctg aaa aac ttc aga atc tat agc ctg gat atg aag      1706
Asn Asp Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys
    515                      520                      525

aag agc ttc ttt cag agg ttc ggc ctg gac aaa tgg agt tcc ctc cca      1754
Lys Ser Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro
    530                      535                      540

gaa aca ccc aca tta cct gct ttc ttc ttg ggt agc ttg tcc atc agc      1802
Glu Thr Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser
    545                      550                      555

tcc acc cct tgt gac acc ttt ctg aag ctg gag ggc tgg gag aag ggg      1850
Ser Thr Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly
    560                      565                      570

gtt gta ttc atc aat ggc cag aac ctt gga cgt tac tgg aac att gga      1898
Val Val Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly
    575                      580                      585                      590

ccc cag aag acg ctt tac ctc cca ggt ccc tgg ttg agc agc gga atc      1946
Pro Gln Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile
    595                      600                      605

aac cag gtc atc gtt ttt gag gag acg atg gcg ggc cct gca tta cag      1994
Asn Gln Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln
    610                      615                      620

ttc acg gaa acc ccc cac ctg ggc agg aac cag tac att aag tgag      2040
Phe Thr Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
    625                      630                      635

cggtggcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc      2100
ctgggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg      2160
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg      2220
ggatggctct gggcctggct ttgttgatga tggttttctt acagccctgc tcttgtgccg      2280
aggctgtcgg gctgtctcta ggggtgggagc agctaatacag atcgcccagc ctttggccct      2340
cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcatctgctg      2400
gactcaggcg tgctctttgc tggttcctgg gaggttggc cacatccctc atggccccat      2460
tttatcccc aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc      2520
tgagctgact ttgttcttc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa      2580
ctcgcgctga gaaacatgtg acttcccctt tcccttccca ctgctgctt cccacagggt      2640
gacaggctgg gctggagaaa cagaaatect caccctgcgt cttcccaagt tagcagggtg      2700
ctctgggtgt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca      2760
catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga agccatggcc      2820
catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag tcctggcaga      2880
agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct cacatgtgag      2940
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggcccagct      3000

```


Gly	Ile	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	
105					110					115						
aac	aac	gct	gct	gga	cag	gcc	ggg	aag	gaa	gca	gac	aaa	gcg	gtc	caa	436
Asn	Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	
120					125					130					135	
ggg	ttc	cac	act	ggg	gtc	cac	cag	gct	ggg	aag	gaa	gca	gag	aaa	ctt	484
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	
				140					145					150		
ggc	caa	ggg	gtc	aac	cat	gct	gct	gac	cag	gct	gga	aag	gaa	gtg	gag	532
Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	Val	Glu	
			155					160					165			
aag	ctt	ggc	caa	ggt	gcc	cac	cat	gct	gct	ggc	cag	gcc	ggg	aag	gag	580
Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	
		170						175				180				
ctg	cag	aat	gct	cat	aat	ggg	gtc	aac	caa	gcc	agc	aag	gag	gcc	aac	628
Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser	Lys	Glu	Ala	Asn	
		185				190					195					
cag	ctg	ctg	aat	ggc	aac	cat	caa	agc	gga	tct	tcc	agc	cat	caa	gga	676
Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser	Ser	Ser	His	Gln	Gly	
200					205				210						215	
ggg	gcc	aca	acc	acg	ccg	tta	gcc	tct	ggg	gcc	tcg	gtc	aac	acg	cct	724
Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly	Ala	Ser	Val	Asn	Thr	Pro	
				220					225					230		
ttc	atc	aac	ctt	ccc	gcc	ctg	tgg	agg	agc	gtc	gcc	aac	atc	atg	ccc	772
Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg	Ser	Val	Ala	Asn	Ile	Met	Pro	
		235						240					245			
taaactgg	catccggcct	tgctgggaga	ataatgtcgc	cgttgtcaca	tcagctgaca											830
tgacctggag	gggttggggg	tgggggacag	gtttctgaaa	tccctgaagg	gggttgtact											890
gggatttgtg	aataaacttg	atacact														917

<210> 145
 <211> 1306
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (74)...(694)

<400> 145	
gaaggaccaa aggcgaccgg tgcaggtgca cgacgccagc tcccttctgg ggggcggggg	60
cctggggggtt gcc atg gcc ccc agc cac ctg tca gtg cgg gag atg agg	109
Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg	
1 5 10	
gaa gat gag aag ccc ctg gtg ctg gag atg ctg aag gcc ggc gtg aag	157
Glu Asp Glu Lys Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys	
15 20 25	
gac acg gaa aac cgc gtg gcc ctc cat gcc ttg aca cgg ccg ccg gcc	205
Asp Thr Glu Asn Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala	
30 35 40	
ctg ctc ctc ctg gcg gcg gcc agc agc ggc ctg cgc ttt gtc ctg gct	253
Leu Leu Leu Leu Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala	
45 50 55 60	
tcc ttc gcc ctg gcc ctc ctc ctg ccg gtg ttc ctg gct gtg gcc gcc	301
Ser Phe Ala Leu Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala	
65 70 75	
gtg aag ctg ggc ctg ccg gcc cga tgg ggc tcg ctg cct ccg ccg ggt	349
Val Lys Leu Gly Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly	
80 85 90	
ggc ctg ggc gcc ccc tgg gtg gcc gtg ccg ggc tcc ggt gac gtg tgt	397
Gly Leu Gly Gly Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys	

```

      95      100      105
ggg gtc ctg gct ctg gcc cct ggc aca aat gca ggg gac ggg gcc cgg      445
Gly Val Leu Ala Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg
      110      115      120
gtc acc cgc ctg tct gtc tct cgc tgg cac cgc cgc cgg ggc gtg ggc      493
Val Thr Arg Leu Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly
      125      130      135      140
agg agg ctg ctg gcc ttc gcg gag gcc cgg gct cgg gcc tgg gct ggg      541
Arg Arg Leu Leu Ala Phe Ala Glu Ala Arg Ala Trp Ala Gly
      145      150      155
ggc atg ggg gag ccc cgg gcc cgg ctc gtg gtc ccc gtg gct gtg gcc      589
Gly Met Gly Glu Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala
      160      165      170
gcc tgg ggg gtg gga ggg atg ctg gag ggc tgt ggc tac cag gcc gag      637
Ala Trp Gly Val Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu
      175      180      185
ggg ggc tgg ggc tgc ctg ggc tac acg ctg gtg agg gaa ttc agc aaa      685
Gly Gly Trp Gly Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys
      190      195      200
gac ctg tgaagctaca gactgacagc cagggcaggg gaggagggag gggcgccag      740
Asp Leu
205
cacctgatga tcgcctactg tctgcggggt cttttacctg ctctccctca gtgagtcctc      800
aaccaccctg ggcccagaaa cagaggcctg ccgaggggag gagcctggcc tctgtccacc      860
cgtcagcagt gtgaagtctg ttgtgtttga gcttctcaga gtggaatgac tccttttctt      920
tcttggccct cggggggcctc tcgaggtcag cctctccaac ccctacctca gctcctgtct      980
gcactgagaa acctcccccg gtgatgtctg caaagtctgt gctgtccgtg cccagggctg      1040
ggagagctat ctggggaggg ggagaggagg ccgagcagaa tacaccccag agttagggtt      1100
tgcgactccg cctccctggg acctggattg ggtcagatgc ctgtccttgg aggggacaag      1160
gttgactgct taggaggcgc gacgcacagg gctgccaggc ctggcccctc tctgggaagg      1220
ttgagagctg agacgggcag ccctgtccct tcctccagat ccgtctggtt ttttacaccg      1280
tttgtaata aagcctgaaa ccgctt      1306

<210> 146
<211> 2022
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)...(1416)

<400> 146
cttccgctgg ccgctggctc gctggcgcgt cctggaggcg gcggcgggag cgcagggggc      60
gcggggcccg gggactcgca ttccccgggt cccctccac cccacgggc ctggacc      117
atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc      165
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
      1      5      10      15
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc      213
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
      20      25      30
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc      261
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
      35      40      45
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac      309
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
      50      55      60
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt      357
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
      65      70      75      80
gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc      405

```


Leu	Arg	Arg	His	Lys	His	Arg	Pro	Ala	Pro	Arg	Leu	Gln	Pro	Ser	Arg		
		175					180				185						
acc	agc	ccc	cag	gca	ccg	aga	gca	cga	gca	tgg	gca	cca	agc	cag	gcc		686
Thr	Ser	Pro	Gln	Ala	Pro	Arg	Ala	Arg	Ala	Trp	Ala	Pro	Ser	Gln	Ala		
		190					195				200						
tcc	cag	gct	gct	ctt	cac	gtc	cct	tat	gcc	act	atc	aac	acc	agc	tgc		734
Ser	Gln	Ala	Ala	Leu	His	Val	Pro	Tyr	Ala	Thr	Ile	Asn	Thr	Ser	Cys		
205					210					215					220		
cgc	cca	gct	act	ttg	gac	aca	gct	cac	ccc	cat	ggg	ggg	ccg	tcc	tgg		782
Arg	Pro	Ala	Thr	Leu	Asp	Thr	Ala	His	Pro	His	Gly	Gly	Pro	Ser	Trp		
				225						230					235		
tgg	gcg	tca	ctc	ccc	acc	cac	gct	gca	cac	cgg	ccc	cag	ggc	cct	gcc		830
Trp	Ala	Ser	Leu	Pro	Thr	His	Ala	Ala	His	Arg	Pro	Gln	Gly	Pro	Ala		
			240					245					250				
gcc	tgg	gcc	tcc	aca	ccc	atc	cct	gca	cgt	ggc	agc	ttt	gtc	tct	gtt		878
Ala	Trp	Ala	Ser	Thr	Pro	Ile	Pro	Ala	Arg	Gly	Ser	Phe	Val	Ser	Val		
		255					260					265					
gag	aat	gga	ctc	tac	gct	cag	gca	ggg	gag	agg	cct	cct	cac	act	ggt		926
Glu	Asn	Gly	Leu	Tyr	Ala	Gln	Ala	Gly	Glu	Arg	Pro	Pro	His	Thr	Gly		
	270					275					280						
ccc	ggc	ctc	act	ctt	ttc	cct	gac	cct	cgg	ggg	ccc	agg	gcc	atg	gaa		974
Pro	Gly	Leu	Thr	Leu	Phe	Pro	Asp	Pro	Arg	Gly	Pro	Arg	Ala	Met	Glu		
285					290					295					300		
gga	ccc	tta	gga	gtt	cga	tgagagagac	catgaggcca	ctgggctt									1020
Gly	Pro	Leu	Gly	Val	Arg												
				305													
tccccctccc	aggcctcctg	ggtgtcaccc	ccttacttta	attcttgggc	ctccaataag												1080
tgtcccatag	gtgtctggcc	aggccacct	gctgcggatg	tggctctgtg	gcgtgtgtgg												1140
gcacaggtgt	gagtggtgta	gtgacagtta	ccccatttca	gtcatttcct	gctgcaacta												1200
agtcagcaac	acagtttctc	tgatgtc															1227

<210> 148
 <211> 2210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (204)...(1871)

<400> 148

aggggacgcg	aggcggagcg	gggccccaca	caggccgcgg	cggctggctc	gggcccctac												60
ggtcccggcg	gcggctggag	gaggaagcca	ggcggctggc	ggaggaggag	agacggagga												120
ggccgagacc	ggagcgccgc	tcgccgcaga	cttacttccc	cggctcagca	gggaaaggtt												180
cctagaaggt	gagcgcgggac	ggt atg	caa agt	tgt gaa	tcc agt	ggt gac	agt										233
		Met	Gln	Ser	Cys	Glu	Ser	Ser	Gly	Asp	Ser						
		1				5				10							
gcg gat	gac cct	ctc agt	cgc ggc	cta cgg	aga agg	gga cag	cct cgt										281
Ala Asp	Asp Pro	Leu Ser	Arg Gly	Leu Arg	Arg Arg	Gly Gln	Pro Arg										
		15			20		25										
gtg gtg	gtg atc	ggc gcc	ggc ttg	gct ggc	ctg gct	gca gcc	aaa gca										329
Val Val	Val Ile	Gly Ala	Gly Leu	Ala Gly	Leu Ala	Ala Ala	Lys Ala										
		30			35		40										
ctt ctt	gag cag	ggt ttc	acg gat	gtc act	gtg ctt	gag gct	tcc agc										377
Leu Leu	Glu Gln	Gly Phe	Thr Asp	Val Thr	Val Leu	Glu Ala	Ser Ser										
		45			50		55										
cac atc	gga ggc	cgt gtg	cag agt	gtg aaa	ctt gga	cac gcc	acc ttt										425
His Ile	Gly Gly	Arg Val	Gln Ser	Val Lys	Leu Gly	His Ala	Thr Phe										
		60			65		70										
gag ctg	gga gcc	acc tgg	atc cat	ggc tcc	cat ggg	aac cct	atc tat										473
Glu Leu	Gly Ala	Thr Trp	Ile His	Gly Ser	His Gly	Asn Pro	Ile Tyr										


```

ttt gat gtc ctc tac ccg cct gag cgc tac ggc cat gtg ctg agc ggc      1481
Phe Asp Val Leu Tyr Pro Pro Glu Arg Tyr Gly His Val Leu Ser Gly
      415                                420                425

tgg atc tgc ggg gag gag gcc ctc gtc atg gag aag tgt gat gac gag      1529
Trp Ile Cys Gly Glu Glu Ala Leu Val Met Glu Lys Cys Asp Asp Glu
      430                                435                440

gca gtg gcc gag atc tgc acg gag atg ctg cgt cag ttc aca ggg aac      1577
Ala Val Ala Glu Ile Cys Thr Glu Met Leu Arg Gln Phe Thr Gly Asn
      445                                450                455

ccc aac att cca aaa cct cgg cga atc ttg cgc tgc gcc tgg ggc agc      1625
Pro Asn Ile Pro Lys Pro Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser
      460                                465                470

aac cct tac ttc cgc ggc tcc tat tca tac acg cag gtg ggc tcc agc      1673
Asn Pro Tyr Phe Arg Gly Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser
      475                                480                485                490

ggg gcg gat gtg gag aag ctg gcc aag ccc ctg ccg tac acg gag agc      1721
Gly Ala Asp Val Glu Lys Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser
      495                                500                505

tca aag aca gcg ccc atg cag gtg ctg ttt tcc ggt gag gcc acc cac      1769
Ser Lys Thr Ala Pro Met Gln Val Leu Phe Ser Gly Glu Ala Thr His
      510                                515                520

cgc aag tac tat tcc acc acc cac ggt gct ctg ctg tcc ggc cag cgt      1817
Arg Lys Tyr Tyr Ser Thr Thr His Gly Ala Leu Leu Ser Gly Gln Arg
      525                                530                535

gag gct gcc cgc ctc att gag atg tac cga gac ctc ttc cag cag ggg      1865
Glu Ala Ala Arg Leu Ile Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly
      540                                545                550

acc tgagggctgt cctcgctgct gagaagagcc actaactcgt gacctccagc ct      1920
Thr
555

gccccttget gccgtgtgct cctgccttcc tgatcctctg tagaaaggat ttttatcttc      1980
ttagagcta gccgccctga ctgccttcag acctggccct gtagcttttc tttttctcca      2040
ggctgggcgg tgagcagggtg ggccgttgag ttacctctgt gctggatccc gtgccccac      2100
ttgcctaccc tctgtcctgc cttgttattg taagtgcctt caatactttg cattttggga      2160
taataaaaaa ggctccctcc cctgcccctc agcttctctc tggttttctc      2210

```

<210> 149
 <211> 1493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (93)...(845)

```

<400> 149
ctcaagctgg caggtgggtcg ggggagcggc cggagaggag ctgccgggag ttcgtgccct      60
gcaggacatg acaccagtggt catatcacgg cc atg ggg tct cag cat tcc gct      113
                                Met Gly Ser Gln His Ser Ala
                                1                                5

got gct cgc ccc tcc tcc tgc agg cga aag caa gaa gat gac agg gac      161
Ala Ala Arg Pro Ser Ser Cys Arg Arg Lys Gln Glu Asp Asp Arg Asp
      10                                15                20

ggg ttg ctg gct gaa cga gag cag gaa gaa gcc att gct cag ttc cca      209
Gly Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro
      25                                30                35

tat gtg gaa ttc acc ggg aga gat agc atc acc tgt ctc acg tgc cag      257
Tyr Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys Gln
      40                                45                50                55

ggg aca ggc tac att cca aca gag caa gta aat gag ttg gtg gct ttg      305
Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala Leu

```